

## THE GENETIC VARIATION AND STABILITY ANALYSIS OF RICE MUTANT LINES USING AMMI MODEL UNDER NORMAL AND DROUGHT STRESS CONDITIONS

Ali Akbar EBADI<sup>\*1</sup>, Mohammad Taher HALLAJIAN<sup>2</sup>, Mojtaba KORDROSTAMI<sup>1</sup>

1-Rice Research Institute of Iran, Agricultural Research, Education and Extension Organization (AREEO), Rasht, Iran

2- Researcher at Radiation Application Research School, Nuclear Science and Technology Research Institute (NSTRI)

Ebadi Ali Akbar, Hallajian M.T. and M. Kordrostami (2019): *The genetic variation and stability analysis of rice mutant lines using AMMI model under normal and drought stress conditions.*- Genetika, Vol 51, No.2, 687-699.

This study was conducted to investigate the genotype  $\times$  environment interaction and stability analysis of 14 mutant lines (with their parental lines). The study was designed for two years, 2015-2016, in two environmental conditions, normal and drought stress, in Rasht. Based on the results of combined analysis of variance, genotype, environment, and genotype  $\times$  environment effects were significant at 1% probability level. The significance of the environmental effect indicates that the environments were different in terms of genotypes performance. Therefore, the stability analysis was performed with different methods of measuring stability. The results of ANOVA for the additive main effect and multiplicative interaction (AMMI) showed the genotype and environment main effects and genotype  $\times$  environment effects were significant at 1% probability level. Based on the AMMI results, TM6-230-VE-7-5-1, TM6-230-VE-8-4-1, Khazar, and KM5-200-4-2-1 had a positive and negative interaction, respectively. HM5-300-5-1, HM5-250-12-1, TM6-B-19-2 were selected as the stable genotypes. Stability analysis determined through AMMI stability value (ASV) method showed HM5-250-12-1, Tarom, HM5-250-E-1-1, TM6-B-19-2, Hashemi and HM5-300-5-1 with the least stability value were introduced as the most stable cultivars.

*Keywords:* AMMI model; Drought; Mutants; Rice; Stability analysis; G $\times$ E interaction

---

*Corresponding author:* Ali Akbar Ebadi, Rice Research Institute of Iran, Agricultural Research, Education and Extension Organization (AREEO), Rasht, Iran. E-mail: a.ebadi@areeo.ac.ir.

## INTRODUCTION

National flocks in Africa and Asia were used for genetic progress and variation to produce Rice belongs to the Gramineae family and the *Oryza* genus. The *Oryza* genus has more than 20 known wild and two crop species; *O. glaberrima* and *O. sativa*, which are cultivated in different parts of the world (SMITH and DILDAY, 2003). Rice is an annual herbaceous plant with the fibrous roots which does not penetrate deep into the soil. Each rice plant typically produces about 5 to 20 branches during the growth period, which is one of the most important factors affecting the increase the yield production. Rice crops are geographically categorized into three distinct groups, Indian (*Indica*), Japanese (*Japonica*) and intermediate (*Javanica*) (KHUSH, 2005).

Rice is the most important crop in the world and is the first source of food for more than half of the world's population. More than 90 percent of the world's rice is grown in Asia, where more than 60 percent of the Earth's population lives there (KHUSH, 2005). The global rice production in Asia as one of the largest rice producers grew by 3 percent to 653 million tons in 2011. Rice production in Africa also rose to 25.5 million tones by one percent increase. Rice production is expected to reach 732.3 million tons in 2012 (FAOSTAT, 2012).

Stress is a term that was first used by the biologists on living organisms and is defined as any factor potentially causing damage to the living organisms. Stress is the result of the abnormal physiological processes that result from the effects of one or a combination of environmental and biological factors. Stress has potential damage that results from an abnormal metabolism and may occur as growth failure, complete death of the plant, or death of a part of the plant (LICHTENTHALER, 1998). Drought is a meteorological term that indicates a period in which the rainfall is less than the evapotranspiration. Because rain deficiency causes water deficit, the term "drought stress" is used for the cases where stress is caused by the absence of effective rainfall (REDDY *et al.*, 2004). The amount of damage to the plant due to drought stress is different depending on the plant type, intrinsic properties of the soil, the duration, the time of occurrence and frequency of occurrence of the stress. In dry and semiarid regions, in addition to low rainfall, the distribution of rainfall varies from season to season and from year to year. Therefore, it is difficult to predict its amount and distribution. In Iran, other than the Caspian Sea and small parts of the northwest of the country, the rest of the regions are considered as dry and semi-arid areas, while their semi-arid regions are more spacious (KHALILY *et al.*, 2010).

