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AMMI analysis of yield performance in canola (*Brassica napus* L.) across different environments

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Abstract

In order to explore the effect of genotype, environment and genotype × environment interaction (GEI) on grain yield of 15 canola genotypes in four different environments, an experiment was conducted in a randomized complete block design with 3 replications during 2013-2014 growing seasons. Combined analysis of variance exhibited that grain yield was significantly ($p<0.01$) affected by environments (E), genotypes (G) and genotype × environment interaction (GEI) indicating the presence of genetic variation and possible selection of stable entries. AMMI analysis revealed that the first and second interaction principal component (IPCA1 and IPC2) explained 65.11% and 19.64% of the G×E variation, respectively. According to AMMI1 biplot, G2, G3, G4, G5, G7, G8, G11, G12, G13, G15, and G14 with grain yield less than mean indicated specific adaptation for E1 and G1, G6 and G10 for E1, E2 and E3. Distribution of genotypes in the AMMI II biplot displayed that genotypes, G2, G5, G13 and G15 scattered close to the origin, indicating minimum G×E interaction and hence stability. The remaining 11 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental fluctuations.

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Introduction

Rapeseed (*Brassica napus* L.) is now the second most important source of vegetable oil in the world and canola oil is considered healthy for human nutrition due to its lowest content of saturated fatty acids among vegetable oils and moderate content of poly-unsaturated fatty acids (Starner *et al.*, 2002).

Climate changes may result in strong impacts on agriculture, especially on crop growth and yield. Crops are largely determined by climate conditions during growing season; thus, even minor deviations from optimal conditions can seriously threaten yield. Therefore, knowledge on the effect of environmental factors on crop growth and development could reduce the possibilities of significant yield loss and improve the selection of specific cultivars for growing in the target regions (Marjanović-Jeromela *et al.*, 2011).

The genotype × environment interaction (G × E) is the response of each genotype to variations in the environment. It has been one of the principal subjects of study in breeding, allowing the generation of different methodologies for genetic improvement. It has also been a constant worry for breeders, especially when the magnitude of G × E is large, since this impedes the selection and recommendation of stable genotypes, as well as slowing selection advancement (Meziani *et al.,* 2011). G × E has a negative impact on heritability. The lower the heritability of a trait, the greater the difficulty in improving that trait via selection, therefore GE interaction is perquisite to evaluate rapeseed behavior during different environments to find out cultivars with general or specific adaptation or stability before release or any recommendation (Mortazavian and Azizinia, 2014)

The detection of GEI in trials has led to the development of procedures that are generically called stability analyses. The numerous stability statistics available to the plant breeder and to the production agronomist provide different strategies and approaches of dealing with GEI. Stability is an important concept for plant breeders interested in analyzing GEI data (Farshadfar *et al.*, 2012).

Several statistical methods have been developed to characterize and minimize the effect of the G × E interaction in selected varieties and to predict phenotypic responses to environmental changes. However, most statistical stability methods are not able to provide an accurate and complete variety response pattern for this interaction (Oliveira *et al.*, 2014), especially because the genotype response to environmental variation is multivariate and most stability indices have a univariate response (Crossa *et al.*, 1990; Oliveira *et al.*, 2014).

Analysis of variance (ANOVA) is merely an additive model in which the G × E interaction is a source of variation, but its intrinsic effects are not analyzed. In contrast, principal component analysis (PCA) is a multiplicative model and, therefore, does not present additive main effects for the environment nor genotype. However, the newly developed AMMI analysis includes ANOVA and PCA in a unified approach that can be used to analyze multiple yield trials (Zobel *et al.*, 1988; Kang and Gauch, 1996; Oliveira *et al.*, 2014). AMMI uses ANOVA to test the main effects of genotypes and environments, and PCA to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G × E interaction, with a minimum number of degrees of freedom. Because ANOVA and PCA are part of the AMMI model, this model is likely more suitable for characterizing the G × E interaction (Zobel *et al.*, 1988).

