




## Article

# Evaluation of Grain Yield Stability in Some Selected Wheat Genotypes Using AMMI and GGE Biplot Methods

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**Abstract:** Wheat *Triticum aestivum* L. is one of the most important agricultural products, and meets the highest nutritional needs of humans in various countries. This study aims to evaluate the compatibility and stability of 25 wheat genotypes for two crop years in five regions (Karaj, Qazvin, Isfahan, Varamin and Damavand) in a randomized complete block design with three replications. The results of variance analysis in the additive main effects and multiplication interaction (AMMI) method showed that the effect of genotype and the genotype × environment interaction in the first, second, and mean two crop years had a significant difference at the level of one percent probability. Based on the results obtained from the first and second principal components, G8, G4 and G22 genotypes were identified as superior genotypes. Isfahan was an ideal environment for this study. The results obtained from the comparison of the Duncan method showed that G14, G12, and G1 genotypes had suitable ranks. Graphical analysis was used to study the genotypes of wheat and the environment, and the genotype × environment interaction. Based on the ranking genotypes in the first and second principal components and an average of two years, G2 and G21 genotypes were identified as high yielding, and G21 genotypes as stable. G18 and G23 genotypes were selected as the best genotypes in all three experimental periods, based on the multidimensional diagram. The results of the ideal genotype diagram were G12 and G21 genotypes; and based on the results of the ideal environment diagram, Damavand and Varamin environments were identified as ideal environments. AMMI1 covered 69.6% and AMMI2 75.6% of the data variance in the first year of the experiment. In the second crop year, 78.1% of the total variance of the data was explained based on the AMMI1, and 71.1% based on the AMMI2.

**Keywords:** AMMI and GGE biplot methods; genotype × environment interaction; stability; wheat

## 1. Introduction

Food security are the axes of a society's economic and social development. Food, malnutrition, energy, and environmental problems are among the most significant problems today. According to the United Nations, in 2020, at its most optimistic count, about one billion people worldwide suffer from hunger and malnutrition each year [1]. Wheat (*Triticum aestivum* L.) is one of the most important agricultural products, and meets humans' most

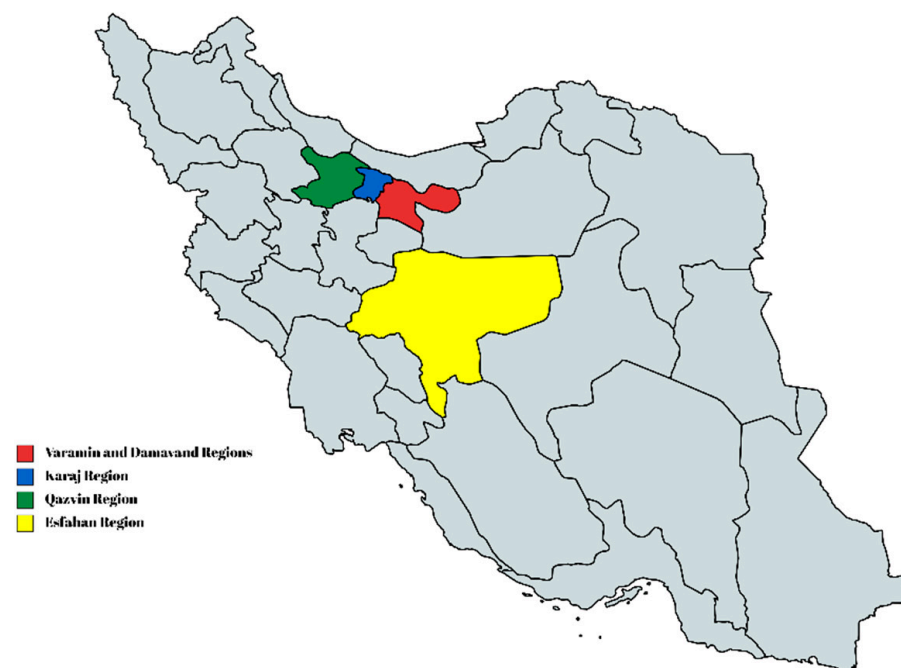
significant nutritional needs in various countries. Due to its high nutritional value, compatibility with the human gastrointestinal tract, variety and quality of product, the abundance and affordability of wheat in the diet of three-quarters of the world's population has an important place. In addition to direct feeding, it is the most critical input in livestock and poultry [2]. Furthermore, as the most adaptable grain to various environmental conditions, due to its high genetic diversity and its strategic and economic nature, wheat has become the most important crop globally [2]. In more than 100 countries, wheat provides 55% of carbohydrates, 20% of protein and 20% of the daily calories needed by humans [3].