The goal of plant breeding is to increase the yield of major crops such as rice. Mutations are one of the important phenomena of nature. This phenomenon has a significant role in the evolution of living organisms. The basis of the mutation is the change in the chemical structure of the genes. These changes are new inherited traits and spread among the individuals in a population. The term mutation is derived from the Latin word *mutatio* meaning a major and sudden change. The genetic variation resulting from artificial mutation seems to be the same as the variation from natural mutation. Therefore, the basic principles of using the diversity of artificial mutations with the diversity of natural mutations are the same. Nowadays, mutation breeding is widely used to create tolerant cultivars for biotic and abiotic stresses. This method is sometimes used to improve the quality or change the characteristics of the plant. This aspect of the mutation in ornamental plants has been used extensively. Nowadays, new plant breeding techniques are used for proper plant response to the environment.

In the plant breeding, the genotype response to the environmental factors is called genotype x environment interaction. This interaction reduces the correlation between genotype and phenotype and consequently decreases the efficiency of selection (BRANDIEJ and MEVERTY,

1994). The presence of the genotype  $\times$  environment interactions indicates that the best genotype in one environment may not be the best one in the other environments (FREEMAN and PERKINS, 1971). The interaction between the genotype and the environment can have different aspects. For example, a specific environmental difference can affect some genotypes more than the other ones. The response of different genotypes is usually due to the different response of the genes or their different apparent power in different environments (FALCONER, 1960). Stability analysis is the most important method used to find out the nature of the interaction between the genotype and the environment and, therefore, identifying stable varieties. The genotype  $\times$  environment interaction has a special significance for the plant breeders and is one of the complex issues of breeding programs for producing high-yielding and sustainable genotypes (CORNELIUS and CROSSA, 1999; GAUCH, 2006; YAN *et al.*, 2007). Awareness of the nature of the genotype  $\times$  environment interaction helps the plant breeders to select genotypes more accurately and select the best genotypes for stability and high yield (ROY, 2000). The criterion for using a variety of sustainability analysis methods depends on the type of experimental design, the plant, the opinion of the researcher, the test environment and other conditions (FATAHI and YOUSEFI, 2006).

Additive main effect and multiplicative interaction (AMMI) analysis are more useful than a conventional two-way fixed-effects model with cross-effects (ZOBEL *et al.*, 1988). The AMMI method is a combination of variance analysis and principal component analysis. In the AMMI method, by using variance analysis, the main effects of genotypes and environments are usually estimated, which are referred to as the main additive effects. Then, by analyzing the main components, the interaction of genotype and environment, which is known as complementary interactions, is analyzed. This study was conducted to evaluate the stability of rice mutant lines to drought stress.

#### MATERIALS AND METHODS

In this project, two improved cultivars "Fajr" and "Khazar" (with relative resistance to drought stress) and two local cultivars "Tarom" and "Hashemi" (sensitive to drought stress) were used as plant material. To determine the optimum irradiation dose, seeds were exposed with different gamma-ray doses (0, 150, 180, 200, 230, 250 and 300 Gy). Survival of the seedlings in different doses was calculated for the four genotypes. Then the  $M_1$  populations were created based on the genotype and optimum dosage. Based on the results of irradiation and determination of optimum dosage, for generating  $M_1$  populations, seeds of the main populations of Tarom cultivar with the optimal dosage (230 Gy) and three other doses (220, 250 and 300 Gy), seeds of the main population of Hashemi cultivar with the optimal dosage (250 Gy) and a higher dose (300 Gy), and seeds of the main populations of Khazar and Fajr cultivars with the optimal dosage (200 Gy) and one higher dose in Khazar (250 Gy) and two higher and lower doses in Fajr (150 and 250 Gy) were irradiated and were sent to the Rice Research Institute of Iran, Rasht, Iran, for planting in the nursery. In order to evaluate the genotype  $\times$  environment interaction and determining the stability of the rice mutant lines, a total of 14 rice mutant lines with their parental lines (Hashemi, Tarom, Khazar, and Gilaneh) were surveyed in a completely randomized block design with three replications in 2 years (2015-2016) and two separate experiments (drought stressed and natural conditions), Table 1. In these environments, the experiments were carried out uniformly and genotypes were considered as the constant factors. In May 2015 and 2016 about 300 seeds of each cultivar were selected and disinfected with sodium hypochlorite 20% for 10 minutes. Seeds then rinsed with sterile distilled water, it was transferred to the Petri dishes containing filter paper. A small amount of sterilized distilled water

was added to the Petri dishes to make the paper and the seeds completely wet. The Petri dishes were placed in the germinator at 35° C and 70% humidity to accelerate the germination process. When the length of the buds (radicles and plumules) reached about 1 to 2 cm, the seeds were removed from the germinator and cultivated, in special boxes of 120 × 60 cm, in greenhouses to produce transplants. All the necessary care was taken to produce strong and proper transplants. After about 25 days, when the transplant size reached about 30 cm, they were transferred to the main field. 18 genotypes were separately studied in a randomized complete block design with three replications in drought-stressed and non-stressed media. The size of the experimental units was considered 2 m<sup>2</sup> with a density of 25 plants/ m<sup>2</sup> so that in each experimental unit, about 50 plants were cultivated. After the random assignment of the treatments to the experimental units, transplanting was carried out (as a single plant) at 20 x 20 cm. Field irrigation was done for all cultivars using flushing method in both stressed and non-stressed environments up to 30 days after transplantation. The irrigation was discontinued until the end of the maturity period for the stressed environment, while it was continued in the non-stressed environment. Evaluation of all the traits except for grain yield, biological yield and harvest index (all plant of each plot was used for evaluation), was performed on 10 plants per plot (which were randomly selected and marked with a specific mark).