In addition, AMMI simultaneously quantifies the contribution of each genotype and environment to the SSG×E, and provides an easy graphical interpretation of the results by the biplot technique to simultaneously classify genotypes and environments (Kempton, 1984; Zobel *et al.*, 1988). Therefore, with this technique, one can readily identify productive cultivars with wide adaptability or mega-environments, as well as delimit the agronomic

zoning of cultivars with specific adaptability and identify environments in which to conduct tests (Kempton, 1984; Gauch and Zobel, 1996).

The present investigation was carried out to quantify GE interaction effects on yield and to determine stable entries within the genotypic pool used in this study.

Materials and methods

Plant materials

This experiment was carried out in four different locations of Kermanshah, Iran during 2013-2014 growing season. A set of 15 canola genotypes selected from advanced experiments of research stations were used as experimental material (Table 1). Experimental layout was a randomized complete block design with 3 replications in each location. Each plot consisted of 4 rows of 6 meter length. Data on seed yield were taken from the middle two rows of each plot. At harvest seed yield was determined for each genotype at each test environments.

Table 1. Genotype code and name of 15 canola genotypes.

No.	Code	Name
1	G1	GK Helena
2	G2	GK olivia
3	G3	Antol
4	G4	GKH1103
5	G5	Billy
6	G6	Liliane
7	G7	GKH 305
8	G8	Lioness
9	G9	Modena
10	G10	Okapi
11	G11	Opera
12	G12	Slm046
13	G13	Talaye
14	G14	Zarfam
15	G15	Oase

Statistical analysis

Analysis of variance was done for obtained data to determine the effects of genotype, environment and genotype × environment interaction using the SAS 9.1 software.

AMMI analysis

The grain yield data were subjected to combined analysis of variance and AMMI analysis which is a combination of analysis of variance and principal component analysis. Briefly, analysis of variance is used to partition variance into three components: genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, multiplication effect analysis is used to partition GE deviations into different interaction principal component axes (IPCA), which can be tested for statistical significance through ANOVA. The IRRISTAT software was used for combined analysis of variance and AMMI analysis.

Results and discussion

Combined analysis of variance

Combined analysis of variance exhibited significant differences among environments (E), genotypes (G) and G×E interaction (Table 2) indicating the presence of genetic diversity and possible detection of phenotypic stability in genotypes. The first and second interaction principal component analysis (IPCA1 and IPC2) explained 65.11% and 19.64% of the G×E variation, respectively.

AMMI model and pattern analysis

In AMMI model, principal component analysis is based on the matrix of deviation from additivity or residual, while pattern analysis employs both classification and ordination techniques. In this respect both the results of AMMI analysis, the genotype and environment will be grouped based on their similar responses (Gauch Jr, 1992; Pourdad and Mohammadi, 2008; Rashidi *et al.*, 2013).

GEI was further partitioned by principal component analysis (Table 2). Ordination technique using an approximate F-statistic (Gollob, 1968) revealed high significant differences for IPC1, IPC2 and IPC3. The Gollob's test most often retains the multiplicative axis terms of little practical relevance that is, axis with a low proportion of explained GE variation. In this

study, the first three multiplicative axis terms were significant.

Table 2. AMMI analysis of grain yield of 15 canola genotypes in four environments.

Source	df	SS	MS	F	F prob
Treatments	59	133226375	2258074	60.03	0.000
Genotypes	14	37522360	2680169	71.25	0.000
Environments	3	34201261	11400420	261.24	0.000
Block	8	349121	43640	1.16	0.3297
Interactions	42	61502753	1464351	38.93	0.000
IPCA	16	41944656	2621541	69.69	0.000
IPCA	14	18530384	1323599	35.19	0.000
IPCA	12	1027713	85643	2.28	0.01259
Residuals	0	0			
Error	112	4213127	37617		
Total	179	137788623	769769		

Biplot analysis

To have a better discussion on the biplots resulted from the AMMI analysis we must consider the following points (Kempton, 1984): (I) The center of biplot shows the mean of a genotype or an environment. (II) A long distance of a genotype (or an environment) from the center of biplot indicates a large interaction with that genotype (or environment). (III) The long length of a genotype on the environmental vector reveals more deviation from the mean and vice versa. (IV) The angle between the vectors of a genotype and an environments shows that the interaction is positive or negative.

