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Genotype × Environment Interaction Analysis for Grain Yield of Durum Wheat New Genotypes in the Moderate Region of Iran Using AMMI Model

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Abstract: To determine stability and different reactions of durum wheat promising genotypes in the moderate region of Iran, 18 durum wheat genotypes were evaluated in Karaj, Varamin, Isfahan, Neishabour, Kermanshah and Gonbad, along with commercial bread wheat and Dena cultivars as control cultivars. The study conducted based on randomized complete block design (RCBD), with three replications in two consecutive years (2008-2010). To evaluate the genotype × environment interaction and to identify the stable genotypes, analysis of stability was performed. In this study, some stability parameters such as the new parameter AMMI Stability Value (ASV) and multivariate and graphical method of AMMI were studied. According to the results of ASV, genotype 13 was identified to be a superior and promising in term of yield stability (7.454 ton per hectare) and was found adaptable genotype. Moreover, in AMMI biplot, genotypes 17, 11, 13 and 15 had the least interaction and genotypes 11 and 13 with the most amount of yield were shown to have high general adaptability and were selected.

Key words: Durum wheat · Genotype × environment interaction · AMMI model

INTRODUCTION

Yield is a polygenic attribute whose related phenotype is considered to be highly affected by the environment and therefore the evaluation of genotype × environment interaction is a matter of great significance in plant breeding. This interaction brings about a major difficulty in plant breeding for it interferes with evaluation and selection of genotypes in different environments; particularly, it would reduce the efficacy of selection on the condition that genotypes are selected only on the basis of yield mean. Having knowledge of genotype × environment interaction allows plant breeders to eliminate the unnecessary places in evaluation of genotypes by reducing this interaction and thus prevent the waste of resources. Consequently, the genotypes with best yield means are selected [1-3].

There are different methods used to evaluate genotype × environment interaction which are usually selected according to plant breeders' and researchers' views. Expertise in statistics and biometry is required in order for the plant breeders to select a correct model for a specific experiment such as stability analysis.

Analysis of genotype × environment interaction entails an investigation of various parameters which fall into two major categories of multivariate and univariate [4]. Environmental variance [5], Ecovalence [6], stability variance [7], coefficient of variation [8], Finlay and

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Wilkinson's method [9], Eberhart and Russell method [10] and Tai Regression [11] are some of the methods examining univariate parameters; among the models investigating multivariate parameters, AMMI and GGEbiplot are proved to be more valid and widely used [12-15]. All methods for stability analysis have both merits and demerits and selection of the most reliable one should be based on a consideration of all conditions including plant type and the region.

The present paper is an attempt to analyze stability and examine the genotype × environment interaction for grain yield of durum wheat's new genotype in the moderate region of Iran. To identify the best genotype, the study employs the multivariate method of AMMI.

MATERIALS AND METHODS

Since zonal tests generally require a number of replications across several years and several research stations, the present study focuses on 18 new genotypes of durum wheat in Karaj, Isfahan, Kermanshah, Varamin, Neishabour and Gonbad along with commercial bread wheat and Dena cultivars as control cultivars; the study follows the randomized complete block design (RCBD) in 3 replications and over two consecutive crop years (2008-2010). The experiments were conducted in two years and in six research stations located in Karaj, Isfahan, Kermanshah, Varamin, Neishabour and Gonbad, all of which are believed to be in the moderate region of Iran. Kermanshah is located in the west, Isfahan, Karaj and Varamin are in the center and Neishabour and Gonbad are in the northeast of Iran. It took two crop years for this study to complete: 2008-2009 (the first year) and 2009-2010 (the second year). There were 12 environments (obtained from the number of years multiplied by the number of research stations). The crop features and the technical aspects of the research were the same in all stations and the genotypes were set to be the dependent variable. Each plot included six 6-meter lines separated from each other with a space of 20 centimeters ($1.2 \times 6 = 7$ m^2). At harvest time, half a meter from either side of each plot was omitted and the rest (6 m^2) was harvested.

The irrigation was done through leakage method. Land preparation had three phases of tilling, disking and furrowing; the necessary amount of fertilizer was applied to the land based on the results of soil test and the recommendations of the soil and water research section of each region. In the tillering stage, puma super and granstar herbicides were used and broad leaf weeds and narrow leaf weeds were removed through hand weeding. In each square meter, 450 seeds were planted. During the growth season, agricultural operations were performed regularly and necessary notes were taken. At harvest, the yield for each variety in the relevant environment was calculated. After harvesting with an experimental combine, the yield of each cultivar was measured with digital scales; after deducting the weigh of the sack, the yield for each experimental unit was calculated and converted into ton per hectare.

