Investigation of the Interaction between Genotype and Environment by AMMI and GGE Models on 28 Bread Wheat Genotypes in Tropical Iran

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Abstract

The interaction of genotype and environment is one of the most important topics and challenges of plant breeding researchers, this research was performed on twenty-eight bread wheat genotypes from two alleles and their parents in six different environments in two consecutive years of investigation of performance stability. The experiment was conducted as a randomized complete block design with four replications. Performance, stability analysis was performed using multivariate parametric methods (AMMI and GGE-biplot). The main effect of genotype and environment on the results of AMMI analysis was significant at the 1 % level, the main components of PC1 and PC2 have used for biplot, based on parameters of AMMI model stability analysis, genotypes 25, 16, 6, 27 were selected as stable genotypes. Based on the results of graphical analysis of genotype interactions ×environment using GGE-biplot genotypes 18, 17, 14, 15, 20 were selected as stable genotypes, where the location of Zabul is different from the others.

Keywords: AMMI analysis, GGE model, Plant Breeding, Wheat performance

Introduction

Plant species with allelic diversity may respond differently to different environments because the reaction of genotypes varies in different environments, so it is necessary to prepare specific data of the region that are suitable for adaptation and performance. Therefore, identification of compatibility, performance, stability components, and performance components in wheat genotypes, one can produce and identify high yielding species. Production of high yielding varieties with adaptation, the main purpose is to produce plants. One of the factors that slow the breeding programs and even the failure to introduce genotypes and sometimes cause the breeder to introduce more varieties for the regions is the presence of GE interactions [1]. Different methods for stability analysis are presented and in general stability analysis methods are divided into two parametric and nonparametric methods; parametric methods are also divided into two univariate and multivariate methods to estimate the nature of gene interaction effects on the environment and their control [2]. The two most commonly used statistical analyzes are multivariate methods to the additive principal effect analysis and multiplicative (AMMI) and biplot (GEE) interactions [3]. AMMI Stability Parameter, IPCA1 (The first major component of the interaction), IPCA2 (The second major component of the interaction) absolute sum of principal component values meaningful genotype interaction in SIPCA environment, AMMI stability value, ASV, AMMI stability

index, Di and YSi performance stability index, the presence of interaction between genotype and environment indicates that the absolute values of the relevant criteria are large and it is small because of no interaction [4]. With the AMMI method, the best model for data analysis can be identified, it is also a suitable method for preliminary analysis of performance. Performance estimation is done more accurately. By reducing the number of replicates, more treatments can be added to the experiment and increase selection efficiency. The importance of the AMMI method is more important in research experiments, which usually include more treatments and fewer repetitions. This advantage in plant breeding is important in hybrids of maize

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with fewer replications in their designs, in which the AMMI method has this advantage [5]. More understanding of the interactions by multiplicative components can be obtained by plotting by biplot, by reducing the number of replicates more treatments can be used in the experiment. Higher genetic yields were obtained in less time. The multivariate GGE biplot, which is the base of principal component analysis, is widely used in various forms to investigate the interaction of genotype in the environment.

