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An Investigation of Common and Specific Adaptability in Canola Cultivars Using Additive Main Effect and Multiplicative Interaction

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Abstract: Canola is one of the most important oily crops in Iran. To evaluate common and specific compatibility of canola cultivars, 10 cultivars were evaluated in a Randomized Complete Block (RCB) designs with three replications. The experiment was carried out in four locations contains Karaj, Birjand, Kashmar and Shiraz in 2009 - 2010. The studied cultivars were including Modena, Okapi, Hoyla401, Licord, Opera, Zarfam, RGS003, SLM046, Sarigol and Hoyla308. The data were analyzed by AMMI method. Genotype, environment and genotype × environment interaction were significant. In this method the first interaction principal component was significant. Licord genotype had the most amount of mean yield but had the least first interaction principal component, which was distinguished as stable genotype. The first two interaction principal components explain 95% of the data variances. Modena and Zarfam genotypes in four environments had the most stability level. Also, Licord and Hoyla308 genotypes in Karaj, Okapi in Kashmar, Hoyla401 and RGS003 genotypes in Birjand and Sarigol genotype in Shiraz had the most specific adaptability.

Key words: Canola, AMMI, Common and Specific Adaptability, Yield.

INTRODUCTION

From the economical point of view, canola is the fifth important crops after Rice, Wheat, corn and Cotton (Cardoza and Stewart, 2003). Iran is one of the biggest importers of oil crops. Canola producing may decrease to some extent Iran's dependency to import the oil. The additive main effects and multiplicative interaction method (AMMI) is a combine analysis of analysis of variance and principal component analysis. In this method genotypes main effect and environment effect is evaluated which is known as additive main effects or increasing effects. Afterward by principle component analysis, genotype environment interaction was analyzed which is known as multiplicative effect (Gauch, 1992). Kempton is the first person who used the AMMI model for analyzing yield data practicality (Kempton 1984). Usefulness of AMMI model is for that, this model justifies some extent of sum of squares, affecting genotype and environment interaction. Thus, this cause increasing the model predictions accuracy level and statistical usefulness (because of increasing noise and increasing degree of freedom) (Gauch, 1992). Another usefulness of the model is dividing the environments to mega-environments (Gauch and Zobel, 1997). AMMI formula is as below: (Gauch,1992).

$$X_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + l_{ge} + \varepsilon_{ger}$$

In this formula x_{ger} is yield of g'th genotype in e'th environment and r'th replication. μ is the mean of whole experiment. α_g and β_e are main genotype effect an environment effect respectively. λ_n is eigen value of principle component axis of n. γ_{gn} is eigen vector for genotype for n axis, δ_{en} is special environment vector for n axis, l_{ge} amount of noise and ε_{er} is related to error.

First part of AMMI model, means additive part, uses usual analysis of variance. Whole mean is determine by ($\bar{X}_{..}$) genotype effect (α_g) is determine as genotype deviation of mean ($\bar{X}_{.j} - \bar{X}_{..}$) and environmental effect (β_E) is determine as environmental effect ($\bar{X}_{.j} - \bar{X}_{..}$) (Gauch, 1992). Second section is AMMI model's multiplicative part, which uses principle component analysis method for genotype environment interaction. But one should consider that in AMMI method, calculation is done on affects genotype and environment interaction amount $(Zinj = X_{ij} - \bar{X}_{\dot{\imath}0} - \bar{X}_{.J} + \bar{X}_{..}$ but in principle component calculation is done on difference main data from whole mean ($X_{ij} - \bar{X}_{..}$) (Gauch,1990).

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Environments portion in whole variance is more than genotype environment interaction, and genotype environment interaction portion is more than genotype portion (Motzo *et al*., 1962).

Annicchiarico in comparison of linear regression model and AMMI in interpreting affect interaction of 3 experiments data on durum wheat, 2 experiments data on corn and an experiment on bread wheat and oat, found out that AMMI's more ability is not limited to special plant, rather this method has more efficiency in a condition that environment restrictions has more effect on genotype reaction (Annicchiarico, 1997).

The aim of this study was to evaluate genotype effect and genotype environment interaction and to determine location's value for yield in ten canola cultivars. Results of this study may simplified apprehension about genotype and genotype environment interaction in canola and also can help to choose appropriate lines for each region.

MATERIALS AND METHODS

To evaluate genotype effect and genotype environment interaction in canola, 10 cultivars in a randomized complete block design (RCBD) with 3 replications were evaluated for grain yield in four regions, Karaj, Birjand, Kashmar and Shiraz in 2009 - 2010. Climate features in this four location is showed in table 1. Usual tillage activities such as: Ploughs, disk, leveling the ground and so on were done regularly and after tillage activities, farming the seeds was done manually. Each plot was included four rows with the length of two meters with 50 centimeters distance to one another. A plant distance on row was choosing to be in 50 centimeters. Irrigation was done regularly and weeding was done each week obsessively. SAS and GGE biplot software's were used for analyzing the data.

Table 1: Geographical and weather information of four farmed regions.