To analyze the data, the multivariate method of AMMI was utilized and its analysis of variance (ANOVA) table was drawn. The mean and IPCA1 biplot, as well as IPCA1 and IPCA2 biplot were drawn for all genotypes and environments and genotypic decomposition reaction was used for a close scrutiny of the genotypes. AMMI stability value parameter (ASV) was calculated for all stabilities. The calculations were made by SAS, SPSS and Excel.

RESULTS

The ANOVA results for grain yield, based on AMMI, are presented in Table 3. The genotype × environment interaction is shown to be significant at 1% level of probability which indicates that the genotypes had differential yields in different environments. Genotype × environment interaction accounted for a relatively large part of the total sum of squares. The effect of the environment accounted for the greatest part of total sum of squares and was significant at 1% level of probability. There was a significant difference among the genotypes suggesting a difference among all the genotypes under study in all experimental environments. To investigate genotype × environment interaction with AMMI, an analysis of principal components was carried out on the remaining matrix and the three first principal components were shown to be significant at 1% level of probability. Therefore, $AMMI_3$ is considered as the principal component of AMMI.

To evaluate stability of cultivars, the present study utilized the new ASV parameter and the results are presented in Table 4. In AMMI stability value, genotypes with lower ASV are assumed to be more stable. In this research, genotype 13 showed the lowest ASV with a yield of 7.454 ton per hectare and above the total average and genotype 2 had the highest ASV and were identified as the most unstable genotype; genotypes 19, 14 and 3 were the next in line regarding instability.

Table 1: Code and the pedigree of durum wheat genotypes.

Code	Pedigree
1	Dena (check 1)
2	Bread wheat (Check 2)
3	CABECA_2/PATKA_4//ZHONGZUO/2*GREEN_3
4	CHEN_11/POC//TANTLO/4/ENTE/MEXI_2//HUI/...
5	CNDO/PRIMADUR//HAI-OU_17/3/SNITAN
6	OSU-3880005/3/STOT//ALTAR84/ALD/4/KUCUK_2
7	GUANAY//TI L0_1 /LOTUS_4
8	SRN 3/AJAIA 15//PICON/3/GREEN/6/CiVlH82A....
9	SULA/AAZ_5//CHEN/ALTAR 84/3/AJAIA_12/F3LO.
10	AMIC
11	BISU_1/PLATA_16//RISSA/3/SNITAN
12	D86135/AC089//PORRON 4/3/SNITAN
13	CAMAYO/ADAMAR
14	GREEN 18/FOCHA 1//AIRON 1/3/SOOTY 9/R.
15	GREEN_38/BUSHEN_4//PORTO_3
16	HESSIAN-F 2/3/STOT//ALTAR 84/ALD
17	MALMUK_1/SERRATOR_1//RASCON_37/TARR.
18	URA/4/CHENJ/TEZ/3/GUIL//CIT71/CII/5/CHEN/.
19	ALTAR 84/STINT//SILVER 45/4/SKEST//HUI/TU.
20	IGUAYACAN INIA/YEBAS 8/3/TOPDY 18/FO.

Table 2: Specifications of geographic and climatic test stations.

Location	Height (m)	Rainfall Ave. (mm)	Temperature (□)	Latitude	Longitude
Karaj	1300	250	14.4	35.47	5.56
Varamin	918	148.7	17.9	35.19	51.39
Isfahan	1570	200	16	32.66	51.67
Neyshabor	1250	365.8	14.8	36.209	58.799
Gonbad	52	500	6.17	35.88	57.73
Kermanshah	1200	456.8	14	33.31	47.06

Table 3: AMMI variance analysis for grain yield of durum wheat genotypes in diverse. environments

Source	Df	SS	MS	SS%
Total	241	2545.327581	10.561525	
Treatment	239	2542.2501	10.63703	
Genotype (G)	19	30.019246	1.579960	1.1
Environment (E)	11	2325.433358	211.403033	91
E × G	209	186.797646	0.893769	7.3
IPCA1	29	51.806	1.786	27.73
IPCA2	27	34.203	1.267	18.32
IPCA3	25	27.423	1.096	14.68
Noise	91	41.229	0.453	22.05
Error	478	230.859408	0.482969	

Ns: non-significant difference. * and ** show significant difference at 0.01 and 0.05 levels of probability respectively.

Table 4: AMMI stability of value and first and second principal components quantities of durum wheat genotypes.