*Table 1. The origin/ pedigree of rice genotypes used in this experiment.*

Genotype code	Genotype	Pedigree
G1	Gilaneh	Saleh×Abjibuji
G2	Hashemi	Iranian landrace
G3	HM5-250-12-1	Parent: Hashemi
G4	HM5-250-6-6	"
G5	HM5-250-7-6	"
G6	HM5-250-E-1-1	"
G7	HM5-250-E-3-2	"
G8	HM5-300-3-1	"
G9	HM5-300-5-1	"
G10	Khazar	IR36/TNAU4756
G11	KM5-200-4-2-E	Parent: Khazar
G12	Tarom	Iranian landrace
G13	TM6-230-VE-7-5-1	Parent: Tarom
G14	TM6-230-VE-8-4-1	"
G15	TM6-250-10-7-1	"
G16	TM6-B-19-2	"
G17	TM6-B-2-1-E	"
G18	TM6-B-7-1	"

Combined analysis of variance was performed assuming the effects of genotype were constant and the effect of the environments was randomized. The AMMI method was used for the data analysis and the analysis of variance was performed for this method. The AMMI model is derived from the following equation:

$$Y_{ijr} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij} + \varepsilon_{ijr}.$$

Where  $Y_{ijr}$  is the  $i^{\text{th}}$  genotype performance in the  $j^{\text{th}}$  environment for the  $r^{\text{th}}$  replication,  $\mu$  is the grand mean,  $g_i$  are the genotype main effects as deviations from  $\mu$ ,  $e_j$  are the environment main effects as deviations from  $\mu$ ,  $\alpha_{ik}$  and  $\gamma_{jk}$  are the genotype and environment IPC scores,  $\rho_{ij}$  is the residual containing all multiplicative terms not included in the model (1);  $n$  is the number of axes or principal components (PC) retained by the model, and  $\varepsilon_{ijr}$  is the experimental error, assumed independent with identical distribution. Classic concept of  $(G \times E)_{ij}$  normally indicates the interaction of the  $i^{\text{th}}$  genotype with the  $j^{\text{th}}$  environment, but in the AMMI model is written as:

$$\sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \rho_{ij}$$

The degree of freedom of the main component of the interaction was calculated using the following formula:  $(g-1)-(e-1)-(2k-1)$ . Where  $g$  represents the number of genotypes,  $e$  represents the number of environments and  $k$  is used for the main components of the interaction. In the AMMI model, several models are fitted to predict data. The AMMI stability value (ASV) as described by (PURCHASE *et al.*, 2000) and Yield Stability Index was calculated as mentioned by (BAVANDPORI *et al.*, 2015). All the analyses were performed using GenStat ver. 12. In this study, the studied environments are abbreviated as E1-E4, which are E1: 2015, normal; E2: 2015, drought; E3: 2016, normal; E4: 2016, drought respectively.

## RESULTS AND DISCUSSION

To perform analyzes, for the combined analysis of variance, the uniformity of the variance of the experimental error was tested using Bartlett's test. The test results indicated the variances were uniform within the test and the combined analysis of variance could be performed for the whole data. Results of the combined analysis of variance, genotype, environment, and genotype  $\times$  environment effects were significant at 1% probability level (Table 2). The significance of the environmental effect indicated that the environments were different in terms of the performance of the genotypes. The significance of the genotype  $\times$  environment interaction showed a difference in relative performance between the genotypes differs from one environment to another one.

Table 2. Combined analysis of variance and AMMI analysis for evaluating the stability of 14 rice mutant lines and their parents in 4 environments during 2 years.

Source of variation	df	SS	MS
Genotype (G)	17	11.80	0.69**
Environment (E)	3	437.30	157.75**
G $\times$ E	51	19.90	0.39**
IPCA1	19	11.30	0.59**
IPCA2	17	5.30	0.31**
IPCA3	15	3.30	0.22**
Residuals	13	0.22	0.11
Error	136	4.00	0.03
Total	215	510.10	10.37

The genotype and environment main effects and genotype  $\times$  environment effects were significant at 1% probability level. The presence of significant differences between the

environments indicated that the studied locations for the cultivation of rice mutant lines had significant differences. The Gollob test was used to determine the number of components which were significant at 1% probability level, (GOLLOB, 1968). The three main components of the model were retained and the rest of the main components for the interaction effects were presented as the residuals (Table 2).

