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## Using AMMI model and its parameters for yield stability analysis of rice (*Oryza sativa* L.) advanced mutant genotypes of Tarron-Mahalli

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### Abstract

Genotype×environment interaction is one of the most important production challenges for plant breeders. Line selection with desirable yield is severely affected by genotype×environment interaction. In order to consider this interaction, 13 M8 mutant genotypes derived from Tarron-Mahalli rice land races along with 3 control, Tarron-Mahalli, Tarron-Jelodar and Neda were used to evaluate their grain yield stability and adaptability using a RCBD design with 3 replications and two regions in Mazandaran province in 2016-2017. Analyses were carried out using the AMMI method. Effects of genotype, environment and their interactions were significant. Two components of the first model covered more than 91% of the interaction variance. The bi-plot showed that genotypes 15, 18, 31, 30 and 33, Tarron-Jelodar and Tarron-Mahalli were the stable genotypes. Results of AMMI model statistics showed that according to AMGE statistics, Neda, genotypes 26 and 31, based on ASI, MASI and MASV statistics, genotypes 33, 26 and 30 and based on AVAMGE, DA, FA, SIPC and ZA statistics, genotypes 33, 30 and 31 had the highest stabilities, respectively. According to the results of the indices of simultaneous selection for grain yield and stability for each of AMMI statistics it is observed that genotypes 33, 31, Tarron-Jelodar, genotypes 26

and Neda cultivar are identified as the stable high yielding genotypes. Results showed that most of stability statistics based on the AMMI model are appropriate stability indices for identifying stable genotype with high grain yield.

**Key words:** AMMI model, Rice mutant, Simultaneous selection, Stability analysis.

### INTRODUCTION

Rice is an important and popular food plant worldwide and more than half of the world population consume rice as their daily food (Park *et al.*, 2014; Zuo and Li, 2014; Nili *et al.*, 2017). According to the geometric growth rate of the world population, improving rice yield is very important (Oladosu *et al.*, 2017).

Inducing mutation is a method for increasing genetic diversity by which we can detect agronomical and economically useful alleles in crop genomes and then select desirable mutant lines in the following generations (Samadi-Gorji *et al.*, 2015). Induced mutation has been recorded as an effective method to improve production in rice and many other crop varieties. Many characteristics of rice have been improved by mutation, resulting in a high yield, a shorter duration and a shorter height (Xuan *et al.*, 2019).

Genotype×environment interaction reduces the

correlation between phenotypic and genotypic values, and therefore, the difficulty in identifying truly superior genotypes across environments is magnified (Kang, 1998). The genotype×environment interaction provides valuable information for cultivar performance in different environments and has an important role on stabilizing breeding materials (Karadavut *et al.*, 2010). Genotype×environment interaction points out the relative yield of cultivars at different environments. It implies the difference in genotype classification, in the other words, it emphasizes the different expression levels in genetic variations among environments (Li *et al.*, 2017).

Additive main effect and multiplicative interaction (AMMI) model or consideration of cumulative main effects and multiplicative interactions is a multivariate method for the consideration of genotype stability that has comprehensively been used for the estimation of genotype×environment interaction and a number of stable genotypes (Askarinia *et al.*, 2009). The reason behind comprehensive usage of AMMI method is that this model considers a great part of sum of squares in interactions and separates main effects and interactions (Ebdon and Gauch, 2002). Moreover, the results of this method can be used for breeding programs with specific adaptation and desirable environmental selection (Gauche and Zoble, 1997). AMMI method is a combining analysis of variance and principal components analysis that can be used for the consideration of genotypes stability. In AMMI method using analysis of variance, the main and cumulative effects of genotype and environment will be firstly estimated and then, the multiplicative interactions (non-cumulative) will be analyzed by principal components analysis (Zoble *et al.*, 1988).

Oladosu *et al.* 2017 considered genotype×environment interaction and yield stability of 15 rice genotypes including 12 mutant lines and 3 registered cultivars in ten environments in Malaysia. The combined analysis of variance showed that main effects of genotypes, environments and their interactions for all traits (yield and its components) were significant. They classified the rice genotypes into 3 main groups based on multivariate stability parameters of AMMI model, so that, the high stability with high yielding varieties were classified into the first group in which they had comprehensive adaptation with diverse environments. Musila *et al.* (2017) performed a study using 56 genotypes including 45 from an F3 population together with their parents and one control genotype in order to consider genotype×environment