As well as live stresses, including pests, diseases and weeds, threshing stresses, including dehydration, cold and heat, are major limiting factors in wheat production [4]. Grain yield and stability have always been used as essential criteria in selecting and introducing cultivars in different regions and years [5–8]. The genotype in the environment interaction on yield has made it impossible to recommend high yielding hybrids for all regions. Therefore, it is necessary to study the genotype in the environment interaction before introducing new high-yielding hybrids with high stability, due to the interaction of the genotype  $\times$  environment, for the evaluation of new lines in different environments. The best genotype in one environment is not necessarily the best genotype in another environment [9–13]. Many statistical methods have been developed to determine the state of the effect of the environment, which are usually divided into two groups, parametric and non-parametric. The parametric methods themselves are divided into two groups: univariate and multivariate. Univariate methods include Finley and Wilkinson variance [14], and Eberhart and Russell [15], who proposed the regression method between hybrid yield and environmental index. Francis and Kannenberg [16] used the coefficient of environmental variation among all experimental environments. The essential multivariate methods used to analyze the data of yield comparison experiments are: statistical methods GGE by plot, AMMI, and principal component analysis (PCA) used to determine the stability and compatibility of genotypes based on quantitative analysis singular value decomposition (SVD) [17]. For example, the GGE biplot method and the AMMI model are powerful analytical tools to study the genotype in environment interaction [17,18]. In evaluating genotypes in different environments, the environment's effect cannot be exploited very much in most cases. Therefore, removing the effect of the environment from the data and focusing on the main effect is essential to genotype (G) and to the interaction of genotype in the environment (GE) [17]. The sum of genotype and genotype effects in the environment is significant in selecting stable genotypes. Of course, the study of genotype effects and the interaction of genotype in the environment simultaneously should be noted. The GGE biplot method allows these two effects to be examined simultaneously and graphically [18]. Therefore, the main effect of genotype and the interaction of genotype in the environment are separated in the GGE biplot. Gauch [17] stated that the AMMI method, due to the separation of these effects from each other, is always superior to the GGE biplot, or at least has equal inaccuracy. However, Yan et al. [19] believe the GGE biplot method is more successful than the AMMI method in analyzing genotype data in the environment. In terms of breeds, genotype selection is based on the main effect of genotype or genotype interaction, and it was not considered in the environment alone [20]. Many researchers have introduced the GGE biplot method as an efficient method for investigating the interaction of genotype  $\times$  environment. It is stated that this method provides helpful information about the genotypes and environments under study. GGE biplot has been reported in selecting suitable hybrids for bread wheat [21,22]. According to the above, the purpose of this study was to evaluate wheat genotypes and genotypes in the environment interaction by graphical analysis of GGE biplot and AMMI, and to identify genotypes with stable yield and superior environments, by identifying and introducing genotypes with the sustainability of high yield and adaptation to environmental conditions, which can be a step towards meeting the country's needs for wheat production. The objectives of this research include the following: (1) Evaluation of stability and compatibility of genotypes, (2) Selection of stable genotypes in different environments, (3) Selection of genotypes with high yield in different environments, (4) Investigation of

the reaction of genotypes in different environments, (5) Investigation of the interaction of genotype  $\times$  environment.

## 2. Materials and Methods

This study evaluated the stability and compatibility of 25 wheat genotypes in five regions (Karaj, Qazvin, Isfahan, Varamin and Damavand) (Figure 1) and two cropping years, an experiment in a randomized complete block design (RCBD). Planting was done in four rows with a distance of 50 cm and a length of 3 m. To eliminate marginal effects the two middle rows were sampled. After planting in mid-November, irrigation is done, and the field is green. In mid-April, in the three to five-leaf stage, according to the region's climatic conditions, a suitable herbicide (with specific broad-leaved and narrow-leaved pesticides) was used to control weeds. Urea fertilizer was used in each of the stems and clustering stages. The names and codes of the genotypes are given in Table 1, and the names, codes, and geographical and climatic conditions of the experiment sites are given in Table 2. All methods are performed according to the relevant guidelines/regulations/legislation. Plots in an area of one-third of a hectare will be selected for the experiment, and soil sampling will be performed for soil analysis and fertilizer recommendation. In September 2019 and 2020, land preparation was carried out by operations such as autumn plowing of two discs perpendicular to each other, rolling and fertilizing according to recommendations from the soil decomposition experiment. According to the result of soil decomposition, ammonium phosphate fertilizer and urea fertilizer were spread on the field and mixed with the soil by disk. Nitrogen fertilizer was applied in three stages before planting, tillering and early flowering of the plant. Phosphorus and potassium fertilizers were applied before planting. Seeds were disinfected with a suitable fungicide before sowing to control blackheads.



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Figure 1. Experiment Locations in Iran.

**Table 1.** Names and code of wheat genotypes studied in the experiment.

Genotype No.	Genotype	Genotype No.	Genotype	Genotype No.	Genotype
G1	ABC Zigmund	G10	Ralitsa	G19	Neven
G2	ABC Lombardia	G11	Faktor	G20	Tervel
G3	A 38/64	G12	Ognyana	G21	Riana
G4	ABC Kolino	G13	ABC Alfio	G22	Vyara
G5	Presyana	G14	A 27/320	G23	Aneta
G6	Bilyana	G15	Apogej	G24	Alisa
G7	ABC Navo	G16	A 18/74	G25	Rakhshan (Control)
G8	LG Anapurna	G17	Pryaspa		
G9	ABC Klauzius	G18	A 47/415		

**Table 2.** Annual rainfall mean, codes, and geographical parameters for the environments.

Location Code	Location	Longitude	Latitude	Elevation AMSL (m)	Average Rainfall (mm)	Average Annual Min Temp (°F)	Average Annual Max Temp (°F)
KRJ	KARAJ	51.00	35.48	1321	295	35	83
QAZ	QAZVIN	49.99	36.31	2347	210	33	79
VAR	VARAMIN	51.64	35.32	918	218	33	101
ESF	ESFAHAN	51.65	32.68	1590	116.9	24	98
DAM	DAMAVAND	52.06	35.72	2300	320	21	83

Graphical decomposition was made using the GGE biplot based on the individual quantities by the following formula:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad (1)$$

where,  $Y_{ij}$  is the mean of  $i$ th genotype in  $j$ th environment,  $\mu$  is the mean of all genotypes,  $\beta_j$  is the main effect of  $j$ th environment,  $\lambda_1$  and  $\lambda_2$  are the special quantities for the first and second components, respectively,  $\xi_{i1}$  and  $\xi_{i2}$  are the special vectors of genotypes, and  $\eta_{j1}$  and  $\eta_{j2}$  are the environmental vectors of first and second components, respectively, and  $\varepsilon_{ij}$  is the remaining quantity for the  $i$ th genotype in  $j$ th environment.