The Biplot of the AMMI1 model is shown in Figure 1. In this Figure, the horizontal axis is the mean performance and the vertical axis is interaction principal component axes 1 (IPCA1). The genotypes with IPCA1 scores close to zero have a low contribution to the interaction, being considered stable and represented wide adaptation reaction whereas the larger scores on the ordinate depicted more specific adaptation to environments with the same IPCA1 sign (GHANBARI *et al.*, 2014; EBDON and GAUCH, 2002; CROSSA *et al.*, 1991). So, TM6-B-2-1-E and HM5-250-E-1-1 with the same sign and higher mean yields than mean were specifically adapted to E1. TM6-230-VE-7-5-1 with higher mean yields than mean was specifically adapted to E2 and TM6-B-7-1 with higher mean yields than mean was specifically adapted to E3. Also, the results revealed that Khazar and KM5-200-4-2-1 genotypes had a positive and negative interaction respectively, and, due to the low average yield, these genotypes were introduced as unstable and low yield genotypes. Considering the magnitude of the interaction between genotype and environment, HM5-300-5-1, HM5-250-12-1, TM6-B-19-2 were selected as the stable genotype and based on this model (AMMI), are recommended for all the studied environments. The stability value of Hashemi, Tarom and Gilaneh cultivars was close to ordinate's zero, and their performance was close to the average yield, or less than the average yield of genotypes (Figure 1).

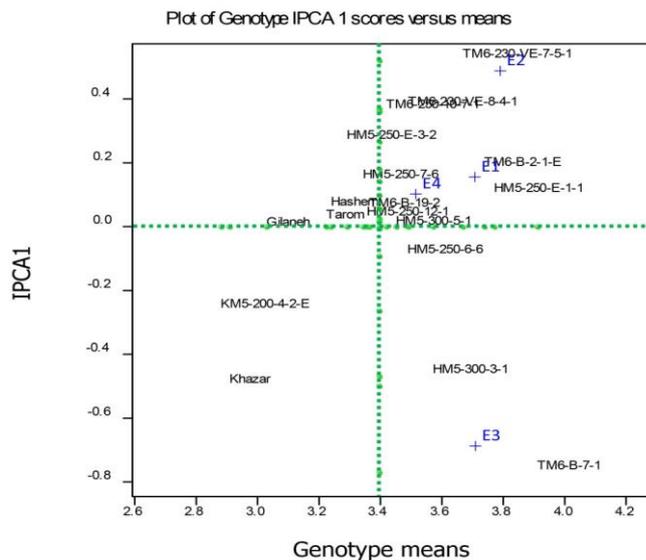


Figure 1 Biplot curve of AMMI1 model for 18 rice mutant lines in 4 different locations. E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016, drought respectively.

In Figure 2, the vertical axis, passing through the mean of all genotypes, divides the genotypes into two main groups: the genotypes with a yield greater than the total mean and the genotypes with a yield less than the total mean. The horizontal axis that crossed the zero point of the interaction principal component axes 1 (IPCA1) axis divides the chart into two parts. The genotypes that were in the upper part of this axis recognized as genotypes with the positive interaction and the genotypes that were located at the bottom of this axis had a negative interaction. The genotypes in the upper and the right side of the graph had a positive interaction between the two interaction principal component axes 1 (IPCA1) and interaction principal component axes 2 (IPCA2) axes and the genotypes located in the lower and the left side of the graph had a negative interaction between the two axes. Since the interaction principal component axes 2 (IPCA2) explained interactions were less than interaction principal component axes 1 (IPCA1), genotypes that had a positive or negative interaction with the interaction principal component axes 1 (IPCA1) axis compared to the interaction principal component axes 2 (IPCA2) axis will be recognized as high-interactions genotypes. The genotypes close to the center of the graph had less interaction with both IPCA1 and IPCA2 axes. HM5-250-6-6, HM5-300-5-1, HM5-250-12-1, TM6-B-19-2 were recognized as stable genotypes with the least amount of interaction between two axes. Khazar and KM5-200-4-2-1 showed the highest levels of interaction (Figure 2).

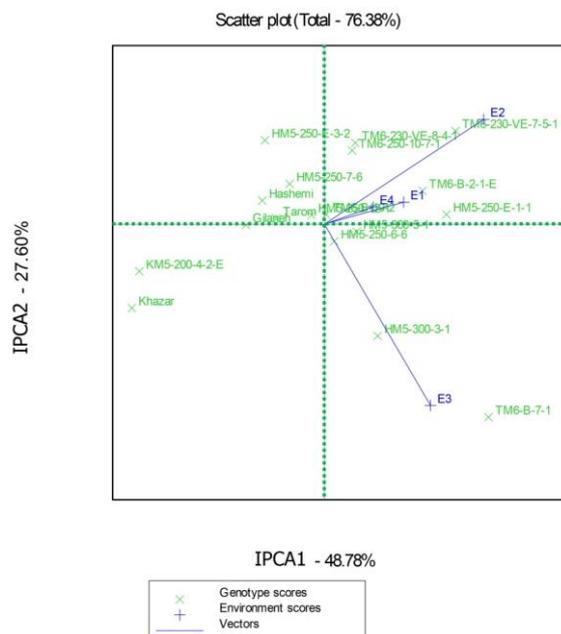


Figure 2. Biplot curve of AMMI2 model for 18 rice mutant lines in 4 different locations. The vertical line represents the grand mean of the experiment. E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016, drought respectively.

