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APPLICATION OF AMMI MODEL FOR EVAULATION SPRING BARLEY GENOTYPES IN MULTI-ENVIRONMENT TRIALS

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Abstract

The aim of study was to evaluate the yield performance of genotypes and stability, environments and G × E interaction of 12 spring barley genotypes in multi-environment trials. The trials were implemented in respect to a integrate arrangement complex style with four replications. The AMMI (Additive main effects and multiplicative interaction) analysis was made to estimate grain yield and understand G × E interaction patterns. Analysis indicated that the major contributions to treatment sum of squares were environments (81.4%), GE (10.3%) and genotypes (8.3%), respectively; suggesting that grain yield of genotypes was effected environmental conditions. PCA 1 and PCA 2 axes (Principal component) were significant (0.01) and supplied to 68.30% of the complete G × E interaction. The AMMI analysis revealed that E3 and E5 were more stable and high productive; mean while E6 and E7 were unstable and nominal efficient environments. According to stability variance, the genotypes (G1, G3, G6 and G9) were the productive and more stable; meanwhile G4 and G5 were low productive and stable genotypes. Moreover, G2 were the best productive to all environments without E2. The G × E model exposed according to AMMI analysis recommended that G2 shown candidates and registered as Kendal, because of wide adaptability with high performances in all environments.

Introduction

Barley (*Hordeum vulgare* L.) is important for cereal crop of Turkey and accounted for nearly 20% of the total cereal production. Barley has been cultivated for many years and has a significant role in South-Eastern Anatolia. It is also grown mainly on rainfall conditions, but genotype × environment interaction (GEI) restricts the progress in yield improvement under rain fed and unpredictable climatic conditions (Kilic 2014). Therefore, G × E interaction is of major importance, because of provides information about the effect of test environments on genotype performance and plays an important key role for assessment of performance yield stability of the breeding genotype (Mohammadi *et al.* 2013). Increasing genetic gain in yield performance is possible in part from narrowing the adaptation of genotypes and so maximizing yield in particular environments are described by GE interaction (Sabaghnia *et al.* 2012b).

Yield is highly affected by many genetic factors as well as environmental fluctuations, because it is a complicated marker which is dependent on somewhat other markers (Akter *et al.* 2014). The model of AMMI is a complex model including both two way data structure and additive multiplicative components which enabled a breeder to get precise prediction on genotypic potentiality and environmental influences on it. The impact of AMMI method has been clearly showed by different researchers using multi-environment. This method is very effective for studying GEI interaction (Tarakanovas and Ruzgas 2006), provide the correlative size and significant affects of GEI and its interaction (Asfaw *et al.* 2009), display more informative in different genotype response over environments, describing specific and non-specific resistance of

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genotypes, identifying most discriminating environments (Mnukherjee *et al.* 2013), demonstrates the presence of GE interactions, and shows highly significant differences for environment, genotype and their interactions (Rad *et al.* 2013), is important for testing promising lines under across environments to estimate stability and performance (Hagos and Abay 2013), reveals the efficiency performances of genotypes under the different effect of conditions and effects of GE interaction (Kilic 2014) and thus, it is useful for breeders and supporting breeding program decisions.

The major objective of study reveal adaptation of barley genotypes using AMMI analysis to estimate the importance of GE interaction on yield, define mega-environments, identity the best acting genotype for every mega-environment and debate the containment of the GE interaction to barley breeding.

Materials and Methods

The experimental material comprising of 12 barley genotypes (Ten new promising lines and two cultivars (Sahin 91-regional and Vamıkhoca 98-national check) were used (Table 1).

Table 1. The information's about varieties, used in experiment.