### 3. Results

#### 3.1. AMMI Analysis

Data analysis based on the AMMI model showed that the interaction of genotype  $\times$  environment was significant in the first and second year, and in two years' data. The results were significant in the first component in the first crop year, in the second year, and in the average of the two crop years and the first two components. The lowest coefficient of variation was related to 14.72% of the average of two crop years, and the highest coefficient of variation of 23.88 was related to the first crop year (Table 3). The values of the first and second significant components of environments and genotypes are presented in Tables 4 and 5. In general, environments with significant first component interaction are more suitable for identifying and sieving genotypes. Accordingly, in the first crop year of the E4 environment, in the second crop year of the E2 environment, and in the average of two crop years, the E4 environment is more suitable for identifying and screening genotypes than other environments (Table 4). Based on Duncan's mean comparison analysis at the 0.01 probability level, the results obtained from the mean yield trait indicate the G14, G12 and G1 genotypes as favourable genotypes, considering that they obtained the highest rank in this analysis, and G10 and G13 genotypes are identified as unfavourable genotypes in grain yield, due to their low rank (Table 5). Such genotypes have high stability, the lowest amount of the significant first component of the interaction, and higher yields. Accordingly, in the first crop year, the G4 genotype was a stable genotype due to having the lowest

amount of the first principal component (0.0003) and a relatively high yield (2.25). In the second crop year, the G8 genotype was identified as a stable genotype due to having the lowest amount of the first principal component (0.00004) and a relatively high yield (2.61) (Table 6). In general, it can be concluded that the E4 environment is a suitable environment for the identification and screening of genotypes, and that genotypes G4, G8 and G22 are suitable genotypes for planting in different regions and years.

**Table 3.** Variance analysis based on AMMI model on 25 wheat genotype in five regions in the first, second, and average of two crop years.

SOV	DF	Year 1		Year 2		Average of 2 Years	
		SS	MS	SS	MS	SS	MS
Block	2	0.0000004	0.0000002 <sup>ns</sup>	0.000002	0.000001 <sup>ns</sup>	0.0000008	0.0000004 <sup>*</sup>
Environment	4	0.000004	0.000001 <sup>*</sup>	0.00006	0.00001 <sup>**</sup>	0.00001	0.000003 <sup>**</sup>
Genotype	24	0.00001	0.0000004 <sup>*</sup>	0.00001	0.0000006 <sup>**</sup>	0.000006	0.000002 <sup>**</sup>
G × E	96	0.00004	0.0000004 <sup>*</sup>	0.00005	0.0000006 <sup>**</sup>	0.00002	0.000002 <sup>**</sup>
IPCA 1	27	0.00002	0.0000008 <sup>**</sup>	0.00002	0.0000009 <sup>**</sup>	0.00001	0.0000004 <sup>**</sup>
IPCA 2	25	0.000008	0.0000003 <sup>ns</sup>	0.00001	0.0000006 <sup>**</sup>	0.000005	0.000002 <sup>*</sup>
IPCA 3	23	0.000006	0.0000002 <sup>ns</sup>	0.00001	0.0000004 <sup>ns</sup>	0.000004	0.000001 <sup>ns</sup>
IPCA 4	21	0.000003	0.0000001 <sup>ns</sup>	0.000004	0.0000002 <sup>ns</sup>	0.0000003	0.0000001 <sup>ns</sup>
Error	248	0.0000003	0.0000001	0.00007	0.0000003	0.00003	0.0000001
CV%		23.88		21.45		14.72	

<sup>\*</sup>, <sup>\*\*</sup>, and <sup>ns</sup>: significant at 5%, 1% and not-significant.

**Table 4.** Average value, first principal component and second principal component in the five studied areas in the first, second and average of two crop years.

Environments	First Year		Second Year			Average of 2 Years		
	Mean	IPCA1	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2
E1	2.28	−0.02	2.9	0.03	0.01	2.59	−0.02	0.001
E2	2.53	0.01	2.85	0.01	0.002	2.69	0.0001	−0.02
E3	2.38	−0.01	2.82	−0.03	0.03	2.6	0.005	0.02
E4	2.48	0.04	1.8	−0.02	−0.02	2.14	0.03	−0.004
E5	2.56	−0.009	2.36	0.007	−0.01	2.46	−0.009	−0.003

**Table 5.** Comparison of Duncan's mean grain yield in two cropping years and five test areas.

Genotype	Rank	Means
G1	3	2.66 a
G2	21	2.409 abcd
G3	23	2.29 bcd
G4	22	2.405 abcd
G5	18	2.482 abcd
G6	10	2.54 abc
G7	17	2.49 abcd
G8	20	2.422 abcd
G9	19	2.447 abcd
G10	25	2.16 d
G11	6	2.58 abc
G12	2	2.67 a
G13	24	2.23 cd
G14	1	2.71 a
G15	14	2.506 abcd
G16	9	2.56 abc
G17	15	2.502 abcd

Table 5. Cont.

Genotype	Rank	Means
G18	5	2.6 ab
G19	16	2.5 abcd
G20	13	2.506 abcd
G21	11	2.53 abc
G22	7	2.577 abc
G23	12	2.52 abc
G24	4	2.61 ab
G25	8	2.572 abc

a–d: Genotypes have at least one letter in the same statistical group at a five percent level with the Duncan test.