Trial	Karaj (KRJ)	Kashmar (KAM)	Birjand (BIR)	Shiraz (SHZ)
Latitude	35°49´ E	35°24´E	32°89´E	29°61´E
Longitude	51° N	58°46 N	59°24 N	52°53 N
Elevation (m)	1360	1065	1503	1531

RESULTS AND DISCUSSION

In this study AMMI analysis, ranked the genotypes base stability and interaction effect with studied environment. AMMI analysis could be useful to genotype screening for plant breeders. This method justifies carefully the affect interaction and shows to compatible genotype to each region graphically. Furthermore in this method by calculating noise sum of squares, genotype effect and environment interaction and also by calculating the rest sum of squares root can be evaluate the appropriateness of model. Finally, AMMI model is a good method for revealing the hidden information in data and cause increasing our understanding to the amount and nature of affect genotype and environment interaction. If both main effects and interacting effect is important for us, AMMI model can be the first choice for analyzing data (Mandel, 1971). AMMI method is evaluated with three main goals: 1- This method is a diagnostic model and has more usefulness compared with the other methods in statistical analysis, it has comparable yield experiments, because it provides appropriate tools for distinguishing the other lateral which are useful for data analyzing. 2-this model is used to illustrate the nature of affect interaction. 3- This method is uses for improving the accuracy of yield estimate, in a way that using this method is as increasing the replication from 2 to 5 (Crossa, 1990). AMMI analysis was done according to suggested method of Gauch. In this method, first principal affects genotype and environment is calculated and then remaining of the model is uses as affect genotype × environment interaction, according to principal component analysis method is extracted and calculates (Gauch, 1988; laxmi and Gupta, 2000).

In a research, nine wheat genotypes in fifty environments and in another experiment eight wheat genotypes in forty-four environments was studied by AMMI model and joint regression. It was illustrated that AMMI analysis in evaluation of affect genotype and environment interaction is more effective and more efficient than regression model (Acciaresi and Chidichimo, 1999).

In another experiment, two researchers used the evaluation of yield comparison of thirty-six pea cultivars that were planted in four areas during three years for grouping the genotypes and environments and used AMMI method to determine cultivars compatibility degree. Obtained results indicated the existence of more affect genotype and environment interaction which this problematized the yield estimate accuracy and also determining compatible genotypes with areas. AMMI analysis shows that 30, 24, 36 genotypes respectively have the most, the average and the least yield among compatible genotypes. In addition AMMI grouping divided genotypes in to five sets, and environments in to two groups. Thus, Ethiopia, from the view of eco-agriculture conditions is divided into eighteen main region and forty-nine sub-region, which this is necessary in varieties allocation into variant environments, and finally this cultivars are appropriate and compatible with subtropical to cold-humid mountainous regions. (Tay and Bejiga, 2000).

Nachit *et al.* in yield stability analysis of 21 durum wheat genotypes used AMMI model in 22 sub-humid Mediterranean areas. By using AMMI model 5 axis of principal component, significant affect interaction was achieved (Nachit *et al*., 1992).

Seed yield's variance analysis results based on AMMI method is showed in table 2. Genotype × environment interaction effect is signified in %1 probability level, which shows genotypes in different environment have different function. Genotype × environment interactions allocate 1.68 from whole sum of squares. Although, interaction effect, is not the main source of variables, but it is approximately 10 times more than genotype effect. This shows the importance of interaction effects. Environment effect is signified in 1% probability too. Also, amount genotypes there were significant differences. For analyzing genotype × environment interaction effect using AMMI model, analysis was done to principal component on remaining matrix that principal component was significant in 1% probability. This component (IPC1) allocates 1.41 of sum of squares interaction effect. The other components were mixed to noise and 25% sum of squares justified interaction effect and furthermore for evaluating cultivars stability, we used stability value which shows genotype yield, environments, the first and the second interaction effect for lines and environments. Results showed in table 2. If a genotype and an environment from the first and second principal components be same sign, they include positive interaction effect and if from this component don't be same sign, they included negative interaction effect. Those genotypes which have less amount of yield but have positive amount for interactions first principle is appropriate for farming in poor areas. By the way, they included positive interaction effect in poor areas. In table 3 you can see that G4, G10, G1, G6, G2 genotypes and Karaj and Kashmar environment also had the most amount of yield. Environments that have the first principal component interaction near to zero, are not appropriate for distinguishing the lines, and vise versa environments that have the big first principal interaction component are appropriate for distinguishing and screening genotypes. Furthermore, G10, G2, G6 genotypes and Karaj (E1), Kashmar (E2) environment have the most amount of IPC1, in the other word they have the most effect in the interaction.

Table 2: Analysis of variance base AMMI model for seed yield genotypes of canola in four environments.

S.O.V.	df	Sum of Squares	Mean Squares
Rep	2	0.2	0.1^{*}
Environment	3	1.32	0.44^{**}
Genotype	9	1.06	0.11^{**}
G × E	27	1.68	0.062^{**}
IPC1	11	1.41	0.12^{**}
Noise	16	0.25	1.44
Error	78	2.06	0.02
Total	119		

Table 3: Seed yield and genotype first and second principal component of canola in four locations.