ASV	IPCA2	IPCA1	Yield mean (t/ha)	Genotype
0.246478	-0.13506	0.13623	7.123	1
1.329151	0.3884	0.83988	7.390	2
0.828777	-0.46185	0.45469	7.414	3
0.358737	0.18107	-0.20462	7.641	4
0.592012	0.46933	-0.23842	7.846	5
0.84827	0.45256	-0.47405	7.193	6
0.612799	0.56179	-0.16173	7.387	7
0.222299	-0.12482	0.12154	7.213	8
0.311925	-0.3085	0.03046	7.886	9
0.489797	0.29144	0.2601	7.287	10
0.202501	0.05462	0.12884	7.426	11
0.293318	-0.26464	0.08358	7.656	12
0.108621	-0.08755	-0.04248	7/454	13
0.859048	0.0008	0.5676	7.376	14
0.175506	-0.15748	-0.05119	7.425	15
0.868679	-0.78527	-0.24541	7.373	16
0.194449	0.12452	0.09868	7.397	17
0.970922	-0.14987	-0.63383	7.201	18
0.440687	-0.10537	-0.28273	7.415	19
0.588571	0.05589	-0.38713	7.707	20

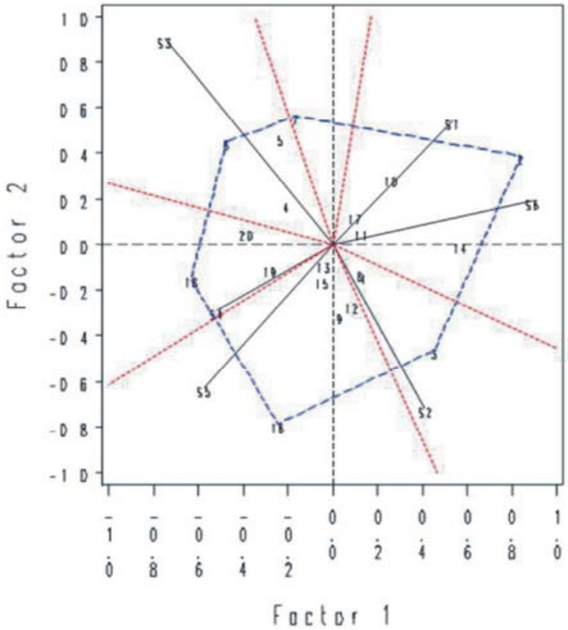

Fig. 1: Biplot based on AMMI$_2$ model (S1 to S6 show Karaj, Varamin, Kermanshah, Isfahan, Neyshabor and Gonbad).

In order to assess the stability of the genotypes and places and to relate differing genotypes to different regions, genotypic reaction analysis with biplot was used. In biplot display, the horizontal axis demonstrates additive main effects or means and the vertical axis presents multiplicative interaction or the values of the first principal components. In the said biplot, two pairs of data are presented on the axes. The first pair contains data on the mean yield of each cultivar (horizontal axis) and the values of the first principal component of each genotype (vertical axis) and the second pair is related to the mean yield of each environment (horizontal axis) and the values of the first principal component of each environment (vertical axis).

The biplot (Fig. 1) illustrates the first and second principal components of the interaction for the genotypes. The genotypes and places are depicted based on the first and second principal components.

In this biplot (Fig. 1), genotypes 7, 6, 18 and 16 have high and unstable interaction. Genotypes 2 and 3 have positive and unstable interaction and genotypes 17, 11, 13 and 15 have the least interaction; hence, genotypes 13 and 11, because of their above-the-average mean yield, are introduced as genotypes with high general adaptability. In investigating private adaptability and deciding on the best genotypes for the places under study, the biplot revealed that genotypes 2, 3, 6, 7, 16 and 18 are those which are located at the angles of the polygon formed in this biplot; these genotypes have the highest private adaptability to their proper places.

The lines perpendicular to the sides of the polygon created spaces containing genotypes and their relevant proper places. Genotypes located at the angles are the wining genotypes and are appropriate for the places located in that space.

In this biplot, Karaj (S_1) and Gonbad (S_6) are located in the first space and the wining genotype in this space is genotype 2; i.e. it has an interaction reaction similar to these two places. In the second space, genotype 3 is located at the angle and is identified as the proper genotype for Varamin (S_2); the third space has genotype 16 at the angle which is the proper genotype for Neishabour (S_5). Genotype 18 is at the angle of the fourth space and is the proper genotype for Isfahan (S_2). Genotypes 3 and 7 in the fifth space are the best for Kermanshah (S_3). When analyzing genotypic reaction based on two principal components, taking the angle between environmental vectors into account will be beneficial to the interpretation of environmental similarities. The angle between two environmental vectors determines the high correlation between the two environments.