Table 6. Average value, first main component, and second main component in 25 wheat genotypes in the first, second and average of two crop years.

Genotype	First Year		Second Year			Average 2 Years		
	Mean	IPCA1	Mean	IPCA1	IPCA2	Mean	IPCA1	IPCA2
G1	2.67	0.007	2.66	0.006	0.013	2.66	−0.005	−0.0006
G2	2.39	−0.0007	2.42	−0.0005	−0.003	2.4	0.001	−0.004
G3	2.31	−0.0006	2.27	0.003	−0.012	2.29	0.0006	−0.007
G4	2.25	0.0003	2.55	0.003	0.0008	2.4	−0.003	0.007
G5	2.71	−0.004	2.25	0.0006	−0.0027	2.48	0.002	0.004
G6	2.64	0.001	2.44	0.015	−0.0011	2.54	−0.006	−0.008
G7	2.39	−0.003	2.59	−0.002	0.011	2.49	−0.001	0.005
G8	2.23	−0.017	2.61	0.00004	0.005	2.42	−0.014	0.003
G9	2.47	−0.004	2.41	0.014	0.008	2.44	−0.011	−0.002
G10	2.1	0.002	2.21	0.001	−0.015	2.16	0.003	−0.009
G11	2.76	0.003	2.4	0.013	−0.016	2.58	−0.007	−0.001
G12	2.73	−0.01	2.62	−0.009	0.009	2.67	−0.006	0.012
G13	2.35	−0.001	2.12	0.017	0.002	2.23	−0.007	−0.008
G14	2.59	−0.01	2.84	0.0008	−0.009	2.71	−0.004	−0.00006
G15	2.56	−0.002	2.44	0.023	−0.009	2.5	−0.01	−0.006
G16	2.23	0.008	2.89	−0.013	−0.007	2.56	0.013	0.002
G17	2.42	0.02	2.58	−0.009	−0.004	2.5	0.015	−0.01
G18	2.69	−0.01	2.5	0.007	−0.007	2.6	−0.009	0.005
G19	2.3	0.005	2.69	−0.003	−0.003	2.5	0.004	−0.014
G20	2.35	0.007	2.65	−0.016	0.005	2.5	0.008	0.013
G21	2.48	0.004	2.58	−0.01	−0.005	2.53	0.008	0.004
G22	2.38	0.001	2.76	−0.0004	0.012	2.57	0.002	0.005
G23	2.52	0.02	2.51	−0.019	0.001	2.52	0.022	−0.0001
G24	2.33	0.009	2.9	−0.013	0.015	2.61	0.009	0.010
G25	2.31	−0.02	2.83	−0.004	−0.019	2.57	−0.003	0.0008

### 3.2. Genotypes Stability by GGe Biplot

Graphic analysis was used to study and interpret the diversity of genotypes and environments, and to study genotype and location interaction. In the horizontal axis biplot diagram (PC1), the main effect of the genotype and the vertical axis (PC2) represent the interaction between the genotype and the environment, which measures the instability of the genotypes. The genotypes close to the origin of this axis have more stability than the genotypes close to the end of this axis. G10 was identified as a low-yield genotype. The order of genotypes in terms of yield traits is as follows:

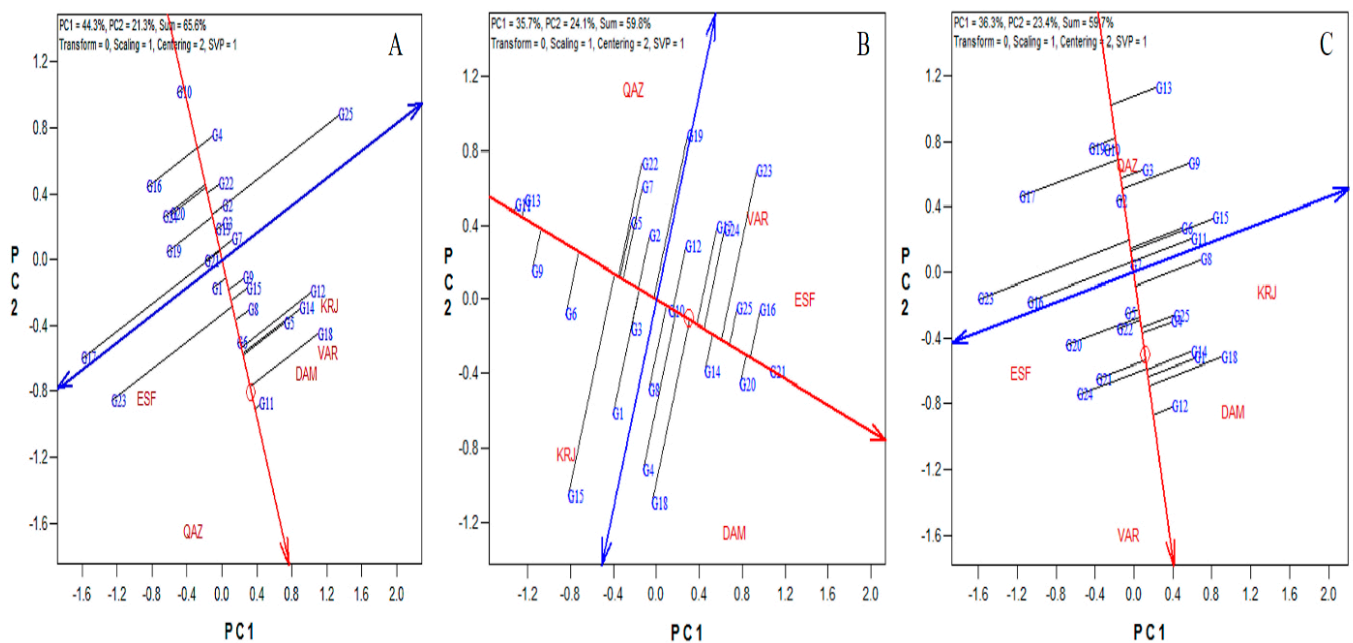
G10 < G4 < G16 < G21 < G20 < G22 < G19 < G2 < G25 < G3 < G13 < G7 < G21 < G17 < G1 < G9 < G15 < G23 < G18 < G6 < G12 < G4 < G5 < G18 < G11.