Identifying high yielding stable genotypes

To investigate the main effects and interactions, AMMI1 biplot was constructed for yield. In Fig. 1, AMMI1 biplot of additive main effects or mean yield are shown along the abscissa and the ordinate represents the first IPCA or multiplicative interaction. The interpretation of a biplot assay is that if main effects have IPCA score close to zero, it indicates negligible interaction effects and when a genotype and an environment have the same sign on the IPCA axis, their interaction is positive; if different, their interaction is negative.

Biplot space of Fig. 1 is divided into 4 sections from low yielding environments in sections 1 (up left) and 4 (low left) to high yielding environments in sections 2 (up right) and 3 (low right). It is clear from the biplot of Fig. 1 that the points for environment are more scattered than the point for genotypes indicating that variability due to environments is higher than that due to genotypes difference which is in complete agreement of ANOVA (Table 2). On the bioplot, the points for the generally adapted genotypes would be at right hand side of grand mean levels (this suggests high mean performance) and close to the line showing IPCA= 0 and (this suggests negligible or no G × E Interaction).

According to the AMMI model, the genotypes which are characterized by means greater than grand mean and the IPCA score nearly zero are considered as generally adaptable to all environment. However, the genotype with high mean performance and with large value of IPCA score are consider as having specific adaptability to the environments.

According to Fig. 1, G2, G3, G4, G5, G7, G8, G11, G12, G13, G15, and G14 with grain yield less than mean revealed specific adaptation for E1 and G1, G6 and G10 with grain yield less than mean are unstable genotypes that revealed specific adaptation for E1, E2 and E3. No genotype was specific adaptation for E2.

AMMI 2 biplot

The IPCA1 versus IPCA2 biplot (i.e. AMMI2 biplot) (Fig. 2) explains the magnitude of interaction of each genotype and environment. The genotypes and environments that are farthest from the origin being more responsive fit the worst. Genotypes and environments that fall into the same sector interact

positively; negatively if they fall into opposite sectors. A genotype showing high positive interaction in an environment obviously has the ability to exploit the agro-ecological or agro-management conditions of the specific environment and is therefore best suited to that environment. AMMI analysis permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific environmental conditions.