interaction for grain yield of rice and identification of high yielding and stable genotypes, under humidity stress in the generative stage (3 regions) and non-humidity stress (one region) in Kenia shore. They used cumulative main effects and multiplicative genotype×environment interactions (AMMI) and genotypes 39 and 40 were identified as the most stable and high yielding. Moreover, they pointed out that these two genotypes with general adaptation are candidates for carrying out intra population simultaneous homozygosity selection toward producing pure lines with desirable yield. Sharifi *et al.* (2017) in a study evaluated genotype×environment interaction in promised genotypes of rice using AMMI model. Results of their combined analysis of variance implied that the main effects of G, E and their interaction for grain yield were significant. They expressed that the significant genotype×environment interaction imply the existence of different responses of genotypes in different environments and emphasized on its severe effects on genotypic yield in different environments. Nevertheless, according to the first Eigen value (EV), genotypes 1, 6, 2 and 9, the second I principal components (SIPC) genotypes 6, 5 and 2, based on AMMI stability value (ASV) genotype 6 and based on bi-plot feature, genotype 6 were known as the most stable genotypes, respectively. Seyou *et al.* (2016) tested 14 narica rice genotypes based on randomized complete block design with 3 replications in 3 regions at west Ethiopia in 2009 and 2010 in order to consider genotype×environment interaction. They found significant differences in main effects of genotypes, environments and their interactions by combined analysis of variance at 1% level and reported that genotype×environment interaction cover about 91.4% of the total variations. Their results showed that in AMMI model the interaction was explained via two significant principal components.

This research aimed to determine genotype×environment interactions for grain yield of progressive mutant genotypes derived from mutation induction in rice cultivar Tarrow-Mahalli and identification of adaptable genotypes in different environments and determining stable genotypes using AMMI model and its related statistics.

## MATERIALS AND METHODS

Thirteen mutant genotypes (mutated by ethyl methane sulfonate at 150 mM) from the eighth generations derived from Tarrow-Mahalli together with 3 controls of Tarrow-Mahalli, two high yielding cultivars of

Tarrom-Jelodar and Neda were evaluated for stability and adaptation of grain yield using randomized complete block design. Tarrom-Mahalli cultivar has the desirable grain quality but has low yield and Tarrom-Jelodar has the desirable quality. Experiments were carried out with three replications in two regions of Mazandaran province (Sari and Tonkabon) in two years (2016 and 2017).

The detailed description of these test regions is given in Table 1. Each plot included 7 rows with 1.6 m length and planting interval of 25×25 cm.

Stability considerations were carried out using AMMI analysis in a unique model of analysis of variance that makes a combination of cumulative and multiplicative parameters (Gauche, 1992). The model is:

$$(1) \quad Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

That  $Y_{ij}$  is the yield of  $i^{th}$  genotype in  $j^{th}$  environment,  $\mu$  is grand mean,  $g_i$  is the yield deviation of  $i^{th}$  genotypes from grand mean,  $e_j$  is yield deviation of  $j^{th}$  environment from grand mean,  $N$  is the number of residual principal components in AMMI model,  $\lambda_n$  is  $n^{th}$  Eigen value of principal component axis,  $\gamma_{in}$  is  $n^{th}$  Eigen vector of principal component axis of  $i^{th}$  genotype,  $\delta_{jn}$  is  $n^{th}$  Eigen vector of principal component axis of  $j^{th}$  environment,  $\rho_{ij}$  residual values of  $i^{th}$  genotype in  $j^{th}$  environment, The multiplicative AMMI parameters means that  $\lambda_n^{0.5} \gamma_{in}$  and  $\lambda_n^{0.5} \delta_{jn}$  of PCA (principle component analysis) scores for interactions or IPCA for  $i^{th}$  genotype and  $j^{th}$  environment, respectively.

In this study, 12 statistics derived from AMMI model were used for the identification of stable genotype (s). Moreover, two indices of Ii and GSI (both are represented in Table 2) proposed by Rao and Prabhakaran (2005) and Farshadfar (2008), were separately calculated for the simultaneous selection of yield and stability based on each statistic (Table 2).

In  $I_i$  index the  $\alpha$  value is the ratio of the weights given to the stability component ( $w_2$ ) and yield ( $w_1$ ) with a restriction that  $w_1 + w_2 = 1$ . The weights considered in index are in general, as per plant breeders' requirement by considering the values of  $\alpha$  as 1 ( $w_1 = w_2 = 0.5$ ), 0.66 ( $w_1 = 0.7, w_2 = 0.3$ ) (Rao and Prabhakaran 2005). Software R 3.5.2 (<https://www.r-project.org>) including package ammistability was used for data analysis.

**Table 1.** The environmental characterization of 16 rice genotypes.

Region	Altitude (m asl)	Longitude	Latitude	Soil texture	Clay (%)	Silt (%)	Sand (%)	Cu (ppm)	Mn (ppm)	Zn (ppm)	Fe (ppm)	K (ppm)	P (ppm)	N (%)	C (%)	EC (mmols/s)	pH
Sari	-11	53°4' E	36° 39' N	Silty clay loam	25	43	32	4	23	2	37	269	20	0.17	1.7	1.17	7.6
Tonekabon	-20	40° 50' E	36° 54' N	Silty clay	45	45	10	5	15	0.5	32	92	4	0.34	3.9	0.53	7.9