According to the AMMI stability score and genotypes yield per environments, four top genotypes per environments Have been selected. According to the results, four genotypes per environments were selected: in Rasht-2015-N, TM6-B-2-1-E, HM5-250-E-1-1, TM6-B-7-1 and TM6-230-VE-8-4-1; in Rasht-2015-D, TM6-230-VE-7-5-1, HM5-250-E-1-1, TM6-250-10-7-1 and TM6-B-2-1-E; in Rasht-2016-N, TM6-B-7-1, HM5-300-3-1, HM5-250-E-1-1 and HM5-300-5-1; and finally, in Rasht-2016-D, TM6-B-2-1-E, HM5-250-E-1-1, HM5-250-6-6 and TM6-230-VE-8-4-1 were selected as the top genotypes in these environments among all the studied genotypes. The results also showed that the parental lines were not included in this list (Table 3).

Table 3. First four AMMI selections per environment. E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016, drought respectively.

Environment	Mean	Score	1	2	3	4
E1	4.483	0.1717	TM6-B-2-1-E	HM5-250-E-1-1	TM6-B-7-1	TM6-230-VE-8-4-1
E2	1.817	0.8312	TM6-230-VE-7-5-1	HM5-250-E-1-1	TM6-250-10-7-1	TM6-B-2-1-E
E3	4.682	-1.0464	TM6-B-7-1	HM5-300-3-1	HM5-250-E-1-1	HM5-300-5-1
E4	2.601	0.0435	TM6-B-2-1-E	HM5-250-E-1-1	HM5-250-6-6	TM6-230-VE-8-4-1

E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016 respectively

In this study, the AMMI model was able to identify high yielding and stable genotypes to some extent. ANANDAN *et al.*, (2009) used the AMMI method to analyze the genotype interaction pattern in 46 rice cultivars and determined the most stable genotypes under salt stress conditions. Like this study, they introduced the AMMI model as a suitable model for investigating the nature of genotype $\times$  environment interaction and identifying stable cultivars. (ASGARNIA *et al.*, 2009) examined the genotype  $\times$  environment interaction patterns for 10 wheat cultivars in 8 media (two nitrogen fertilizer treatments and four irrigation regimes). Analysis of variance and principal components analysis showed that genotypic, environmental and interaction effects were very significant. In conclusion, the first three components explained 89% of the sum of squares of the interaction. Their results were in line with the results of this study. In this study, the first 3 components explained 85.35% of the total interaction (IPCA1= 48.78%, IPCA2= 27.60%, IPCA3= 8.97%). (SHAHMOHAMADI *et al.*, 2005) observed that the first two components had a negligible contribution to interactions. Nevertheless, they used the AMMI-Biplot interpretation for the identification of sustainable genotypes. (MOHAMMADINEJAD and REZAI, 2005) used the AMMI method to interpret the interaction of 9 oat genotypes in six environments. (FATAHI and YOUSEFI, 2006) used the AMMI model to study the stability of 19 barley genotypes in eight moderate region stations, and concluded this model was very effective for identifying the ideal genotype in terms of stability and adaptive performance. Their results were in line with the results of this study.

The average yield of the genotypes varied from 2040 kg.ha<sup>-1</sup> (Tarom) to 3070 kg.ha<sup>-1</sup> (HM5-250-E-1-1) in all 4 environments (Table 4). For consistent use of all components, the AMMI stability value (ASV) was used. The lower the stability value, the more stable the genotype (PURCHASE, 1997). In this study, HM5-250-12-1, Tarom, HM5-250-E-1-1, TM6-B-19-2, Hashemi and HM5-300-5-1 with the least stability value were introduced as the most stable

cultivar among 18 examined genotypes. These genotypes were identified as the most stable cultivars with higher yield and tolerance to drought stress conditions. Hashemi is an Iranian landrace which is tolerant to the drought stress (Rice Research Institute of North of Iran data). On the contrary, TM6-B-7-1, TM6-230-VE-7-5-1, Khazar and HM5-300-3-1 with the highest stability value were introduced as the most unstable genotypes among 18 rice genotypes (Table 4). Although Khazar has a high yield potential, in the face of environmental stresses, its performance was significantly reduced and was not sustainable. Based on the results of this experiment, it seems that the Khazar cultivar has specific compatibility to stress-free conditions and is not recommended for cultivation in conditions of environmental stresses.