Code	Pedigree of line and cultivar name	Origin	IPCAg [1]	IPCAg [2]
01	CARDO/QUIB./3/ROB.//GLORIA-BAR/COPAL . C B S S 96 W M 0 0 2 7 3 T-C-1 M- 1Y- 2M- 0Y	ICARDA	–119.521	158.962
02	LENT/BLLU//PINON -CBSS97M00698T-C-2M-1Y-0M	"	–112.673	881.421
03	CAB./4/GLOR./COPAL//BEN.4D/3/S.PB/5 /ABETO/ /GLORIA-BAR/CBSS97Y00819T-D-2Y-1M-0Y	"	803.197	490.963
04	WI2269/Espe/3/WI2291/Bgs//Hml-02 ICB97-0152-0AP-13AP-0AP	"	338.692	–542.972
05	ŞAHİN-91(Local Check)	GAPIARTC	576.233	–468.294
06	Kv/ /Alger /Ceres.362- 1-1/3/ WI2 269/4 /Sara I C B 9 3-0727- F7SSD- 92AP -0AP	ICARDA	133.104	160.698
07	Mo .B1337 / WI2291 / / Mo. B1337 / WI2291 I C B 9 2-0045- 0AP- 20AP- 0AP- 0AP	"	–680.955	–474.860
08	77s- 409/ Akrash-01 I C B 94-814- 0AP- 7AP- 0AP- 0AP	"	–884.913	–0.15904
09	Kv/ /Alger/ Ceres 362-1-1/ 3 /WI2269/6/ Zanbaka /5 / I C B 9 4- 629-0AP- 7AP- 0AP- 0AP	"	–377.964	0.37109
10	VAMIKHOCA-98(National check)	AARI	170.038	–314.086
11	PATTY/ 3 /WEEAH 11/ / WI 2291/ BGS S E A 92-3396- 3S-0S- 7S-0	"	–159.308	297.823
12	PATTY / 3/ WEEAH 11 // WI 2291 / BGS SEA 92- 3396- 2S- 0S- 15S- 0	ICARDA	314.070	–210.861

ICARDA: International Center for Agricultural Research in the Dry Areas. GAPIARTC: GAP International Agricultural Research and Training Center. AARI: Aegean Agricultural Research Institute

The barley multi-environmental trials were conducted at seven test environment and different years (Table 2).

Test environments shown different growing season and the conditions regions characterized by differences in climatic conditions. The location of Suruc was chosen as a very drought location and Adiyaman for heat stress. Also there were different climatic conditions among years. The trial carried out in a randomized block design with four replications and 450 seeds were used for m^{-2}. Plot magnitude was 7.2 m^{-2} (1.2 × 6 m) occurring in 6 rows spaced with 20 cm separate. Sowing was done by Wintersteiger drill. The fertilization rates for all plots were used 60 kg N/ha and 60 kg P/ha with sowing time and 60 kg N/ha was applied to plots at the early stem elongation. Harvest was done using Hege 140 harvester up on 6 m^2.

Table 2. Years, the status of environment and long term of precipitation.

Years	Sites	Code of sites	Altitude (m)	Latitude	Longitude	Annual rainfall (mm)
2007-08	Adiyaman	E1	685	37° 46' N	38^0 17' E	554
2008-09	Adiyaman	E2	685	$37^0$46' N	38^0 17' E	654
2008-09	Diyarbakir	E3	499	36^0 97' N	38° 42' E	429
2009-10	Adiyaman	E4	685	37^0 46’ N	38^0 17' E	560
2009-10	Diyarbakir	E5	496	36^0 97' N	38° 42' E	518
2009-10	Suruc	E6	496	$36^0$95' N	38^0 41' E	245
2009-10	Hilvan	E7	593	37^0 35' N	38° 59' E	580

The data on grain yields of 12 genotypes in seven environments were evaluated by AMMI analysis (Gauch 1988). All statistical analyses were performed using Gen Stat Release 14.1 (Copyright 2011, VSN International Ltd.).

Results and Discussion

The variance of AMMI analysis showed that as 0.01, all factors had significant effect on barley grain yield of 12 genotypes tested in seven environments and total sum of squares explained 81.4% for environmental effects, only 8.4% for genotypic effects and 10.3% GEI effects (Table 3).

Table 3. The variance of AMMI analysis on grain yield of barley.

Resource of variance	df	SS	MS	F value	G+E+GE SS explained (%)	GE SS explained (%)
Total	335	6835576	20405			
Treatments	83	6027159	72616	27.38**		
Genotypes	11	503127	45739	17.24**	8.35	
Environments	6	4903951	817325	87.70**	81.4	
Block	21	195716	9320	3.51**	10.3	
Interactions	66	620082	9395	3.54**		
IPCA1	16	287112	17944	6.77**		63.3
IPCA2	14	166806	11915	4.49**		36.7
Residuals	36	166165	4616	1.74		
Error	231	612700	2652			

df - degrees of freedom; SS - sum of squares; MS - mean square. **, 0.01; G - genotypes; E - environments.