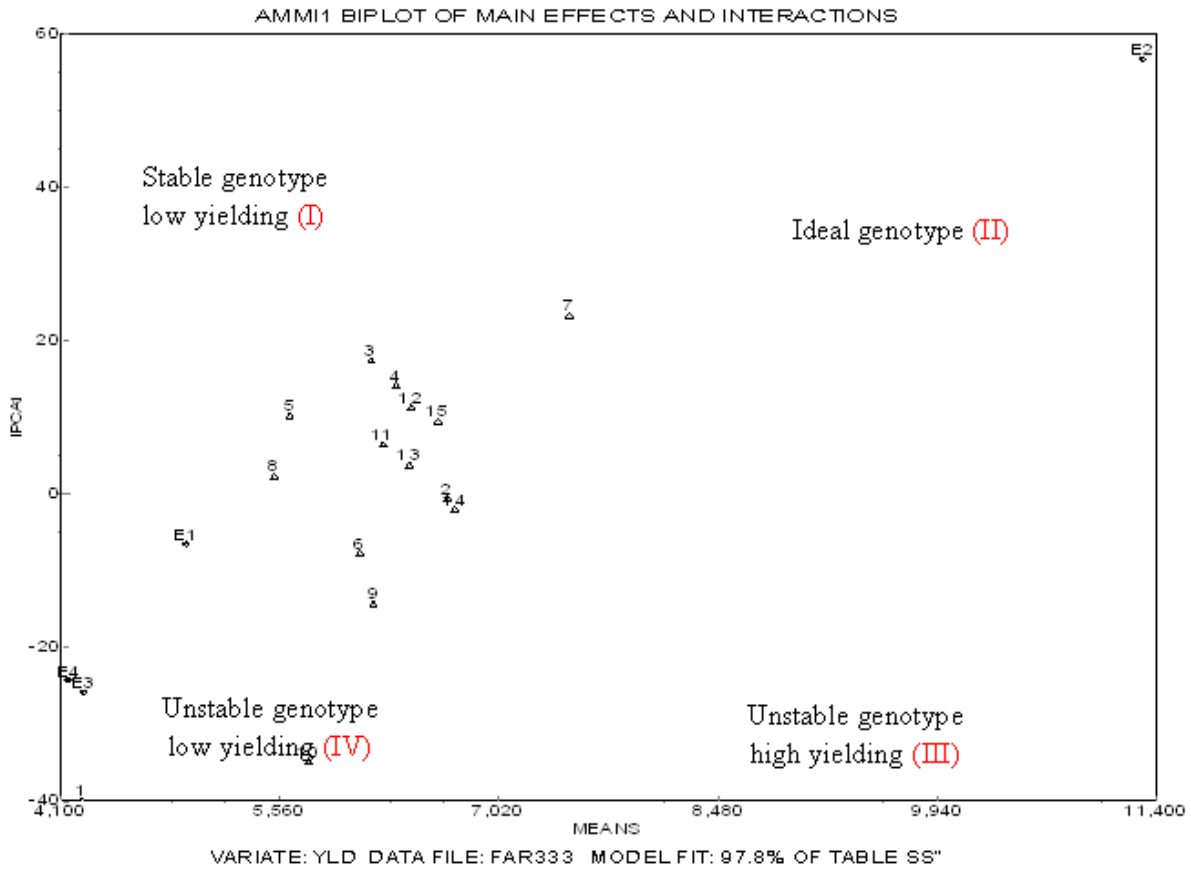

Fig. 1. Biplot of the first interaction principal component axis (IPCA1) versus mean yields.

Fig. 2 gives the AMMI2 biplot for yield. The IPCA1 and IPCA2 components accounted for 96.1% of G×E interaction. Distribution of genotype points in the AMMI II biplot revealed that the genotypes, G2, G5, G13 and G15 scattered close to the origin, indicating minimum interaction of these genotypes with environments. The remaining 11 genotypes scattered away from the origin in the biplot indicating that the genotypes were more sensitive to environmental fluctuations. Interaction of genotypes with specific environmental conditions was judged by projection of genotype points on to environment spokes. On this basis, the genotypes G6, G9, G10 and G14 had positive interaction with environments E4, hence exhibited specific adaptation with irrigated environments. G8 and G11 displayed positive interaction with irrigated environment E1 and E3. Genotypes G3, G4, G12 and G7 indicated specific adaptability and positive interaction with environments E2.

In Fig. 2 genotypes and environments are depicted as points on a plane. The position of the point for genotype i is given by the estimates for the genotypic scores, similarly, the point coordinates for environment j originate from the estimates for the environmental scores. Distances from the origin (0,0) are indicative of the amount of interaction that was exhibited by either genotypes over environments or environments over genotypes (Rashidi *et al.,* 2013).

For example, the genotypes G10 and G7 and environment E2 displayed a highly interactive behavior, whereas the environment E1 exhibited low interaction. In a vector representation, the genotype and environment points determine lines starting at the origin (0,0). The interaction effect of genotype i in environment j is approximated by projecting the genotype point onto the line determined by the environmental vector, where distance from the origin provides information about the magnitude of the interaction. The angle between the vectors of genotype i and environment j tells us something about its nature: the interaction is positive for acute angles, negligible for right angles, and negative for obtuse angles. Genotypes G2, G6, G9 and G14 showed acute angle with the vectors of E4 and obtuse angles with the vectors of environments E1, E2 and E3. Genotypes G3, G4, G5 and G15 exhibited acute angle with environment E2, while obtuse angle with environments E4, E3 and E1. The accessions G8, G11, G12 and G13 revealed acute angle and positive interactions with vectors E1, E2 and E3.