Yield stability analysis cannot be beneficial on its own. In practice, sustainable cultivars are welcomed by farmers if they have high grain yield. Hence, stability indices are usually measured along with grain yield, and ultimately for selecting the high yielding stable genotypes. For this purpose, the stability value (ASV) and YSI were plotted against the mean grain yield (Figure 3).

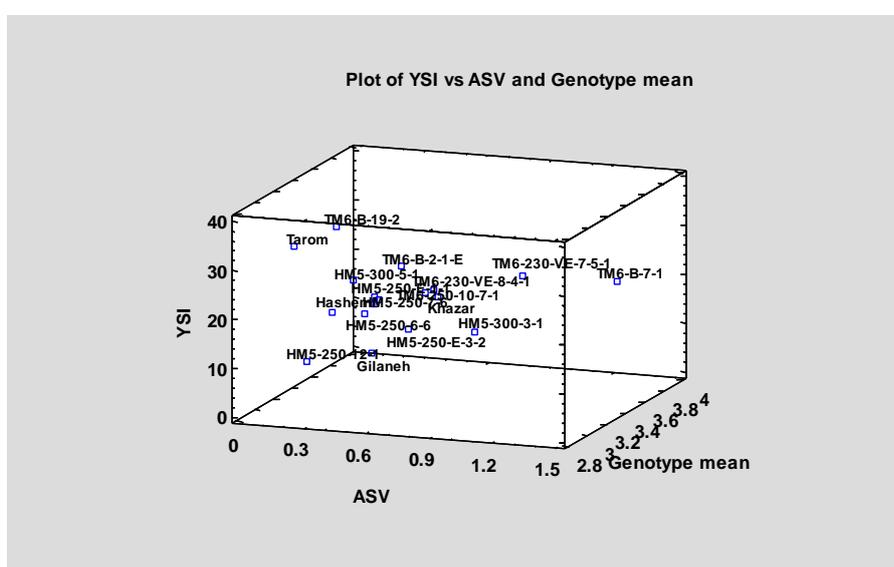


Figure 3. Scatter plot of rice mutant lines based on ASV, YSI and grain yield.

Accordingly, no genotypes with high yield and stability were found in this study. HM5-250-12-1, HM5-250-E-1-1, and Hashemi, with high yield and medium stability, were identified as suitable cultivars for cultivation in these four environments. Khazar had specific compatibility to stress-free conditions and is not recommended for cultivation in conditions of environmental stresses. The results of ASV-YSI were fully consistent with the results of the AMMI model. (ALBERTS, 2004) also reported the same results for the AMMI stability and Biplot. Although these results are generally consistent, if there is a difference between the results of these two methods, the AMMI stability value is more accurate and should be cited, since the ASV includes all the significant components, but the Biplot only considers the first two components (ALBERT,

2004), Figure 3. PURCHASE *et al.*, (2000) used the ASV parameter and concluded that this parameter is a good way to rank the genotypes. Their results were in line with our results.

Table 4. First and second IPC scores, ASVi and YSI of genotypes investigated. E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016, drought respectively.

Genotype	E1	E2	E3	E4	Genot	Yield	IPCA1	IPCA2	ASV	YSI
Gilaneh	3.6	1.86	4.560	2.090	3.028	16	-0.00568	0.49697	0.50	12
Hashemi	4.16	1.62	4.380	2.790	3.237	14	0.05785	-0.19868	0.22	17
HM5-250-12-1	4.08	1.88	4.630	2.830	3.355	11	0.02622	0.00854	0.04	5
HM5-250-6-6	4.65	1.68	4.770	2.850	3.487	7	-0.09155	-0.21534	0.26	14
HM5-250-7-6	4.67	1.64	4.330	2.730	3.343	12	0.14252	-0.31761	0.39	19
HM5-250-E-1-1	4.63	2.38	5.000	3.070	3.77	2	0.09957	0.08838	0.18	14
HM5-250-E-3-2	4.43	1.7	4.130	2.900	3.29	13	0.26653	-0.37264	0.56	14
HM5-300-3-1	4.57	1.72	5.430	2.560	3.57	5	-0.46779	0.18691	0.75	11
HM5-300-5-1	4.47	2.02	4.840	2.470	3.45	8	-0.00244	0.22021	0.22	21
Khazar	4.02	0.64	4.530	2.440	2.908	17	-0.49839	-0.40485	0.87	26
KM5-200-4-2-E	4.38	0.73	4.240	2.170	2.88	18	-0.2627	-0.41443	0.58	24
Tarom	4.78	1.58	4.490	2.040	3.223	15	0.01682	0.03186	0.04	30
TM6-230-VE-7-5-1	4.91	2.79	4.610	2.360	3.667	4	0.52112	0.45368	0.93	22
TM6-230-VE-8-4-1	4.59	2.16	4.340	2.870	3.49	6	0.37041	-0.11246	0.59	20
TM6-250-10-7-1	4.78	2.18	4.380	2.330	3.418	9	0.36154	0.13714	0.58	20
TM6-B-19-2	4.25	1.97	4.670	2.560	3.362	10	0.05395	0.15731	0.18	33
TM6-B-2-1-E	4.96	2.19	4.760	3.040	3.737	3	0.18131	-0.15748	0.32	21
TM6-B-7-1	4.76	1.97	6.190	2.720	3.91	1	-0.76928	0.4125	1.27	19
Mean	4.48	1.817	4.682	2.601	3.39	-	-	-	-	-
IPCA	0.17	0.83	-1.05	0.04	-	-	-	-	-	-