The high addition of environment effects showed that there were important differences among environments for grain yield. On the other hand, the GEI effect was higher than G effect.

Farshadfar and Sutka (2006) reported that the same source E G and GEI explained 86.0, 2.0 and 12.0%. Bantayehu (2013) reported 75.24, 9.32 and 15.44%, Rezene (2014), reported 89.6, 1.8 and 8.6% respectively. Yan and Rajcanw (2002), reported the environment effect had the highest effect than other factors on soybean yield. The results of environment, genotype and GEI effects obtained from this study illustrated similar results of the studies described above and the effect of environment > G × E > genotype. According to Stanisavlievic *et al.* (2013), E explained 50 - 84% of treatment variation, G accounted for 5.3 - 13.6%, while GE explained 6.7 - 36.3 of treatment variation.

The existence of G × E interaction displayed by AMMI model, especially when the interaction divided between two interaction principal component axis (IPCA) (Table 3).The obtained data from confirmed adequacy to the AMMI model (Gauch and Zobel 1996,Yan and Hunt 2001).This status of AMMI made it establish and the biplot calculate effects of genotype and environment. The results of mean square of the PCA1 and PCA2 interaction axis showed that there is significant (0.01). Results of AMMI analysis also indicated that the PCA1 axis accounted 51.0%, and the second accounted for 17.3%. The total of IPCA1 and IPCA2 accounted for 68.3% (Fig. 1). The first IPCA principal component axis explained 63.3% and IPCA2 33.7% (Table 3). AMMI model showed existence interactions of GEI, so it was portioned between first and second IPCA (Interaction principal component axes). The barley grain yield variation is depending on genotypic and environment factors as shown Tables 1 and 2. Gauch and Zobel (1996), suggested that the AMMI model is the most accurate one, because it can predict using the first two IPCAs. The closer the IPCAs scores to zero mean that genotypes are the most stable across their environments. Actually, these biplots is removed two types, model of AMMI 1 and model of AMMI 2 (Carbonell *et al.* 2004). In AMMI 1, the genotype and environments means are plotted on coordinate, the IPCA scores of same genotypes and environments, which are on the ordinate. For interpretation of AMMI, size and signal scores of the IPCA1were observed, score near to zero was typical of genotypes and environments, which contribute little to the interaction i.e., they are stable (Tarakanovas and Ruzgas 2006).

The model of AMMI 1

In the AMMI model 1, x-axis represents the genotypes and environment main effect and y-axis represents the effects of interaction (Fig. 1). The environment and genotypes indicated much more variability in both main effect and interaction. According to AMMI 1, E2, E3, E5 and G1, G2, G3, G6, G9, G7 showed good performance, because of they took place above on axis (mean yield). It is believed that these genotypes and environments were high yielding. On the other hand, E1, E4, E7, E6 and G4, G5, G8, G10, G11, G12 demonstrated low performance, due to they located under on axis (mean yield).

These genotype and environments, which located under on axis (mean yield) were low yielding. Moreover, E3 and E5 were both high potential environments, G1, G6, G9 were broad adaptability for most of test environments. Also G2 and G3 could be recommended for most test environments with high potential and IPCA values (Table 1), while G4 and G5 were unstable. According to Mirosavlievic *et al.* (2014), the genotypes have small IPCA1 values are more stable, Becker and Leon (1988), the basic static concept of stability shows minimal variance of stable genotype across different environments. Genotype with a constant high yield referred to as dynamic stability concept is preferred option in commercial plant breeding (Flores *et al.* 1998). G7 and E2 were high mean yield, but they had low IPCA 1 values. Similar outputs were recorded in barley by (Mohhamadi *et al.* 2013).