G1, G21, G6, and G11 genotypes were more stable than the other genotypes, and G22, G17 and G25 genotypes were identified as unstable genotypes. In the graph related to the second year of the experiment, the G21 genotype had a high yield compared to other genotypes, and the G11, and G13 genotypes had a low yield. Based on this graph, the order of genotypes in terms of yield traits is as follows:

G11 < G13 < G9 < G6 < G15 < G22 < G7 < G5 < G1 < G3 < G2 < G19 < G8 < G12 < G10 < G4 < G18 < G17 < G24 < G14 < G23 < G25 < G20 < G16 < G21.

G21 and G10 genotypes were more stable than the other genotypes, and G19, G15, G18 and G23 genotypes were identified as unstable genotypes. The analysis results on the average of the data obtained in two years showed that the G12 genotype had a higher yield and the G13 genotype had a lower yield than other genotypes. The order of genotypes in terms of yield traits is as follows:

G13 < G19 < G10 < G17 < G3 < G9 < G2 < G23 < G16 < G15 < G7 < G16 < G11 < G8 < G5 < G20 < G22 < G25 < G4 < G21 < G24 < G14 > G1 > G18 < G12 (Figure 2).

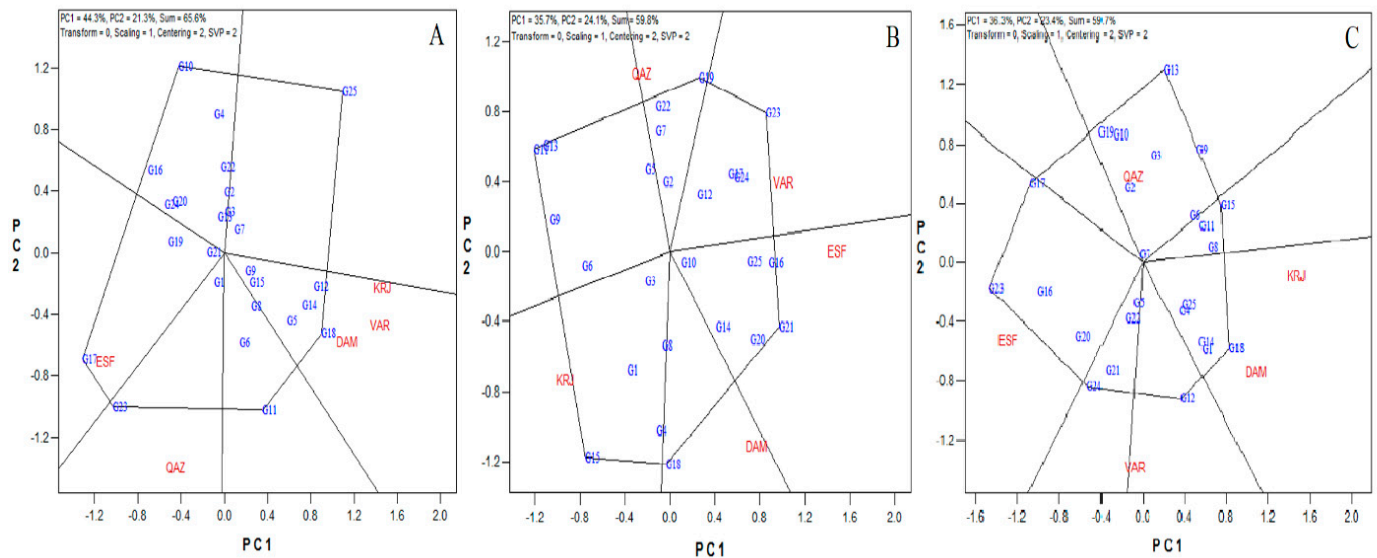


**Figure 2.** The average genotype coordination view for evaluating 25 wheat cultivars in five environments simultaneously classifies cultivars. (A): First year, (B): Second year, (C): Average of two years. G1:, G2:, G3:, G4:, G5:, G6:, G7:, G8:, G9:, G10:, G11:, G12:, G13:, G14:, G15:, G16:, G17:, G18:, G19:, G20:, G21:, G22:, G23:, G24:, G25: (DAM: DAMAVAND, VAR: VARAMIN, KRJ: KARAJ, ESF: ESFAHAN, QAZ: QAZVIN).

### 3.3. Adaptability Analysis

Multidimensional figures are used to determine the best genotype for each region. This shape is obtained by connecting the farthest genotypes from the origin so that other genotypes fall within this polyhedron. A linear polygon is perpendicular to each side, dividing the shape into several parts from the origin. In this figure, the genotypes in a section with a specific environment have performed well in that environment. Genotypes close to the origin do not respond well to changes in genotype or to environments close to the origin. Based on this, the results of the year crop graph indicate that G25, G18, G11, G23, G17 and G10 genotypes are identified as superior genotypes. The G18 genotype in the Damavand region had a higher yield than other genotypes. The G17 genotype had an excellent yield in the Isfahan region. G21, G1, and G7 genotypes did not react much to changes in different environments, according to their proximity to the origin of this

diagram. The results of the polyhedral diagram in the data obtained from the crop year show that G23, G19, G11, G15, G18 and G21 genotypes are identified as superior genotypes. The G23 genotype was more desirable than other genotypes in the Varamin region, the G22 in the Qazvin region and the G16 in the Isfahan region. The G10 genotype did not react to environmental changes, according to its proximity to the graph's origin (Figure 3).