**Table 2.** Parameters, indices and the equations used for the calculation of simultaneous selection.

Parameters and indices	Equation	Author(s)
SIPC <sub>i</sub>	$\sum_{n=1}^N  \lambda_n^{0.5} \gamma_{in} $	Sneller <i>et al.</i> , 1997
AMGE	$\sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn}$	Sneller <i>et al.</i> , 1997
EV	$\sum_{n=1}^N \frac{\gamma_{in}^2}{n}$	Zobel, 1994
D <sub>a</sub>	$\sqrt{\sum_{n=1}^N (\lambda_n \gamma_{in})^2}$	Annicchiarico, 1997
ASTAB	$\sum_{n=1}^{N/} \lambda_n \gamma_{in}^2$	Rao and Prabhakaran, 2005
AVAMGE	$\sum_{j=1}^E \sum_{n=1}^{N/}  \lambda_n \gamma_{in} \delta_{jn} $	Zali <i>et al.</i> , 2012
D <sub>z</sub>	$\sum_{n=1}^{N/} \gamma_{in}^2$	Zhang <i>et al.</i> , 1998
MASI*	$\sqrt{\sum_{n=1}^{N/} PC_n^2 \times \theta_1^2}$	Ajay <i>et al.</i> , 2018
MASV	$\sqrt{\sum_{n=1}^{N/-1} \left( \frac{SSIPC_n}{SSIPC_{n+1}} \right) \times (PC_n)^2 + (PC_{N/})^2}$	Zali <i>et al.</i> , 2012
Z <sub>a</sub>	$\sum_{i=1}^{N/}  \theta_n \gamma_{in} $	Zali <i>et al.</i> , 2012
ASI	$\sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$	Jambhulkar <i>et al.</i> , 2014
FA	$\sum_{n=1}^{N/} \lambda_n^2 \gamma_{in}^2$	Raju, 2002
I <sub>I</sub>	$\frac{\bar{Y}_i}{\bar{Y}_{..}} + \alpha \frac{1}{\frac{1}{T} \sum_{i=1}^T \frac{1}{SP_i}}$	Rao and Prabhakaran, 2005
GSI**	$R_{SP} + R_Y$	Farshadfar, 2008

AMGE: Sum Across Environments of GEI Modelled by AMMI, ASI: AMMI Stability Index, ASTAB: AMMI Based Stability Parameter, AVAMGE: Sum Across Environments of Absolute Value of GEI Modelled by AMMI, DA: Annicchiarico's D Parameter, DZ: Zhang's D Parameter, EV: Averages of the Squared Eigenvector Values, FA: Stability Measure Based on Fitted AMMI Model, MASI: Modified AMMI Stability Index, MASV: Modified AMMI Stability Value, SIPC: Sums of the Absolute Value of the IPC Scores, Za: Absolute Value of the Relative Contribution of IPCAs to the Interaction, GSI: Genotype stability index.

\*θ: In MASI, Za and ASI is the percentage sum of squares explained by the *n*th principal component interaction effect.

\*\**R*<sub>SP</sub> is the stability parameter/index rank of the genotype and *R*<sub>Y</sub> is the mean yield rank of the genotype.

**RESULTS**

Grain yield analysis of variance for rice genotypes based on AMMI model showed that the random main effect of environments, the fixed main effect of genotypes and genotype×environment interactions were significant (Table 3). Results showed that 13.46, 44.14% and 21.51% of total sum of squares were related to environmental effects, genotypic effects and genotype×environment interactions, respectively. AMMI model for separating genotype×environment interactions showed that only two first principal components were significant.

The first interaction principal component (IPCA1) had the highest contribution (73.1%) in the genotype×environment interaction and the first two components (significant) totally expressed 92.1% of sum of squares of genotype×environment interaction

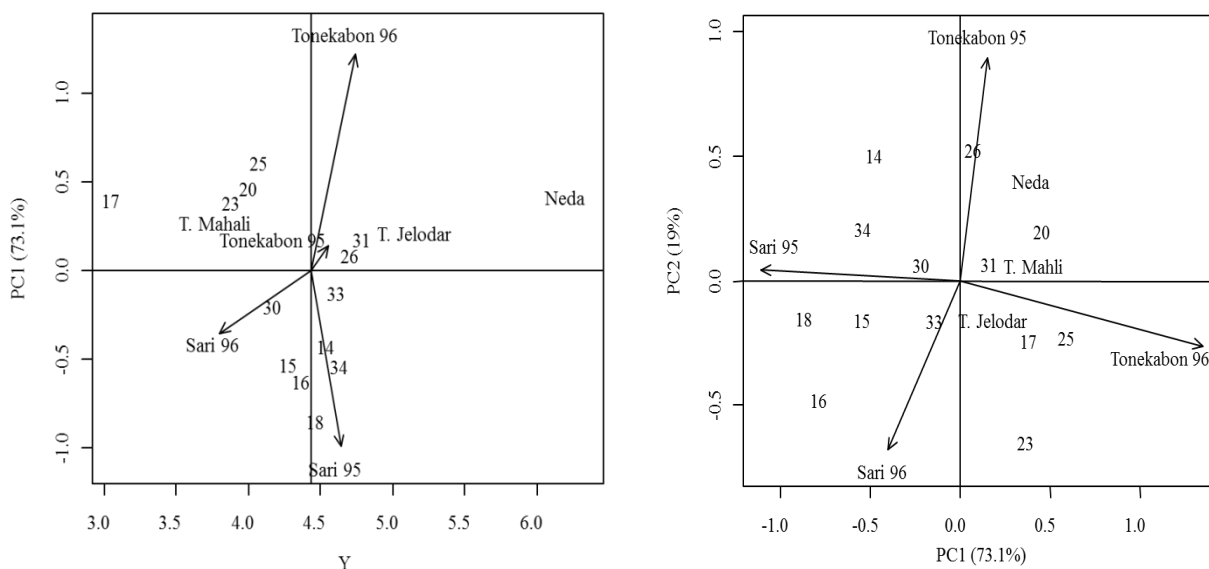
(Table 3). Thus, model AMMI2 was used because of significant mean of squares for the two principal components of genotype×environment interactions.