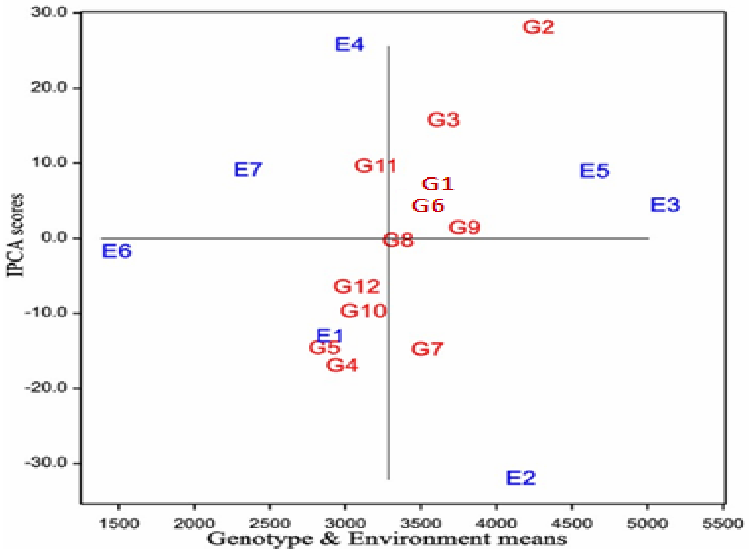

Fig.1. The AMMI 1model showing grain yield (kg/ha) of 12 barley genotypes (G) in 7 environments (E).

The Model of AMMI 2

The AMMI 2 biplot provides good explanation of the pattern, regarding first two IPCs (Fig. 2).

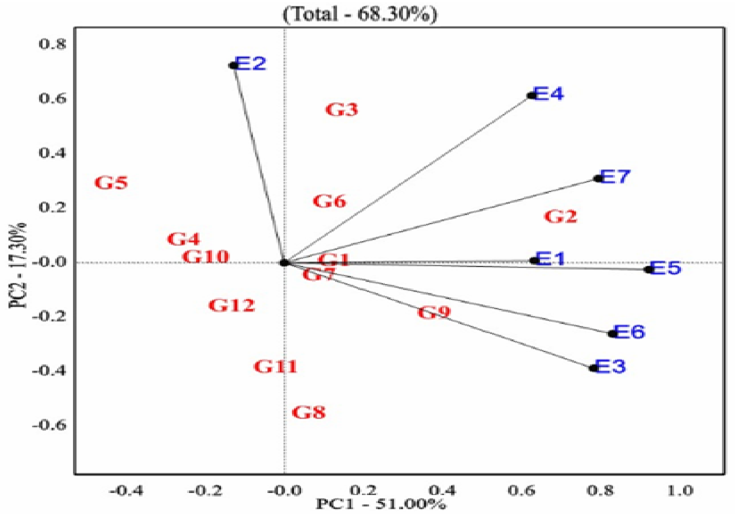

Fig. 1. The AMMI 2 biplot showing interaction genotypes (G) and environments (E).

This model including in first two interactions axis of genotype and environment scores (Vargas and Crossa 2000, Sayar and Han 2015). The AMMI-axes can establish of the GE interaction, in terms of differential sensitivities of the genotypes to the most discriminating environmental variables. Also, AMMI 2 clearly demonstrates "which - won where" pattern and also reveals the sensitivity degree of genotypes to environment (Li *et al.* 2006.Purchase (1997) explained that the genotypes, which are positioned to the center of the biplot, they are more stable than other which are far from center of biplot. Genotypes (G1, G2, G7 and G9) indicated low IPC scores with relatively moderate mean yield and are project static concept of yield stability. Moreover, these genotypes could be recommended for the most test environments with broad adaptability. The biplot also occurred four sectors, which is called mega-environments including; all environment except E2 with wining genotype G1, G2, G6, G7 and G9; E2 with wining G3. On the other hand, G4, G5, G8, G10, G11 and G12 could not associate with any environment (Fig. 2). The results of Islam *et al.* (2014) indicated that interact is positively, when genotypes and environments took place in same sectors. Whereas, interaction is negative, when they took place in against sectors. If they fall into contiguous sector, interaction is somewhat more complex. On the other hand, according to Akter *et al.* (2014), the genotypes are close to each other on the plot, they are looking nearly productive in across environments, while genotypes are away from each other they show different response over the environments. The polygon view of AMMI 2 described genotypes "which-wins-where" models on grain yield in multi-environmental trial data analysis (Figs 3 and 4). The figure divided on two-mega environment with four sectors, which are apart from center to out axis of biplot graph. The G2 took place vertex polygon of sector 1 and show favorable to all environments, except E2. Also the G9 was sufficient for E3 and E6, G1 and G7 for E1 and E5, while G3 and G6 for E2 (Sector 2). The G4, G5, G10 and G12 were located in sector 3 and did not associate with any test environment, like G8, G11and G12, which located in sector 4. On the other hand, G5 and some other genotypes, which were not located in same sector with any test environment, were unfavorable for test environments. According to Sabaghnia *et al.* (2010), the polygon view model are mostly validated from the original data, but, not totally. Nevertheless, Gauch (1988), demonstrated that the outcome of this model is suitable and widely to recommendation purposes. Compared with conventional methods, the AMMI model has some advantages (Gauch *et al.* 2008).