**Figure 3.** Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments. (A): First year, (B): Second year, (C): Average of two years. G1:, G2:, G3:, G4:, G5:, G6:, G7:, G8:, G9:, G10:, G11:, G12:, G13:, G14:, G15:, G16:, G17:, G18:, G19:, G20:, G21:, G22:, G23:, G24:, G25: (DAM: DAMAVAND, VAR: VARAMIN, KRJ: KARAJ, ESF: ESFAHAN, QAZ: QAZVIN).

### 3.4. Ideal Genotypes and Environments

Figure 3 shows the ranking of genotypes based on the best genotype. For this purpose, linear coordinates from the origin are connected to the point of the averages, and continue to the sides. The best genotype is a genotype inclined to the positive end of this axis, and its vertical distance from this line is the most negligible value. In this figure, the best point of the center of the circle is the center, which is marked with an arrow. Other genotypes are grouped according to this point. The shorter the genotype, the better the genotype. Based on the results obtained from the ideal genotype diagram, the G11 genotype was identified as the closest genotype to the positive end in the first crop year, and the G10 genotype was identified as the farthest genotype from the positive end. The order of genotypes is as follows:

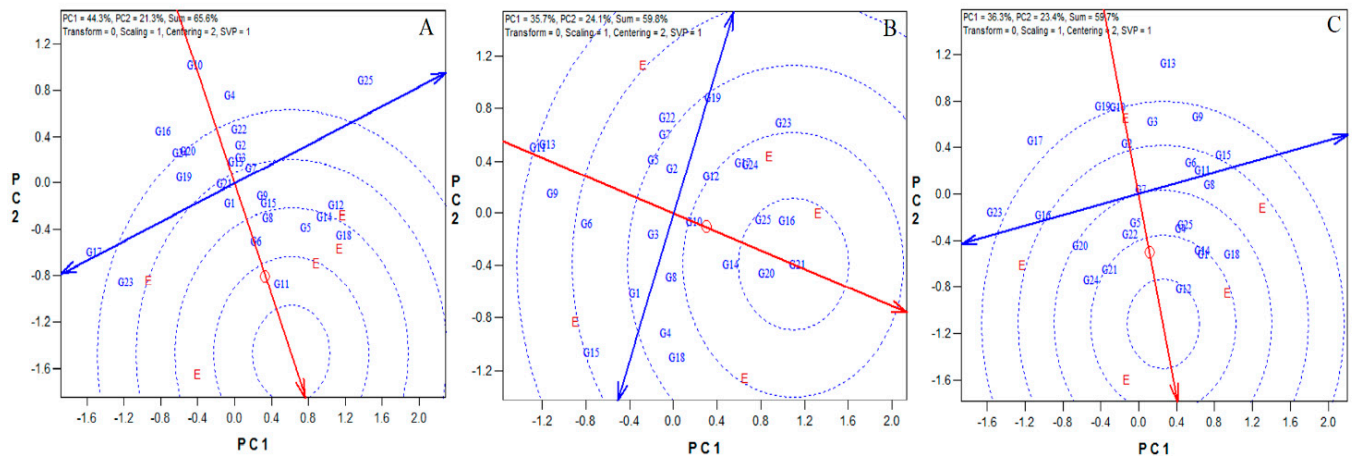
$$G10 < G25 < G17 < G4 < G16 < G20 < G24 < G22 < G2 < G19 < G3 < G13 < G21 < G7 < G23 < G1 < G9 < G15 < G12 < G18 < G14 < G8 < G5 < G6 < G11.$$

Based on the results obtained from the biplot from the second crop year data, genotype G21 was identified as a superior genotype, and genotype G13 as an unfavourable genotype. The order of genotypes in the second crop year is as follows:

$$G13 < G11 < G9 < G6 < G15 < G22 < G5 < G7 < G7 < G1 < G19 < G2 < G3 < G12 < G10 < G8 < G4 < G18 < G23 < G24 < G17 < G12 < G10 < G14 < G25 < G20 < G16 < G21.$$

The results of this biplot, in the average of the data obtained from the first and second year of cultivation, show that the G12 genotype is identified as a superior genotype, and G13 genotype as an unfavourable genotype. The order of genotypes based on the ideal genotype is as follows:

G13 < G23 < G17 < G19 < G10 < G9 < G3 < G2 < G16 < G15 < G6 < G11 < G7 < G8 < G20 < G18 < G25 < G5 < G24 < G1 < G14 < G14 < G4 < G22 < G21 < G12 (Figure 4).



**Figure 4.** Ranking biplot for comparison of the genotypes with the ideal genotype. (A): First year, (B): Second year, (C): Average of two years. G1:, G2:, G3:, G4:, G5:, G6:, G7:, G8:, G9:, G10:, G11:, G12:, G13:, G14:, G15:, G16:, G17:, G18:, G19:, G20:, G21:, G22:, G23:, G24:, G25: DAM: DAMAVAND, VAR: VARAMIN, KRJ: KARAJ, ESF: ESFAHAN, QAZ: QAZVIN).