E1: 2015, normal; E2: 2015, drought, E3: 2016, normal; E4: 2016 respectively.

### CONCLUSION

Generally, in this experiment, different methods of the stability determination showed similar results and overall, HM5-250-12-1, HM5-250-E-1-1 TM6-B-19-2, HM5-300-5-1 and Hashemi were recognized as superior and high-performance genotypes among the 4 environments. In this research, ASV parameter, due to its ease of interpretation, was a suitable and powerful method for stability analysis than other methods, and it is recommended that researchers use this parameter for stability analysis. However, in the AMMI model, the calculations are a bit complicated and for data analysis, there is a need for computer software such as GENSTAT and IRRISTAT, but its results are more reliable. On the other hand, in studies where variances are not homogeneous, the use of the AMMI model is necessary for data analysis.

## ACKNOWLEDGMENT

We gratefully acknowledge the research funding provided for this project (No. 03-04-0455-9411) by Rice Research Institute of Iran, Agricultural Research, Education and Extension Organization (AREEO), Rasht, Iran.

Received, May 2<sup>th</sup>, 2018

Accepted April 28<sup>th</sup>, 2019

## REFERENCES

- ALBERTS, M.J. (2004): A comparison of statistical methods to describe genotype x environment interaction and yield stability in multi-location maize trials. The University of the Free State.
- ANANDAN, A., T., SABESAN, R., ESWARAN, G., RAJIV, N., MUTHALAGAN, R., SURESH (2009): Appraisal of environmental interaction on quality traits of rice by additive main effects and multiplicative interaction analysis. *Cereal Res. Comm.*, 37: 131-140.
- ASGARNIA, P., G.A., SAEIDI, A., REZAEI (2009): Pattern analysis of genotype× field environments interaction for grain yield in wheat using AMMI method. *Electron. J. Crop Prod.*, 2: 75-89.
- BAVANDPORI, F., J., AHMADI, S., HOSSAINI (2015): Stability analysis of bread wheat landraces and genotypes using GGE-Biplot. *J. Biodivers. Environ. Sci.*, 7: 482-489.
- BRANDIEJ, E. and B., MEVERTY (1994): Genotype× environmental interaction and stability of seed yield of oil rapeseed. *Crop Sci.*, 18: 344-353.
- CORNELIUS, P.L. and J., CROSSA (1999): Prediction assessment of shrinkage estimators of multiplicative models for multi-environment cultivar trials. *Crop Sci.*, 39: 998-1009.
- CROSSA J., P.N., FOX, W.H., PFEIFFER, S., RAJARAM and H.G., GAUCH (1991). AMMI adjustment for statistical-analysis of an International wheat yield trial. *Theor. Appl. Genet.*, 81: 27-37.
- EBDON, J.S. and H.G., GAUCH (2002). Additive main effect and multiplicative interaction analysis of national turfgrass performance trials: I. Interpretation of genotype x environment interaction. *Crop Sci.*, 42: 489-496.
- FALCONER, D.S. (1960): Introduction to quantitative genetics. Oliver And Boyd; Edinburgh; London.
- FAOSTAT (2012): Food and Agriculture Organization of the United Nations. FAOSTAT database.
- FATAHI, F. and A., YOUSEFI (2006): Evaluation of yield stability of barley genotypes (*Hordeum vulgare* L.) using repeatable stability parameters and pattern analysis of the AMMI model. *Iran. J. Agric. Sci.*, 317-326.
- FREEMAN, G. and J.M., PERKINS (1971): Environmental and genotype-environmental components of variability VIII. Relations between genotypes grown in different environments and measures of these environments. *Heredity*, 27:15.
- GHANBARI, J. and G.R., KHAJOIE NEJAD (2014): Evaluation of yield and agronomic traits of cumin (*Cuminum cyminum* L.) ecotypes in different sowing dates at Kerman region. *J. Agroecol*, 6: 142-151.
- GAUCH, H.G. (2006): Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.*, 46: 1488-1500.
- GOLLOB, H.F. (1968): A statistical model which combines features of factor analytic and analysis of variance techniques. *Psychometrika*, 33: 73115.
- KHALILY, M., M., MOGHADDAM, H., KANOUNI, E., ASHERI (2010): Dissection of drought stress as a grain production constraint of maize in Iran. *Asian J. Crop Sci.*, 2: 60-69.
- KHUSH, G. S. (2005): What it will take to feed 5.0 billion rice consumers in 2030. *Plant Mol. Biol.*, 59:1-6.
- LICHTENTHALER, H.K. (1998): The stress concept in plants: an introduction. *Ann. N.Y. Acad. Sci.*, 851:187-198.
- MOHAMMADINEJAD, G. and A., REZAI (2005) Analysis of genotype× environment interaction and study of oat (*Avena sativa* L.) genotypes pattern. *JWSS-Isfahan University of Technology*, 9: 77-89.
- PURCHASE, J. (1997): Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. The University of the Free State.