In order to consider yield stability and special adaptation of genotypes with the studied regions, the yield bi-plot with the first principal component (Figure 1, Left) and bi-plot of the first two principal components (Figure 1, Right) were used.

In regard to bi-plot diagram (Figure 1, Left) genotypes 26, 30, 33, 31 and Tarrom-Jelodar in addition to having a higher performance than gross mean, had also less principal component coefficients for genotype×environment interaction (positive or negative). Therefore, they were identified as genotypes with general adaptation for all environments. Three environments of Tonkabon in years 2016 and 2017 and Sari in year 2016 had higher performances

**Table 3.** ANOVA of genotype, environment and genotype×environment interactions of grain yield.

Source	df	SS	MS	TS (%)	G×E-SS (%)
ENV	3	26.68	8.89**	13.46	
REP(ENV)	8	4.43	0.55	2.24	
GEN	15	87.49	5.83**	44.14	
ENV:GEN	45	42.64	.94**	21.51	
PC1	17	31.17	1.83**		73.1
PC2	15	8.11	0.54*		19.0
PC3	13	3.36	0.25 <sup>ns</sup>		7.9
Residuals	120	36.95	0.3	18.64	
Total	191	198.2			



**Figure 1.** AMMI-1 model bi-plot for PC1 and grain yield of 16 rice genotypes in 4 environments (Left). AMMI-2 model bi-plot for IPCA1 and IPCA2 for 16 rice genotypes in 4 environments (Right).



than gross mean and by considering the Tonkabon environment vector length in 2016, the least value for genotype×environment interaction was observed based on the first principal component.

According to Figure 1 (Right), genotypes 15, 18, 31, 30, 33, Tarron-Jelodar and Tarron-Mahalli were closer to axis center in comparison with the other genotypes (bi-plot). In the other words, these genotypes showed the least variations and were considered as the most stable genotypes. Since genotype 23 is located far from the axis center, it has no suitable general stability. However, it, together with genotype 25, have suitable specific adaptabilities with environment Tonkabon 95.

Accordingly, genotypes 14, 34 and 18 with environment Sari 95 and genotype 16 with environment Sari 96 had suitable specific adaptabilities.

Stability statistics of AMMI and their classification are demonstrated in Tables 4 and 5, respectively. According to AMGE stability statistics, the highest stability was identified with the less amount of this statistic for genotypes Neda, 26 and 31. Genotype 17 and the genotypes with the highest values for this statistic were introduced as the most unstable genotypes. According to statistics ASI, MASI and MASV, genotypes 33, 26 and 30 with the least values for these three statistics had the highest stabilities. Meanwhile,