According to the results of the experimental years, G12 and G21 genotypes were identified as superior genotypes, and G13 genotype as an undesirable genotype. Figure 4 shows the ranking of environments based on the ideal environment. According to this biplot, in the first crop year, Damavand was identified as a superior environment, and Isfahan as an unfavourable environment compared to other environments. The order of the environments based on the ideal environment is as follows:

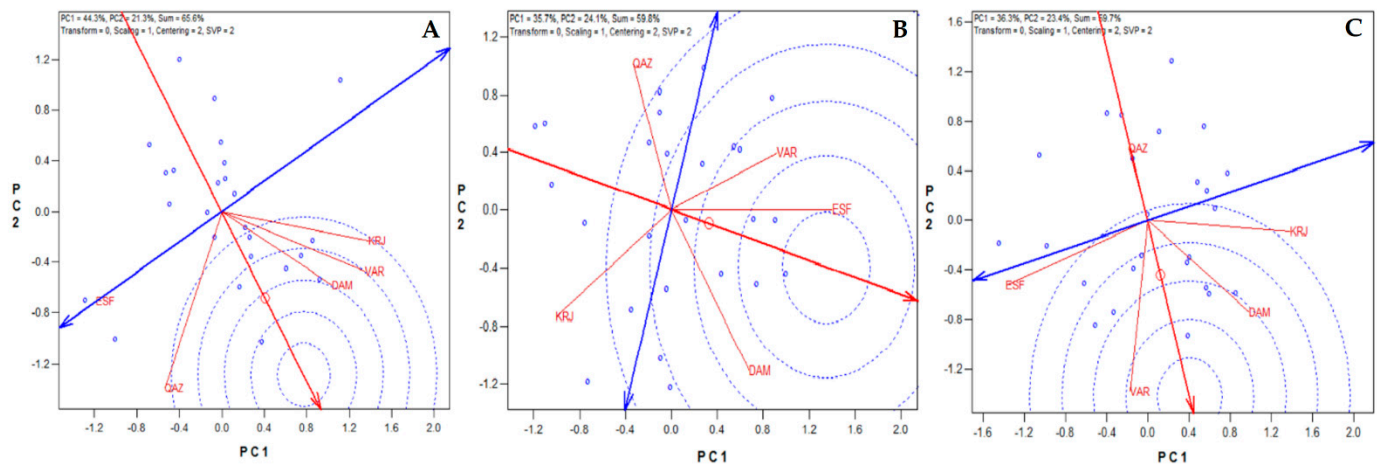
ESFAHAN < QAZVIN < KARAJ < VARAMIN < DAMAVAND

In the second year of the experiment, Isfahan and Damavand regions were identified as superior regions, and the Qazvin region as an unfavourable environment. Based on this, the ranking of regions in the second year is as follows:

QAZVIN < KARAJ < VARAMIN < DAMAVAND < ESFAHAN

Based on the ideal environment biplot results obtained from the average data of the two crop years studied, Varamin and Damavand regions were identified as superior environments, and Isfahan and Qazvin regions as undesirable environments. The ranking of the environments is as follows:

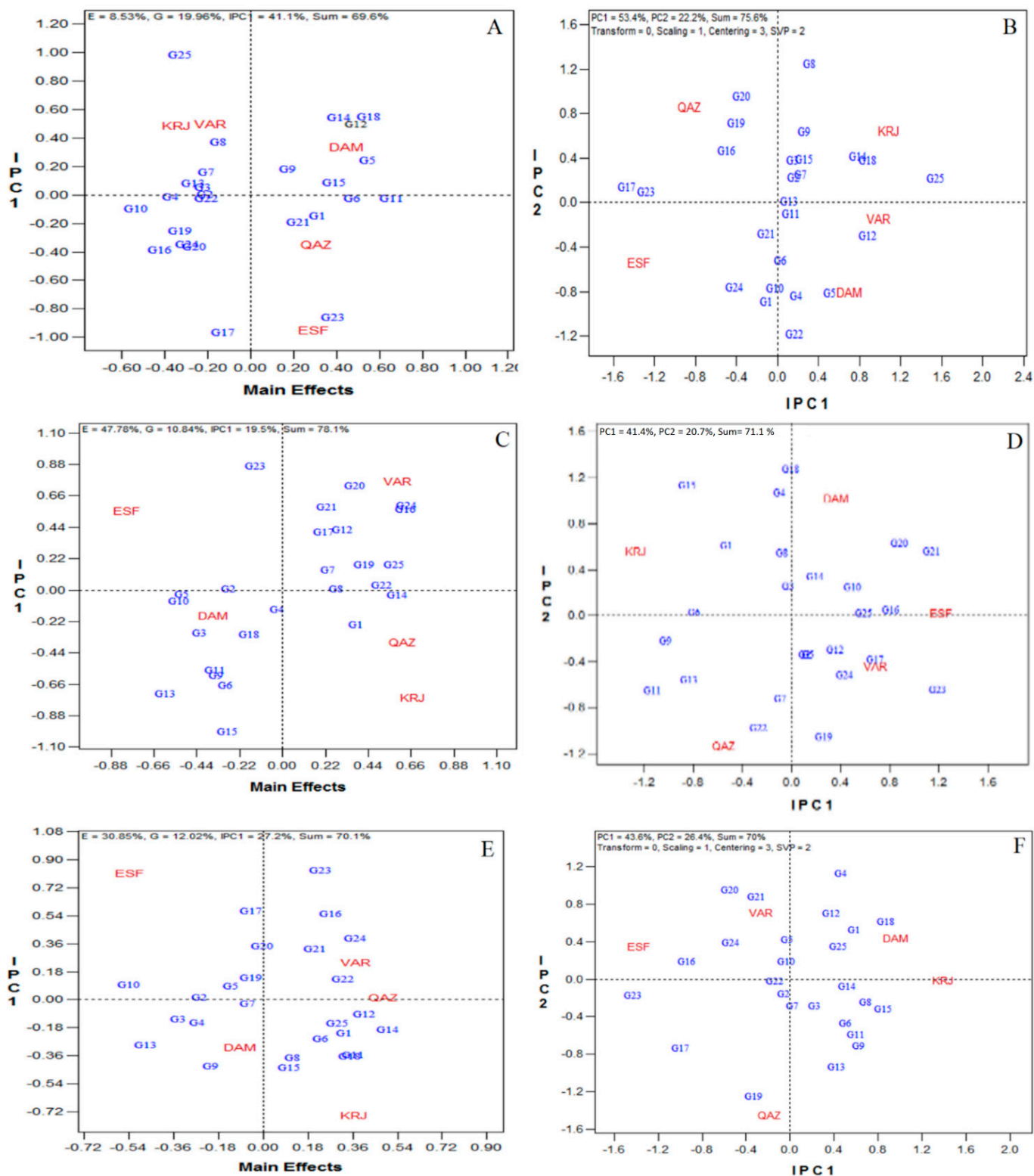
ESFAHAN < QAZVIN < KARAJ < DAMAVAND < VARAMIN (Figure 5).