DISCUSSION

The Additive Main effects and Multiplicative Interaction model (AMMI) includes an analysis of variance along with an analysis of principal components. In this model, in the first step the main effects of genotypes and environments are estimated using analysis of variance (ANOVA) and these estimations are called additive main effects. Then through an analysis of principal components, the genotype by environment interaction – generally known as multiplicative interaction - is analyzed [16]. AMMI model will prove to be our best model of analysis when both additive main effects and multiplicative interaction are significant to us [17]. The first researchers to adopt this model for data analysis were Kempton, [18] and Zali *et al*., [19].

To analyze genotype-environment interaction in yield zonal experiments, Gauch and Zobel [20] employed AMMI model which was in effect the modified version of the model previously used by Gollob [21] and Mandel [17] in social sciences and basic sciences. The AMMI converts the structure of the data which are originally in form of matrices into smaller scale data through the use of a number of axes such as genotype and environment means as well as individual values for principal components [22]. AMMI is a very efficient model in analyzing and interpreting large matrices of genotype × environment because using biplot, it offers reasonable inferences about the interaction and consequently it facilitates the selection of genotypes with high adaptability to specific environments [23]. Generally, AMMI model is widely employed for it pursues for the following three prime objectives:

- It is a diagnostic model and in statistical analysis of the experiments aiming at yield comparison, it has proved to have a higher utility compared to other methods; this is owing to the fact that it offers a tool to identify other secondary models that are beneficial to the examination of the data;
- It is employed to explain the nature of interaction and can easily summarize and present the patterns and relations of varieties and environment [24].
- It improves the accuracy of yield estimation to the extent that the greater accuracy in calculating yield by AMMI is equal to an increase in replications from two to five [24].

Put it differently, the statistical efficacy of this model is two times and a half more than that of randomized complete block design (RCBD). In fact, by cutting the number of repeats and increasing the number of treatments in an experiment, one can drive the cost of the experiment down and improve the selection of the better varieties [24].

AMMI analysis is more efficient than two-way fixed effects model along with interaction [23]. The efficacy of this model is due to the fact that it can explain the sum of squares of genotype × environment interaction to a great extent, which improves its prediction accuracy and statistical efficacy (due to noise decrease and df increase). 2 replications with AMMI equal 3 to 6 replications with other models [16]. Another advantage is that AMMI divides regions into mega-environments [20]. AMMI analysis provides homogeneous sub-regions which, with regard to their environmental conditions in an area specific to planting a certain crop, share similar genotype × environment interaction. Division into mega-environments can help to determine desired genotypes for the environments under study [25].

AMMI is in fact a combination of Analysis of Variance (ANOVA) and Principal Component Analysis (P.C.A.) which has a new parameter of AMMIS Stability Value or ASV. Motzo *et al*. [26] concluded from their studies that in yield zonal tests the role of environment in total variance is bigger than the role of genotype × environment interaction, which in turn performs a bigger role than that of genotypes. In another experiment by Sivapalan *et al*. [27], the main effects of genotypes accounted for merely 2 per cent of the total difference whereas the environment's sum of squares was responsible for 87% of the total sum of squares and the remaining 11% was the effect of genotype × environment interaction. These results, regardless of the percentages, were similar to those obtained by Zali *et al*. [19].

Karimizadeh *et al*. [28] analyzed genotype × environment interaction for 10 corn genotypes with AMMI model and used four parameters of SIPC4, AMGE4, ASV and EV4. Since they obtained fairly reliable results from ASV, they introduced this parameter as the best from among AMMI parameters. In their studies, ASV parameter had a positive and significant correlation with Wricke's Ecovalence as well as the non-parametric parameter of S2. In another study on cotton, ASV and Shukla's stability variance proved to have a high and positive correlation with each other [29].

Albert [30] in his study of genotype × environment interaction in corn hybrids compared different methods of stability analysis and finally introduced AMMI as the best method for this purpose. Burgueno *et al*. [31], in their graphic analysis of AMMI_2 biplot, in order to interpret the biplot and identify the superior genotypes for each place, concluded that the genotypes located at the angles in each space are the wining genotypes for the places within that same space. Given these findings, genotypes 13, 11 and 15 were identified to be the stable genotypes in this method.

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