**Table 4.** Values of AMMI stability parameters and mean grain yield for 16 rice genotypes across 4 environments.

Genotype	AMGE	ASI	AVAMGE	DA	DZ	EV	FA	MASI	MASV	SIPC	ZA	ASTAB	Y
Gen.14	-1.388E-	0.344	1.937	1.04	0.47	0.112	1.09	0.343	1.806	0.967	0.26	0.470	4.5
Gen.15	5.551E-17	0.380	1.761	0.94	0.31	0.048	0.90	0.379	1.995	0.664	0.23	0.290	4.2
Gen.16	1.110E-16	0.457	2.498	1.25	0.49	0.124	1.57	0.457	2.402	1.079	0.31	0.594	4.5
Gen.17	1.110E-16	0.304	1.268	0.79	0.29	0.042	0.63	0.304	1.599	0.643	0.20	0.223	3.0
Gen.18	0.000E+0	0.613	2.714	1.51	0.47	0.114	2.29	0.613	3.221	0.978	0.36	0.722	4.4
Gen.20	-2.776E-	0.354	1.740	0.90	0.31	0.049	0.81	0.354	1.860	0.691	0.22	0.276	4.0
Gen.23	1.665E-16	0.313	2.085	1.08	0.54	0.147	1.11	0.313	1.646	1.032	0.25	0.562	3.8
Gen.25	2.776E-17	0.454	1.795	1.14	0.38	0.073	1.30	0.454	2.386	0.832	0.28	0.429	4.0
Gen.26	-1.631E-	0.127	1.106	0.71	0.42	0.090	0.51	0.127	0.668	0.642	0.12	0.302	4.7
Gen.30	-3.469E-	0.138	0.551	0.35	0.11	0.007	0.12	0.138	0.726	0.262	0.08	0.040	4.1
Gen.31	-2.776E-	0.140	0.684	0.35	0.12	0.007	0.12	0.140	0.738	0.269	0.08	0.043	4.8
Gen.33	5.551E-17	0.088	0.548	0.27	0.13	0.008	0.07	0.087	0.461	0.260	0.06	0.035	4.6
Gen.34	6.245E-17	0.375	1.506	0.95	0.33	0.055	0.91	0.375	1.971	0.731	0.24	0.309	4.6
T.Jelodar	6.939E-17	0.169	0.734	0.44	0.16	0.014	0.20	0.169	0.888	0.371	0.11	0.073	4.9
T.Mahali	-8.327E-	0.274	1.223	0.67	0.21	0.023	0.45	0.273	1.438	0.444	0.16	0.145	3.7
Neda	-2.220E-	0.324	1.872	0.93	0.40	0.080	0.87	0.323	1.700	0.843	0.23	0.356	6.3

**Table 5.** Ranks of AMMI stability parameters and mean grain yield for 16 rice genotypes across 4 environments.

Genotype	AMGE	ASI	AVAMGE	DA	DZ	EV	FA	MASI	MASV	SIPC	ZA	ASTAB	Y
Gen.14	4	10	13	12	13	13	12	10	10	13	13	13	8
Gen.15	12	13	10	10	7	7	10	13	13	8	9	8	10
Gen.16	14	15	15	15	15	15	15	15	15	16	15	15	7
Gen.17	16	7	7	7	6	6	7	7	7	7	7	6	16
Gen.18	8.5	16	16	16	14	14	16	16	16	14	16	16	9
Gen.20	5	11	9	8	8	8	8	11	11	9	8	7	13
Gen.23	15	8	14	13	16	16	13	8	8	15	12	14	14
Gen.25	12	14	11	14	10	10	14	14	14	11	14	12	12
Gen.26	2	2	5	6	12	12	6	2	2	6	5	9	4
Gen.30	10	3	2	2	1	1	2	3	3	2	2	2	11
Gen.31	3	4	3	3	2	2	3	4	4	3	3	3	3
Gen.33	7	1	1	1	3	3	1	1	1	1	1	1	6
Gen.34	8.5	12	8	11	9	9	11	12	12	10	11	10	5
T.Jelodar	6	5	4	4	4	4	4	5	5	4	4	4	2
T.Mahali	11	6	6	5	5	5	5	6	6	5	6	5	15
Neda	1	9	12	9	11	11	9	9	9	12	10	11	1

genotype 18 was the most unstable genotype. Similar results were obtained using AVAMGE, DA, FA, SIPC and ZA statistics, so that, genotypes 33, 30 and 31 with the least values for these statistics were the most stable genotypes. Based on SIPC, genotype 16 was identified as the most unstable genotype but according to the other stability indices, genotype 18 was known as the most unstable genotype. According to DZ and EV, genotypes 30, 31 and 33 were the most stable and genotype 23 was the most unstable genotype, respectively.

Results obtained for the yield stability of genotypes using simultaneous selection for grain yield and stability based on each of AMMI statistics and their classification are demonstrated in Tables 6 and 7, respectively. Using Ii and GSI indices (introduced by Rao and Prabhakaran, 2005; Farshadfar, 2008, respectively), in which each AMMI statistic is separately calculated, genotypes 33, 31, Tarron-Jelodar, 26 and Neda were identified as high yielding and the most stable genotypes. While, genotypes 17, 18 and 23 were low yielding and unstable genotypes, based on the simultaneous selection index.

## DISCUSSION

Results showed that the principal components of genotype, environment and their interactions were significant for grain yield. Mostafavi *et al.* (2014); Akter *et al.* (2015) and Sharifi *et al.* (2017) reported similar results for grain yield in rice. Genotype effects had the highest contribution (4.14%) in sum of squares of the model. The high sum of squares implied that there were great variations among the studied genotypes, because of their differences in mean yield (Mukherjee *et al.*, 2013). Also, genotype×environment interaction consisted of 24.51% of the total sum of square and it shows importance of evaluation of the genotype×environment interaction. The AMMI model of genotype×environment interaction was analyzed into its constructed components. In this regard, the first two principal components were significant and in overall included 62.1% of the interaction variations. Mostafavi *et al.* (2014) reported similar results and found that totally 66% of interaction variance belonged to the first two principal components and Lakew *et al.* (2014) found 79.92% contribution for genotype×environment variation.