GGE-biplot simultaneously examines the effect of genotype and genotype interaction in the environment at the same time, the operating environment is uncontrollable, so in the GGE-biplot method, they use genotype and GE interactions to obtain acceptable results. This method was first developed by Yan et al. (2000) has been used. The GGE-biplot method allows these two effects to be studied simultaneously and graphically. GGE-biplot's features are a powerful and comprehensive tool in quantitative genetics and plant breeding [6]. In all one-year and two-year experiments, data from multiple environments and one year (MET) of E values are dominant over G and GE, so only G and GE should be considered simultaneously in evaluating data for evaluation of data, to make a meaningful result in the selection. The concept of GGE is a combination of G and G×E that is called biplot, indeed, the biplot shows the main effect of genotype and the interaction of genotype in different environments, statistical analysis of the data focuses on the useful part of the G and GE data. In the analysis of stability, Shukla, Weric, Ebert, Russel, Lin, and Beans found a significant relationship between ASV stability values, but Finelli, Wilkinson, Lin, and Beans showed less association with either of these methods. It is important to use the AMMI and GGE-biplot method for comparisons of adaptation and stability. The use of GGE-biplot facilitates the comparison and introduction of top wheat genotypes for each region [7]. In an experiment carried out on oats in Canada's eastern region for three years, the results of the GGE-biplot show that three large environments were divided into six small environments, and genotypes corresponding to each small environment were identified and a strategy was developed for compatible oat data were provided. The aim of the research in determining large environments has been favorable in both AMMI and GGE and so far, the results of the comparisons have shown similar results as would be expected to be very effective for MET analysis. In recent years, this approach has often been illustrated by a data which-won-where pattern which may lead to the identification of high-yielding and stable data in useful experimental environments. The purpose of this study is to investigate the interaction of G×E by analyzing two AMMI and GGE diagrams for wheat seed yield obtained from two-allele transplantation to identify stable hybrids in different environments.

RESULTS AND DISCUSSION
AMMI Analysis

The results of the analysis of variance with the AMMI model in Table 1 show significant differences for genotype, environment, and genotype-environment interaction, which constitute genotype 1.1, environment 92.56 and genotype-environment interaction at 6.3 percentage of the total sum of squares, the 92 percent of the total sum of squares is related to the environment, which indicates a large difference between the environments since the experiment was conducted in different environments, so the major assignment of variation to environmental variance is justifiable. The low contribution of genotypes to the justification of the existing variations maybe because wheat breeding programs selection of stable and superior genotypes was selected in terms of yield and thus this genotype effect has little role in justifying the changes which are in agreement with the results of some researchers. The methods of the existence of significant first two components are best for investigating genotype-environment interaction. For this purpose, genotype-environment interaction was analyzed by principal component analysis of the residual matrix such that the first two components were significant. The first component 34.811 and the second component accounted for 26.28 percent of the total sum of squares of interactions. In general, the AMMI model justified 61.1 percentages of the interactions, indicating good fitting of the model and they create reliable results. The most stable genotypes based on the ASV parameter calculated based on the first two components in the AMMI model and their sum of squares have significant correlations between Shukla, Rig, and Eberhart and Russell [8]. Accordingly, the most stable genotypes 25 and 27 and genotypes 3 and 10 were selected as the most unstable genotypes.

The environments are at the bottom of the vectors, the numbers 1 through 28 represent the genotypes. Figure 1 shows the biplot based on the first two components of the AMMI model. Genotypes with small images on the peripheral vector show less than mean deviation. One of the most important applications of the AMMI method is the specific adaptation of genotypes and the introduction of one or more genotypes for one or more regions. Genotypes located in the center of biplot have small interactions and general stability (genotypes 14, 15, 16, 19, 27), genotypes 20, 25, 26, have private adaptation with Dezful environment, genotypes 15 and 17 have private adaptation with Iranshahr environment, Genotypes 2, 7, 10 and 22 are privately compatible with Khorramabad. Using the AMMI method in the studies, stable genotypes can be identified and stated that the above methods can be used to determine genotypes with general and specific compatibility for different locations.

Table 1. AMMI variance analysis for twenty-eight genotypes studied in bread wheat in 6 environments

Source	Df	SS	MS	%Total SS	
Treatment	167	528.69**	3.165		
Genotype	27	578.788**	21.2143	1.1	
Environment	5	489371**	97874	92.56	
Block	3	1.987	0.6623		
Interaction between genotype and environment	135	3353**	24.84	6.3	
IPCA1	31	11765**	376.6		34.8119
IPCA2	29	881.45**	30.39		26.2826
IPCA3	27	725.9**	26.88		21.6466
IPCA4	25	342.7**	13.70		10.2195
IPCA5	23	236**	10.26		7.0395
Residual	20	0	0		
Test error	501	57.14	0.114		
Total	671	587.8			