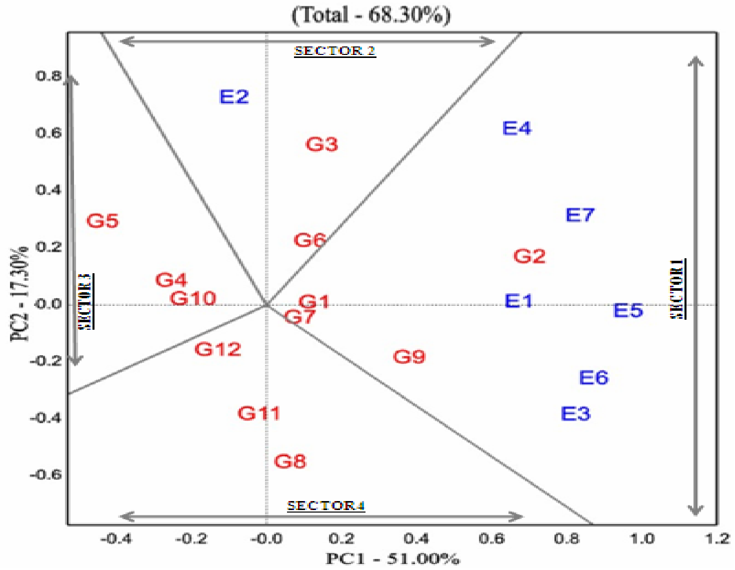

Fig. 3. The biplot showing "which-won-where" and sectors of 12 barley genotypes (G).

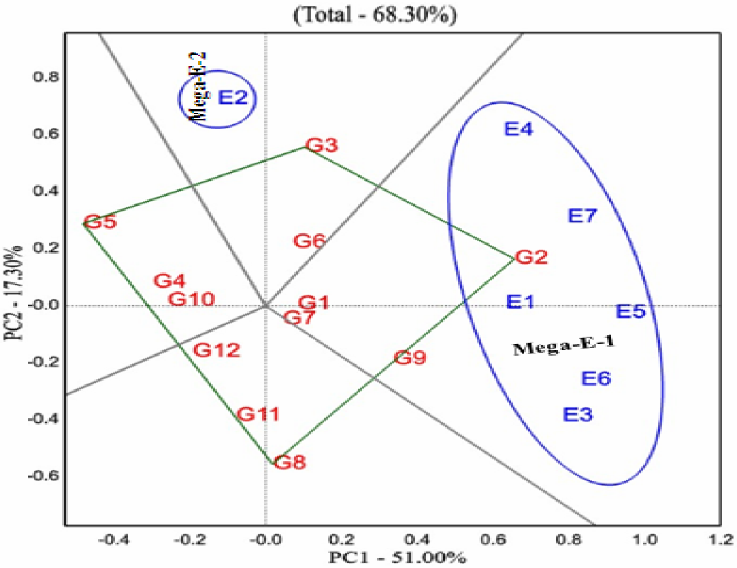

Fig. 4. The Biplot showing mega-environments and the representative of genotypes.

The fact that the different stability methods are used, the AMMI analysis supply more useful information for acquiring certain results and the identity of mega-environments and wining genotypes are inevitable. Moreover, this analysis makes possible developed comprehension of GEI by using the first two principal component axes. The biplot showed that the genotype G2 was the best suitable in large environments, while G3 and G9 were the best available for specific environments. Also, G1 showed more stable for all environments, although it was average yielding for large environment. The results of this study, displayed that genotype (G2) could be candidate for studied environments. Finally, it was registered as Kendal cultivar for spring conditions of Turkey.

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