To identify a genotype with general or specific adaptability, study of the degree and feature of genotype×environment interaction are very important. Therefore, scatter diagram of genotypes

and environments on the first two components of AMMI interaction model demonstrated the feature of genotype and environments dependence. Spaces from bi-plot center illustrate the amount of interaction created by genotypes in environments or by environments in genotypes (Yan and Kang, 2003). Therefore, the closer genotypes to the center of bi-plot, the less genotype×environment interaction and the more general stability will be recommendable for most environments. In contrast, genotypes located far from the center have specific adaptabilities (Aghaei-Sarbarze *et al.*, 2012). According to the results, genotypes 30, 31, 31 and Tarron Jelodar had the highest yield stability in all environments and genotypes 15, 16 and 18 showed specific adaptability to the Sari 96 environment. Sharifi *et al.* (2017); Seyou *et al.* (2016); Ogunbayo *et al.* (2014); Bose *et al.* (2014); Tarang *et al.* (2013) in rice and Damavandi-Kamali, 2007 in cotton introduced stable genotypes with specific adaptability to different environments using AMMI model and bi-plot results.

If a genotype and environment have similar or different symbols for the first component, then they will have either a positive or negative interaction, respectively (Mostafavi *et al.*, 2014). Tonkabon 95 and 96 environments had a positive interaction with genotypes Neda, Tarron-Jelodar, 31 and 26 and a negative interaction with genotypes 33, 14, 34, 18 and 16. In this diagram genotypes and environments located in the direction of a vertical line had similar yields and those located in the direction of a horizontal line, had similar interactions. For example, genotypes 33 and 34 and Sari 95 had similar yields and genotypes 34 and 15 had similar interactions. Genotypes with low yield but a positive interaction with poor environments, are suitable and adaptable for those environments. In this study genotypes 30 and 15 are good examples for this case (Mostafavi *et al.*, 2014; Rahayu, 2020).

Values of a number of IPCAs relevant to genotypes in an environment had both (positive and negative) symbols (Figure 1). Consequently, genotypes with a high positive IPCA had a positive interaction in a number of environments, and with high negative IPCA symbols showed a negative interaction in other environments. For this reason, the high variation in their genotype×environment interaction, changed them as unstable genotypes (Boss *et al.*, 2014; Akter *et al.*, 2019). Results of AMMI model showed that based on IPCA, genotypes 26, 33, 30 and 31 with a minimum amount had the highest yield stability.

**Table 6.** Simultaneous selection indices for yield and stability of each AMMI stability parameters for 16 rice genotypes across 4 environments.

Genotype	AMGE		ASI		AVAMGE		DA		DZ		EV							
	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI						
	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43						
Gen.14	1.023	1.023	12	1.690	1.310	18	1.629	1.284	21	1.659	1.296	20	1.558	1.253	21	1.241	1.117	21
Gen.15	0.965	0.965	21	1.568	1.224	23	1.631	1.251	20	1.665	1.265	20	1.783	1.316	17	1.473	1.183	17
Gen.16	1.024	1.024	22	1.525	1.239	22	1.493	1.225	22	1.553	1.251	22	1.532	1.242	22	1.220	1.108	22
Gen.17	0.689	0.689	31	1.441	1.012	23	1.614	1.086	23	1.522	1.047	23	1.558	1.062	22	1.263	0.935	22
Gen.18	-	-	17	1.380	1.166	25	1.438	1.192	25	1.444	1.194	25	1.535	1.234	23	1.219	1.097	23
Gen.20	0.903	0.903	14	1.550	1.181	24	1.577	1.193	22	1.637	1.218	21	1.711	1.250	21	1.399	1.116	21
Gen.23	0.876	0.876	30	1.607	1.190	22	1.438	1.117	28	1.489	1.139	27	1.342	1.076	30	1.041	0.946	30
Gen.25	0.919	0.919	21	1.424	1.136	26	1.573	1.200	23	1.500	1.169	26	1.582	1.204	22	1.253	1.063	22
Gen.26	1.061	1.061	7	2.865	1.837	6	2.122	1.519	9	1.988	1.460	10	1.658	1.318	16	1.332	1.177	16
Gen.30	0.939	0.939	18	2.596	1.652	14	3.067	1.854	13	2.832	1.753	13	3.058	1.850	12	4.351	2.406	12
Gen.31	1.088	1.088	9	2.719	1.789	7	2.802	1.825	6	2.946	1.886	6	3.154	1.976	5	4.329	2.481	5
Gen.33	1.047	1.047	17	3.657	2.169	7	3.187	1.967	7	3.437	2.074	7	2.986	1.881	9	3.902	2.275	9
Gen.34	1.053	1.053	17	1.663	1.315	17	1.831	1.387	13	1.745	1.350	16	1.816	1.381	14	1.496	1.243	14
T.Jelodar	1.126	1.126	15	2.482	1.709	7	2.725	1.814	6	2.604	1.762	6	2.627	1.771	6	2.837	1.861	6
T.Mahali	0.853	0.853	20	1.690	1.210	21	1.813	1.265	21	1.833	1.274	20	2.031	1.359	20	1.907	1.306	20
Neda	1.427	1.427	3	2.135	1.731	10	2.054	1.696	13	2.136	1.732	10	2.058	1.698	12	1.730	1.557	12



**Table 6 (Continued).** Simultaneous selection indices for yield and stability of each AMMI stability parameters for 16 rice genotypes across 4 environments.