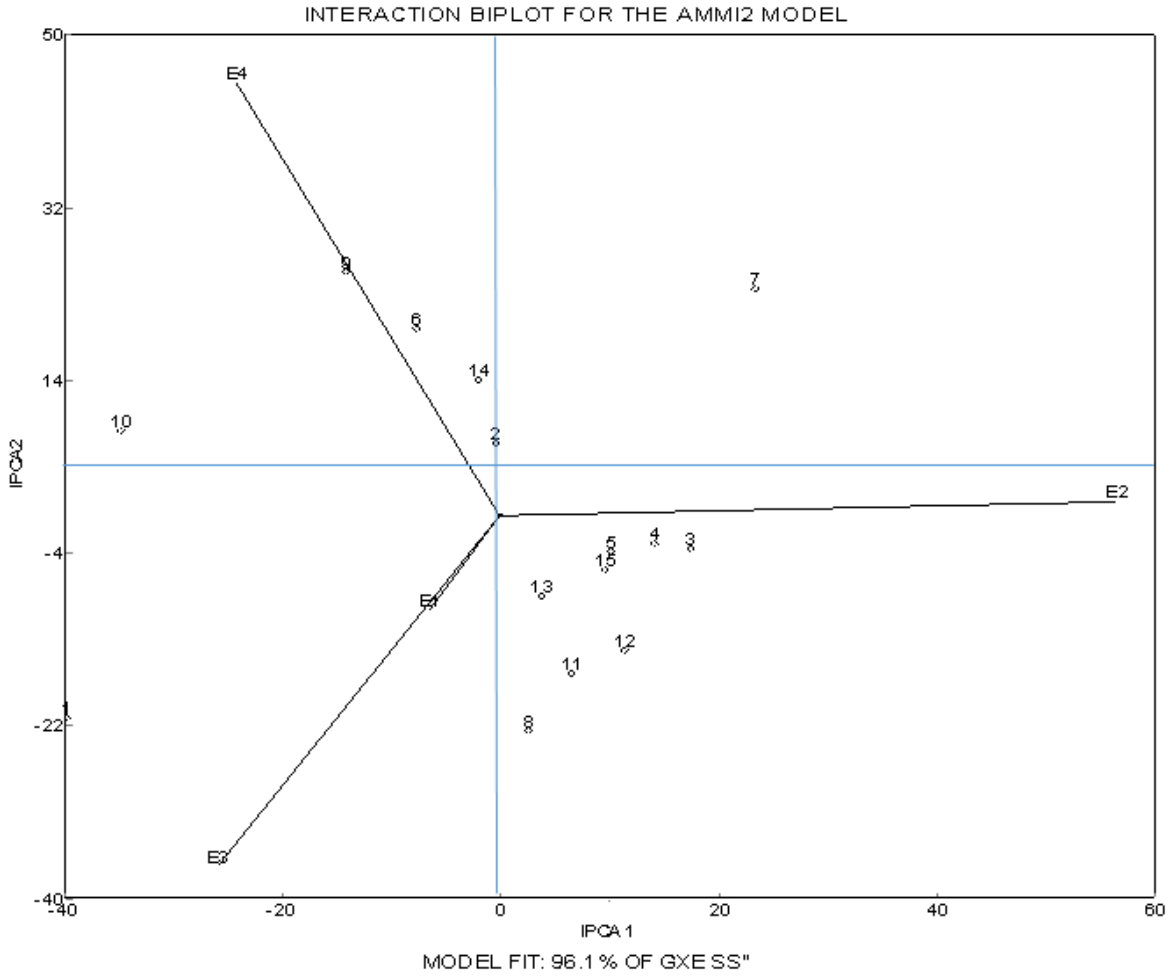

Fig. 2. Biplot of the first interaction principal component axis (IPCA1) versus the second interaction principal component axis (IPCA2) for canola genotypes.

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