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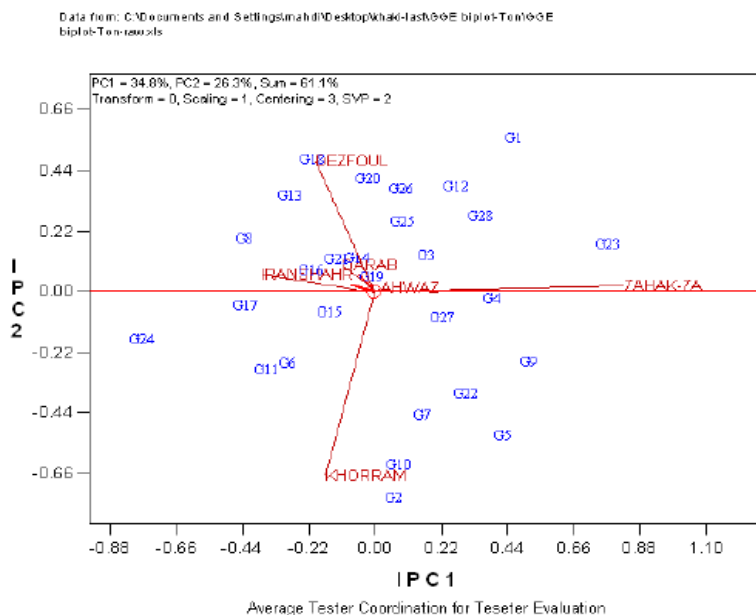

Figure 1. Biplot based on the values of the first and second major components of genotype and environment (AMMI)

Biplot plotted in Fig. 2 depicting the genotype and the environments, using a biplot one can evaluate the optimal shape of the genotypes relative to the environment, the relationships between genotypes and environments are observable, so genotypes can be introduced for specific regions, The AMMI model biplot for the 28 bread wheat genotypes shown in Figure 2 shows the letter G as the genotypes and environments of Khorramabad, Ahvaz, Darab,

Dezful, Iranshahr, Zabolt .The horizontal axis is the mean of yield and the vertical axis is the interaction between genotypes and the environment.
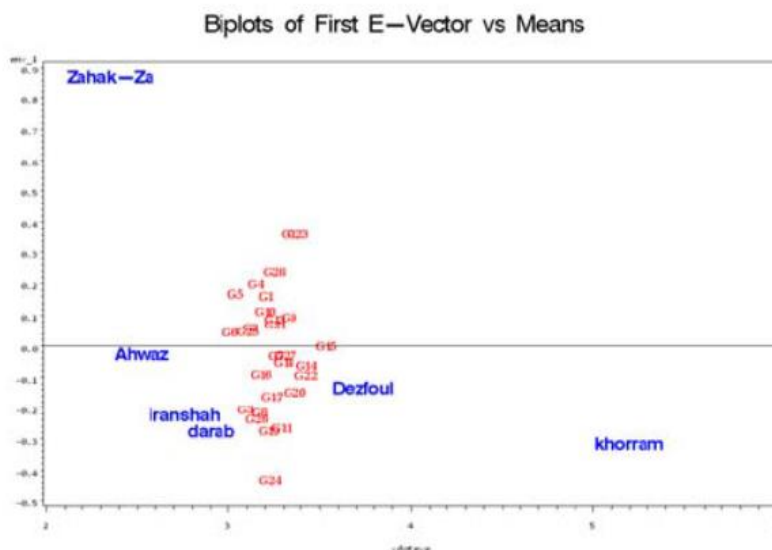

Figure 2. AMMI model biplot chart average performance and environment in 28 bread wheat genotypes