Genotype	FA		MASI		MASV		SIPC		ZA		ASTAB							
	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI	Rao	GSI						
Gen.14	1.330	1.155	20	1.690	1.310	18	1.690	1.310	18	1.5739	1.260	21	1.641	1.289	21	1.290	1.138	21
Gen.15	1.337	1.124	20	1.568	1.224	23	1.568	1.224	23	1.7664	1.309	18	1.655	1.261	19	1.397	1.150	18
Gen.16	1.237	1.115	22	1.525	1.239	22	1.525	1.239	22	1.5167	1.235	23	1.527	1.240	22	1.234	1.114	22
Gen.17	1.216	0.915	23	1.441	1.012	23	1.441	1.012	23	1.5160	1.044	23	1.483	1.030	23	1.249	0.093	22
Gen.18	1.152	0.107	25	1.380	1.166	25	1.380	1.167	25	1.5503	1.240	23	1.449	1.197	25	1.179	1.080	25
Gen.20	1.312	1.079	21	1.550	1.181	24	1.550	1.181	24	1.6434	1.234	22	1.610	1.207	21	1.357	1.098	20
Gen.23	1.162	0.998	27	1.607	1.190	22	1.607	1.190	22	1.3912	1.097	29	1.504	1.146	26	1.098	0.971	28
Gen.25	1.175	1.029	26	1.424	1.136	26	1.424	1.136	26	1.5588	1.194	23	1.485	1.163	26	1.211	1.045	24
Gen.26	1.714	1.342	10	2.865	1.837	6	2.863	1.836	6	1.8898	1.417	10	2.380	1.628	9	1.476	1.239	13
Gen.30	3.660	2.109	13	2.596	1.652	14	2.597	1.652	14	2.9664	1.810	13	2.771	1.727	13	3.999	2.255	13
Gen.31	3.710	2.215	6	2.719	1.789	7	2.720	1.789	7	3.0599	1.935	6	2.882	1.859	6	4.021	2.349	6
Gen.33	5.386	2.913	7	3.657	2.169	7	3.657	2.169	7	3.0881	1.924	7	3.404	2.060	7	4.673	2.606	7
Gen.34	1.417	1.209	16	1.663	1.315	17	1.663	1.315	17	1.7807	1.365	15	1.720	1.339	16	1.458	1.226	15
T.Jelodar	2.790	1.842	6	0.482	1.709	7	2.482	1.709	7	2.5595	1.742	6	2.533	1.731	6	2.853	1.868	6
T.Mahali	1.583	1.167	20	1.690	1.213	21	1.690	1.213	21	2.0503	1.367	20	1.840	1.277	21	1.718	1.225	20
Neda	1.809	1.591	10	2.135	1.731	10	2.135	1.731	10	2.0580	1.698	13	2.107	1.719	11	1.779	1.578	12

**Table 7.** Ranks of Simultaneous selection indices for yield and stability of each AMMI stability parameters for 16 rice genotypes across 4 environments.

Genotype	AMGE		ASI		AVAMGE		DA		DZ		EV			
	Rao		GSI		Rao		GSI		Rao		GSI			
	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43		
Gen.14	8	8	4	7	8	6	10	8	6	12	10	13	10	9
Gen.15	9	9	11	11	10	5	10	10	6	8	9	8	8	7
Gen.16	7	7	13	13	9	7	12	11	8	15	12	14	12	10
Gen.17	15	15	15	14	16	8	16	16	9	12	16	16	16	10
Gen.18	-	-	8	16	14	9	14	13	10	14	13	15	13	11
Gen.20	12	12	5	12	13	8	13	12	7	9	11	9	11	9
Gen.23	13	13	14	10	12	10	15	15	12	16	15	16	15	12
Gen.25	11	11	12	15	15	9	14	14	11	11	14	11	14	10
Gen.26	4	4	2	2	2	3	6	6	3	8	8	10	9	6
Gen.30	10	10	9	4	6	4	2	4	4	2	3	8	2	4
Gen.31	3	3	3	3	3	1	3	2	1	1	1	1	1	1
Gen.33	6	6	7	1	1	2	1	1	2	3	2	3	3	3
Gen.34	5	5	8	9	7	4	7	7	5	6	6	7	7	5
T. Jelodan	2	2	6	5	5	1	4	4	1	4	4	4	4	2
T. Mahali	14	14	10	7	11	7	7	9	6	7	7	5	6	8
Neda	1	1	1	6	4	4	5	5	3	5	5	6	5	4

**Table 7 (continued).** Ranks of Simultaneous selection indices for Yield and Stability of each AMMI stability parameters for 16 rice genotypes across 4 environments.