Genotype/Environment	Seed yield (Kg/ha)	IPC1	IPC2
Modena (G1)	4.9	0.01	0.009
Okapi (G2)	4.1	0.23	-0.13
Hyola 401 (G3)	3.1	-0.13	-0.1
Licord (G4)	5.7	-0.35	0.1
Opera (G5)	2.6	-0.43	0.04
Zarfam (G6)	4.6	0.14	0.13
RGS 003 (G7)	3.3	-0.15	-0.26
SLM 046 (G8)	4	0.01	-0.14
Sarigol (G9)	3.1	-0.37	0.25
Hyola 308 (G10)	5	0.33	0.09
Karaj (E1)	5.2	0.52	0.14
Kashmar (E2)	4.8	0.29	-0.18
Birjand (E3)	2.7	-0.38	0.27
Shiraz (E4)	3.4	-0.42	0.3

To evaluate and to interpret cultivars diversity, environments and study of genotype effect and genotype environment interaction we used graphical analyzed. This graph explained 95 percent of variance of data (PC1= 86%, PC2=9%). Figure 1 shows AMMI1 graph which indicates each genotype that is near the mean axis and is located in positive part of graph, has more stability and according to this G1 and G6 genotypes have more compatibility than the other genotypes. Figure 2 shows AMMI2 graph. In this graph each genotype which is near to graph center, in positive part of graph has more stability. Also, genotypes near to each area have the more stability than the other genotypes in each area. In result, G10, G4 genotypes in Karaj, G2 genotype in Kashmar, G3, G7 genotypes in Birjand and G9 genotype in Shiraz showed the most stability.

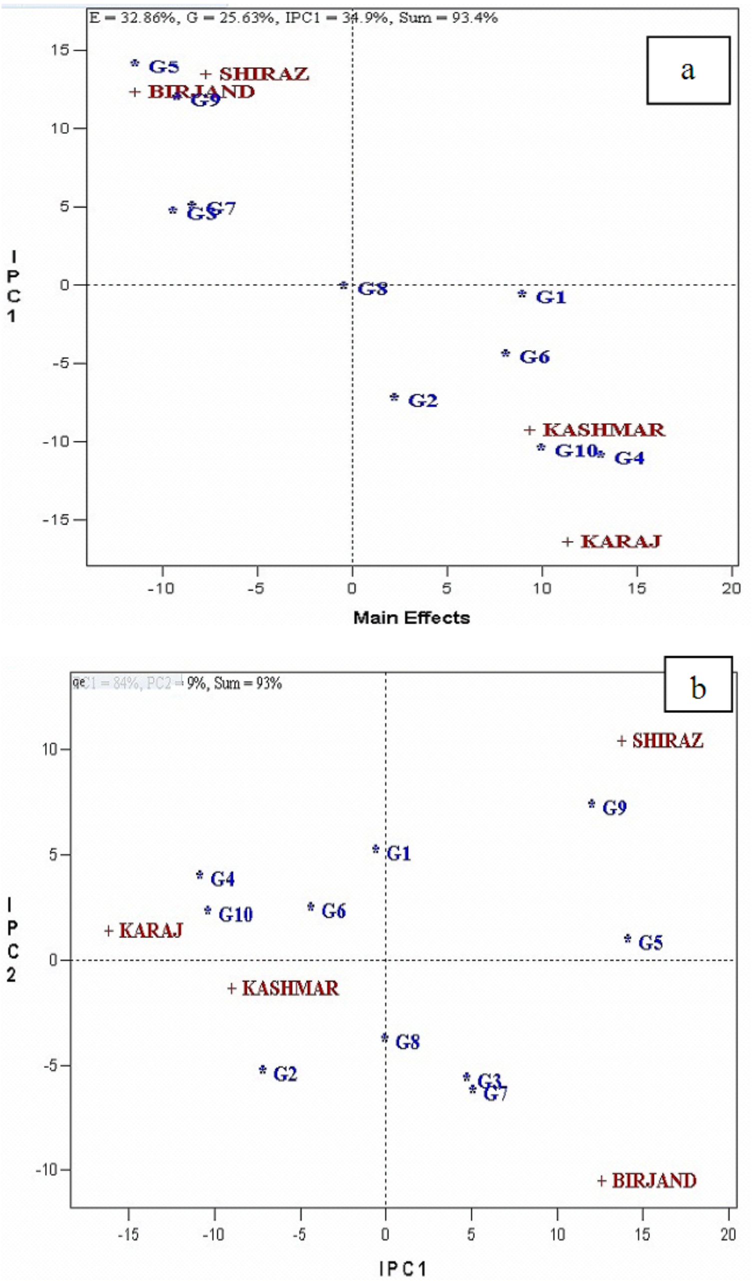

Fig. 1: GGE biplot graph regarding the grain yield of ten cultivars of canola studied in four regions. A: The determination of genotypes based on AMMI1 model. B: The determination of genotypes based on AMMI2 model. G1: Modena, G2: Okapi, G3: Hyola401, G4: Licord, G5: Opera, G6: Zarfam, G7: RGS 003, G8: SLM 046, G9: Sarigol, G10: Hyola 308.

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