Genotypes 6, 16, 25, 27 have values close to zero (horizontal axes) genotypes and environments that have close values have more general stability, so having higher performance than average performance is shown as stable genotypes, genotypes 4, 12, 19 had the highest interaction and the least average yield of the most unstable genotypes.
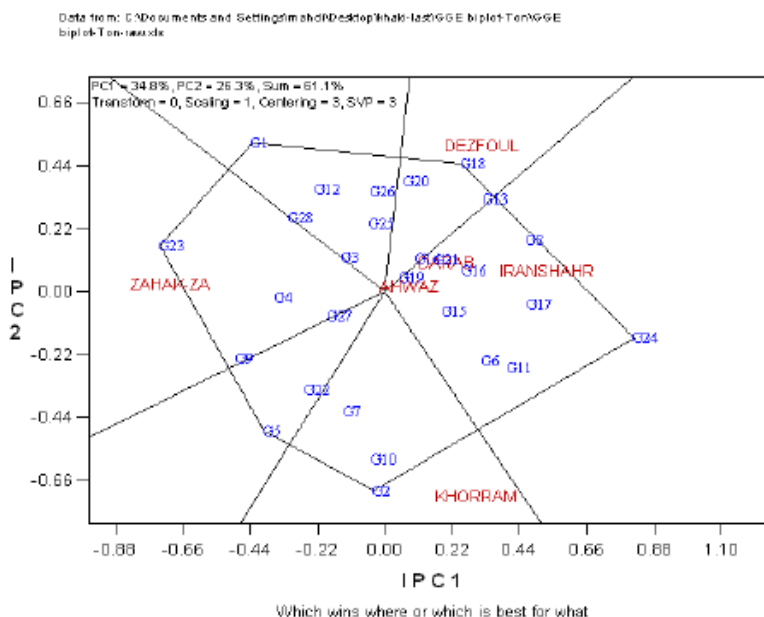

Figure 3. Which "genotype for where" model for the 28 genotypes studied in bread wheat

Which-win where model

In Figure 3, the genotypes with the greatest distance to the center of the biplot are connected by lines and form a polygon, genotypes 1, 13, 18, 20, 22, 24, 28 are the most distant from the center of the biplot, so they are located on the polygon and are among the most reactive data and have the highest or lowest performance in one or more environments. The digits in the center of the biplot are less reactive and have

the same rank in all environments and therefore do not react to the environment[9, 10]. A line passes through the center of the biplot in the polygon that divides the polygon into sections, in each of these sections the environments are located, the environments that are in the same area are similar, these environments are highly correlated, they are closer together in this biplot, so they fit into a large environment, here, location 1 is the environments of Iranshahr, Darab, Ahvaz, where they are located in one area, indicating identical conditions, in the second location is Dezful, in third location Zabul and fourth location Khorramabad. In each environment, the genotypes at the top are the genotypes that have the highest or the least performance in one environment. In location 1, genotype 2 has the highest performance, in place 2 the highest genotype is No. 1, genotype 2 is suitable for the third location, and genotype 2 is for location 4. Although genotypes 1, 5, and 23 are in top and superior, they do not perform well in any environment, genotypes located at the center of the biplot are less responsive and more stable. In south-eastern Ethiopia, a study was carried out on 18 barley genotypes in eleven environments using the biplot method. The environments were divided into two large environments, each environment containing several sub-environments, and a suitable genotype was determined for each large environment, biplot is used to determine the stability of other products such as soybean, rapeseed, barley, lentil, pea, and safflower. It is important to use AMMI and GGE-biplot for comparability and sustainability comparisons, the use of GG-Ebiplot facilitates comparison and introduction of top wheat genotypes for each region. In an experiment conducted on oats in Canada's eastern region for three years, the results of the GGE-biplot indicated the identification of three large environments in the region, divided into six small environments and the genotypes for each small environment were identified and a breeding strategy was presented for compatible oats.