Genotype	FA		MASI		MASV		SIPC		ZA		ASTAB		
	Rao		GSI		Rao		GSI		Rao		GSI		
	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	a=1	a=0.43	
Gen.14	10	9	7	6	8	6	8	6	11	10	8	10	8
Gen.15	9	10	7	10	10	9	10	9	9	10	8	10	6
Gen.16	12	11	9	12	9	8	10	14	12	11	7	9	9
Gen.17	13	15	10	13	16	9	10	15	16	16	10	12	16
Gen.18	16	16	11	15	14	11	11	13	11	13	11	15	13
Gen.20	11	12	8	11	13	10	10	10	13	12	11	12	12
Gen.23	15	14	13	9	12	8	10	16	15	15	8	16	15
Gen.25	14	13	12	14	15	12	12	12	14	14	12	14	14
Gen.26	6	6	3	2	2	1	2	7	6	6	5	7	6
Gen.30	3	3	5	4	6	4	4	3	3	4	3	3	3
Gen.31	2	2	1	4	3	2	3	2	1	2	2	2	2
Gen.33	1	1	2	3	3	2	1	2	1	1	1	1	1
Gen.34	8	7	6	1	1	5	5	8	4	7	3	8	4
T.Jelodar	4	4	1	8	7	2	2	4	4	4	1	4	4
T.Mahali	7	8	7	6	5	7	5	7	7	7	7	6	8
Neda	5	5	4	5	4	3	4	5	5	5	4	5	5

According to the second principal component of genotype×environment interaction, the highest grain yield stabilities were attributed to genotypes Tarron-Jelodar, Tarron-Mahalli, 30, 31, 33, 15 and 18. Alemu *et al.* (2017); and Ebadi *et al.* (2007) used values of IPCA for selecting stable genotypes. Moreover, Mofidian and Moghaddam (2013) and Ghodrati-Niari and Abdolshahi (2014) used principal components of genotype×environment interaction, in medicago ecotypes and in bread wheat, respectively.

This study demonstrated that AMMI stability parameters based on AMGE statistics, can identify high grain yielding genotypes as the suitable stable genotypes, also verified by Sabaghnia *et al.* (2013) in durum wheat genotypes.

Plant breeders pay the first attention only to genotypic stability (static concept) for genotypic identification with fixed yield. However, they propose then simultaneous consideration of mean yield and stability (dynamic conception) (Dehghani *et al.*, 2010). MASV statistic is profited from dynamic concept of stability and can be useful for simultaneous selection of yield and stability. Results of current study showed agreement with those of Mohammadi *et al.* (2015) who reported that the AMMI statistic is trustable for explaining genotype×environment interaction and simultaneous selection of yield and stability.

Results of AVAMGE statistic has excessive similarity with that of the other AMMI statistics (DA, FA, SIPC, ZA, DZ, EV) that is calculated based on the first two IPCAs. Achievements of this work is similar to the findings of Sharifi *et al.* (2017) and Karimzadeh *et al.* (2016). They showed that the most punctual model in AMMI is predictable using the first two IPCAs. In spite of various stability methods, the AMMI model provided useful information for reaching the certain results (Sharifi *et al.*, 2017). In the present study most of stable genotypes based on twelve AMMI stability statistics, had moderate yield performance, although Ajay *et al.* (2020) reported that according to these twelve AMMI stability parameters, high-yielding genotypes can be identified specially with SIPC, MASI and MASV.

Considering that the stable genotypes have not necessarily the highest yield, the stability parameters cannot be accounted as the only criteria for selecting genotypes (Mohammadi *et al.*, 2007; Mohammadi and Amiri, 2008; Farshadfar *et al.*, 2011). Therefore, there is a need to determine characteristics that use mean yield and stability statistics simultaneously in a unique index to select high yielding and stable

genotypes (Kang, 1993; Rao and Prabhakaran, 2005; Farshadfar, 2008; Babarmanzoor *et al.*, 2009; Farshadfar *et al.*, 2011). Indices that use gross of classes for simultaneous selection of high yielding and stable genotypes, have massive weaknesses since the yield class influences classes weight. Therefore, these indices are not suitable for overall consequences. For this case, Rao and Prabhakaran (2005) proposed a new index free from these obstacles using mean yield and stability values of each genotype (Farshadfar, 2011). Results demonstrated that most of the AMMI statistics are suitable for the identification of stable genotypes (Sabaghnia *et al.*, 2013) for their agreement with the indices considered for yield and stability simultaneous selection. The importance of AMMI model for investigating a genotype environment in agricultural research is that G and E main effect and genotype×environment interaction can be separated from each other and it is suitable for breeders for their focus on G and GE (Gauch *et al.*, 2008).

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