- PURCHASE, J., H., HATTING, C., VAN DEVENTER (2000): Genotype× environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance. *South Afric. J. Plant Soil*, 17: 101-107.
- REDDY, A.R., K.V., CHAITANYA, M., VIVEKANANDAN (2004): Drought-induced responses of photosynthesis and antioxidant metabolism in higher plants. *J. Plant Physiol.*, 161: 1189-1202.
- ROY, D. (2000): *Plant breeding: Analysis and exploitation of variation*. Alpha Science Int'l Ltd.
- SHAHMOHAMADI, M., H., DEHGHANI, A., YOUSEFI (2005): Additive main effects and multiplicative interaction analysis (AMMI) in barley (*Hordeum vulgare*) genotypes. *Seed and Plant*, 405-416.
- SMITH, C.W. and R.H., DILDAY (2003): *Rice: origin, history, technology, and production*, vol 3. John Wiley & Sons.
- YAN, W., M.S., KANG, B., MA, S., WOODS, P.L., CORNELIUS (2007): GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.*, 47:643-653.
- ZOBEL, R.W., M.J., WRIGHT, H.G., GAUCH (1988): Statistical analysis of a yield trial. *Agron. J.*, 80:388-393.
- VENABLES, W.N., B.D., RIPLEY (2002): *Modern Applied Statistics with S*. Fourth Edition. Springer, New York. ISBN 0-387-95457-0.
- YOUSEFI-ZONUZ, A., S., ALJANI, H., MOHAMMADI, A., RAFAT, H., DAGHIGH KIA (2013): Estimation of genetic parameters for productive and reproductive traits in Esfahan native chickens. *J. Livest. Sci. Techno.*, 1:34-38.
- ZEREHDARAN, S., A.L.J., VEREIJKEN, J.A.M., VAN ARENDONK, E.H., VAN DER WAAIJT (2004): Estimation of genetic parameters for fat deposition and carcass traits in broilers. *Poultry Science.*, 83:521–525.

**ANALIZA GENETIČKE VARIJACIJE I STABILNOSTI MUTANTNIH LINIJA  
PIRINČA KORIŠĆENJEM AMMI MODELA U NORMALNIM  
I USLOVIMA STRESA**

Ali Akbar EBADI\*, Mohammad Taher HALLAJIAN, Mojtaba KORDROSTAMI

Istraživački Institut za pirinač, Poljoprivrednaistraživačka, obrazovna i savetodavna organizacija  
(AREEO), Rasht, Iran.

Izvod

Ovo istraživanje je sprovedeno kako bi se ispitala interakcija genotip x spoljašnja sredina i analiza stabilnosti 14 mutantnih linija (sa njihovim roditeljskim linijama). Istraživanje je sprovedeno tokom dve godine, 2015-16, u dve spoljašnje sredine (normalnoj i stresu suše), u Rasht-u. Na osnovu rezultata kombinovane analize varijanse, genotipa i spoljašnje sredine, interakcija genotip x spoljašnja sredina je bila značajna na nivou verovatnoće od 1%. Značajnost efekta spoljašnje sredine ukazala je na njihov efekat na performase genotipova. Stoga je analiza stabilnosti izvedena različitim metodama merenja stabilnosti. Rezultati ANOVA-e za aditivni glavni efekat i multiplikativnu interakciju (AMMI) pokazali su glavne efekte genotipa i spoljašnje sredine i efekte genotip × spoljašnja sredina sa nivoom verovatnoće od 1%. Na osnovu AMMI analize, TM6-230-VE-7-5-1, TM6-230-VE-8-4-1, Khazar i KM5-200-4-2-1, imali su pozitivne i negativne interakcije. Analiza stabilnosti određena kroz metod AMMI nivoa stabilnosti (ASV), pokazala je da HM5-250-12-1, Tarom, HM5-250-E-1-1, TM6-B-19-2, Hashemi i HM5-300-5-1, predstavljaju najstabilnije kultivare.

Primljeno 02.V.2018.

Odobreno 28. IV. 2019.