Simultaneous evaluation of stability and performance of genotypes

By plotting the average environment coordinates (AEC) in the biplot, the mean and stability of the genotypes can be shown, the line that crosses the biplot and the medium environment is the medium or AEC axis. An average axis is determined using PC1 and PC2 moving to the arrows decreases stability, thus environments with longer corresponding line lengths are less stable. The arrow at the bottom of the AEC axis indicates the direction of increased performance. A line passes through the middle of the biplot perpendicular to the AEC axis, which is an estimate of the genotype-environment (GE) interaction while the AEC axis is an estimate of the original G effect. In Figure 4, the genotypes on the shorter AEC axis are more stable based on genotypes number 3, 4, 14, 15, 16, 17, 19, 20, 21, 27 are stable. But genotypes are considered by the researchers which simultaneously have high stability and high performance. In Figure 5, simultaneous stability and performance are possible. Ideal genotypes can be ranked based on distance from genotypes. An ideal genotype is a genotype that has high stability and yield. In this model, the ideal genotype is located on the AEC axis and in the center of the concentric circles. In this model, the ranking of genotypes with performance and suitable stability belongs to genotypes 11, 14, 15, 17, 18, 20.
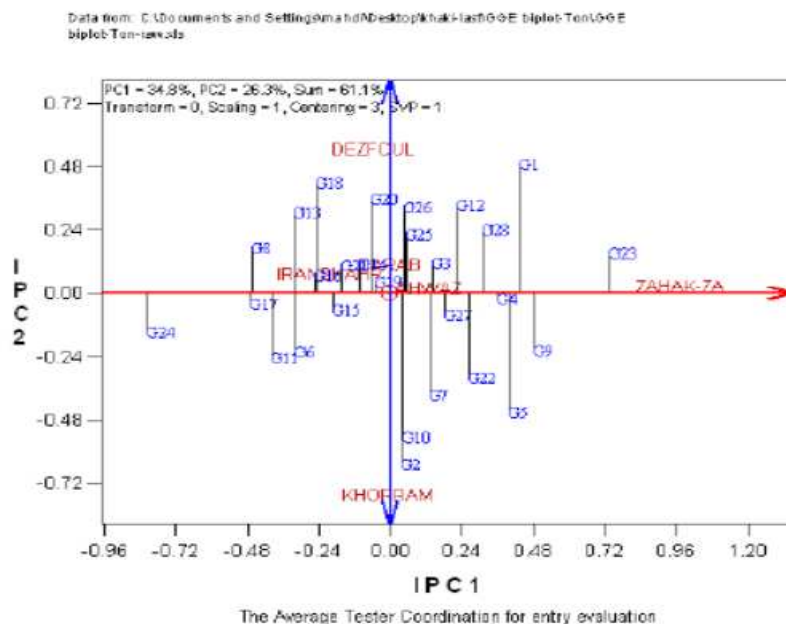

Figure 4. Model for evaluation of stability and performance of genotypes based on medium environment coordinates
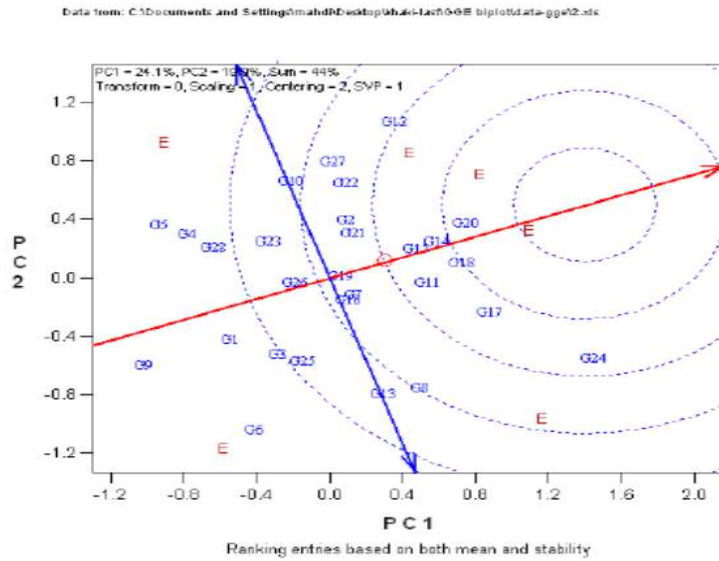
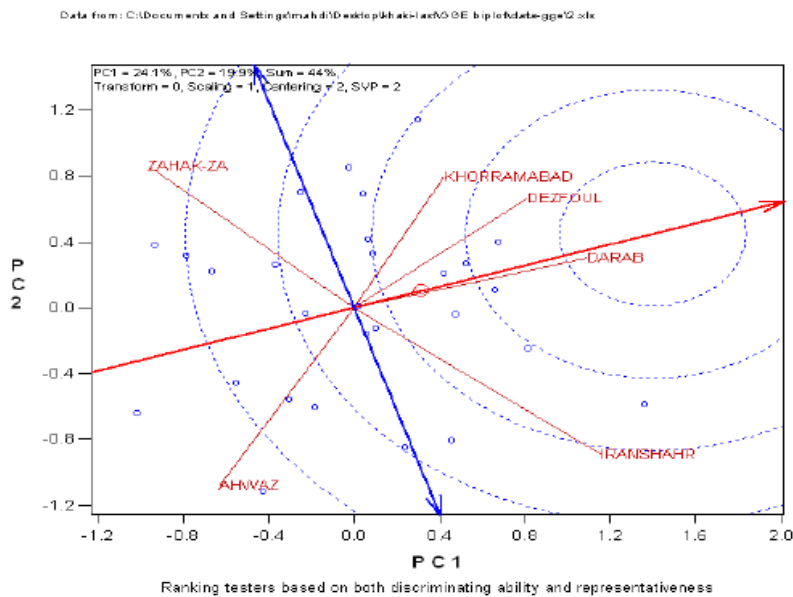**Figure 5.** Ranking 28 bread wheat genotypes by ideal digit

Figure 6. Ranking of environments in terms of power and ideal environment

Ranking of environments based on differentiation and representative of environments

The ability to differentiate environments is one of the ideal environment's evaluation. If there is no distinction between the two environments, then no information about the data is available to the researcher. One of the features of the biplot is the estimation of the standard deviation within any environment with environmental vector length, this criterion for the ability and differentiation of the environment, and whatever the vectors are longer, the environment will be more differentiated [5]. In other words, the length of environmental

vectors is proportional to the standard deviation of the genotypes in the environments. The longer environmental vectors are, the more environmentally relevant the environment is for variability in grain yield. According to Figure 6, Darab, Dezful, Khorramabad, Iranshahr environments show more differentiation than the other two environments. An important criterion in evaluating environments is the test of their representativeness, which is representative or exemplary of the original environment if an environment does not representative of the environments, then the researcher receives misleading information. In

biplot, an environment considered an average criterion, and whenever the environments are closer to this environment, then the chance of being representative will be more. The AEC line crosses the center of the biplot and the medium environment, and the angle of each vector with the AEC axis is a criterion for identifying the sample environment. Khorramabad, Darab, Dezful, and Iranshahr have the lowest angles with the AEC axis and thus it is the most representative of the medium environment. But a suitable environment is an environment that has two criteria at the same time: distinctive and a target environment. The resolution and differentiation of an environment are in a showing of the maximum variation among genotypes but being representative indicates that that environment can be as representative of other environments. As shown in Figure 5, because the genotypes are not present, the dotted arrow points to the center of the concentric circles, suggesting an ideal environment that is defined as the most distinctive and representative of all environments, so Desirability of environments will be Darab, Dezful, Khorramabad, Iranshahr, Zabol, Ahvaz, respectively, where Among the environments, Darab is the most distinctive and most representative environment.

Experimental Designs:

The experiment was carried out in a randomized complete block design with four replications, using 28 wheat genotypes, 26 lines with 2 witness during years 2016-2017 and 2017-2018 at Ahwaz, Darab, Dezful, Iranshahr, Zabol and Khorramabad research fields. After performing the basic statistical calculations, including Bartlett's test, one-way ANOVA and mixed variance analysis were performed to determine the main effects (year, location, and genotype) of the two-way interactions (year ×location, genotype ×location) and three-way interactions (genotype ×location × year) on the data. Grain performance and its components including straw performance, grain performance per spike, biological performance, thousand-grain weight, plant height, spike length, and root length were studied. Stability analysis methods (univariate and multivariate) were used to evaluate compatibility and sustainability. The genotypes used are 1-Chamran 2-Pishtaz 3-Attila 4-Kauz / Luco 5-Irina/Babax 6-Becard/Akuri. Introducing superior wheat to farmers requires its acceptance by farmers and the adaptability and sustainability of the yields given to the specimens compared to the native samples. Therefore, in breeding programs, the Institute of Agricultural Research uses samples that are available for different regions and indigenous populations of the country. Excel software was used for simpler calculations on data and data transferring and SAS and Genstat. 8 software was used for data analysis.

Analysis of two AMMI and GGE models

The AMMI method is a combination of the variance analysis model (ANOVA) and principal components analysis [11]. Using ordinary variance analysis, the main effects of genotype and environment can be estimated which are known as summable effects, principal components analysis (PCA) is

called a multiplicative model, each genotype and environment is assigned a score and the result of multiplying that performance by that genotype is estimated in that environment [12]. AMMI method and GGE-biplot analysis were used to calculate multivariate parameter stability.

Summable model is as follows

$$Y_{ger} = \mu + \delta_g + \beta_e + \theta_{ge} + \varepsilon_{ger}$$

Where μ is grand mean, δ_g is genotype, β_e is environment and θ_{ge} is the residual. The multiplicative model is as follows

$$Y_{ger} = \mu + \sum \lambda_n \xi_{gn} \eta_{en} + \rho_{ge} + \varepsilon_{ger}$$

Where λ_n is the correlation between values of genotype and environment components, ξ_{gn} is genotype singular vector for nth axis, η_{en} is a singular vector for the environment.

Using AMMI in the region performance tests is introduced in 1988 by Zobel et. al. and Guach [13] and its the mathematical is as follows [3]:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_n \delta_{en} P_{ge} + \varepsilon_{ger}$$

where Y_{ger} is genotype performance, μ is grand mean, δ_{en} is environment vector for the nth axis, α_g is the genotype main effects, β_e is the environment main effects, P_{ge} is the residual value, λ_n is the value for the nth main component, γ_n is the genotype vector for the nth axis and ε_{ger} is the experimental error.

AMMI model stability parameter is defined by Purchase [14] as follows:

$$ASV = \sqrt{\left[\frac{SSIPCA1}{SSIPCA2} IPCA1 \right]^2 + IPCA1^2}$$

Where $SSIPCA1$ and $SSIPCA2$ are the sum of the absolute values of the first and second principal components of interaction ICPA1 and ICPA2, respectively. The existence of an interaction between genotype and environment indicates that the sum of the absolute values of the relevant criteria is large and that there is no interaction.

CONCLUSIONS

Analysis of variance showed significant differences among genotypes, environment, and interaction. Which shows the different reactions of genotypes at different locations and years. Based on AMMI model stability parameters, genotypes 6, 16, 25, 27 were selected as stable genotypes. Based on the results of GGE-biplot genotypes 14, 15, 17, 18, 20 were introduced as stable genotypes. The AMMI and GGE method

can be easily interpreted and more information can be obtained, which increases the accuracy of experiments as the number of locations increases

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