**Figure 5.** Ranking biplot for comparison of the genotypes with the ideal genotype. (A): First year, (B): Second year, (C): Average of two years. G1:, G2:, G3:, G4:, G5:, G6:, G7:, G8:, G9:, G10:, G11:, G12:, G13:, G14:, G15:, G16:, G17:, G18:, G19:, G20:, G21:, G22:, G23:, G24:, G25:(DAM: DAMAVAND, VAR: VARAMIN, KRJ: KARAJ, ESF: ESFAHAN, QAZ: QAZVIN).

### 3.5. Stability Based on the AMMI Analysis

According to the AMMI1 graph in the first crop year, which explains 69.6% of the total variance of the data, the share of environment was 8.53%, the share of genotype was 96.19%, and the share of the first component was 41.1%. According to this biplot, any genotype close to the mean axis and in the positive part has higher stability. Accordingly, the G9 genotype was identified as a stable genotype. G14, G18, G12, and G5 genotypes in the Damavand, G8 genotype in Karaj and Varamin regions, G1 and G21 genotypes in Qazvin regions, and G23 genotype in Isfahan region all had higher yield than the other genotypes. According to the AMMI2 biplot, 75.6% of the total data variance was covered, of which 53.4% related to the first component and 23.2% related to the second component. The biplot had high yield G14 and G18 genotypes in Karaj region, G12 genotype in Varamin region, G5 genotype in Damavand region, and G2, G19 and G16 genotypes in Qazvin region. Accordingly, the G13 genotype was more stable than other genotypes. According to the AMMI1 biplot in the second crop year, 78.1% explained the data variance, of which 47.78% related to the effect of environment, 10.04% related to the effect of genotype, and 19.5% related to the first component. Based on the biplot, G8 and G7 genotypes were identified as stable genotypes. According to the biplot, G20, G24 and G10 genotypes in Varamin region, G1 genotype in Qazvin region, and G3, G18, G2 and G10 genotypes in Damavand region showed higher performance than the other genotypes. The AMMI2 biplot explains 71.1% of the data variance, of which 41.4% belonged to the first component and 20.7% to the second component. The biplot shows that G16 genotypes in the Isfahan region, G17 and G24 genotypes in the Varamin region, and G22 genotypes in the Qazvin region had better performance. G14 and G3 genotypes were stable due to their proximity to the biplot's origin. Based on the results from the AMMI1 biplot obtained from the average data of the two crop years tested, 70.1% of the variance of the data was justified, of which 30.85% related to the effect of the environment, 12.02% related to the effect of genotype, and 27.2% related to the effect of the first component. Based on the biplot, G5 and G19 genotypes were identified as stable genotypes. G22, G24, and G21 genotypes had higher yields in the Varamin region, and G9 genotypes in the Damavand region than other genotypes. The results obtained from the AMMI2 biplot explained 70% of the variance, of which 43.6% related to the first component and 26.4% related to the second component (Figure 6).



**Figure 6.** AMMI1 and AMMI2 of genotypes and environments based on biplot analyses. (A): First year AMMI1, (B): First year AMMI2, (C): Second year AMMI1, (D): Second year AMMI2, (E): Average of two years AMMI1, (F): Average of two years AMMI2. G1:, G2:, G3:, G4:, G5:, G6:, G7:, G8:, G9:, G10:, G11:, G12:, G13:, G14:, G15:, G16:, G17:, G18:, G19:, G20:, G21:, G22:, G23:, G24:, G25: (DAM: DAMAVAND, VAR: VARAMIN, KRJ: KARAJ, ESF: ESFAHAN, QAZ: QAZVIN).

#### 4. Discussion

Zulkiffal et al. [23] stated that the best model is when only the first two principal components are significant, and the other components have slight variance. The results obtained from the average data of two crop years identified stable genotypes. The G3 genotype had the lowest amount of the first principal component (0.0006), due to its low yield (2.29); the G22 genotype had 0.002 of the first principal component, and a mean yield of 2.52. It is connected to the mean of the linear coordinates from the origin (a dotted circle indicates the location of the mean of the locations); this axis line is called the mean of the locations. At the optimistic beginning of this axis, the genotypes have more performance and vice versa. A line perpendicular to the origin of the past and on the axis of the mean of the environments (two arrow signs in the biplot indicate this line) is used to determine the stability of the genotype. In this study, G2, G7 and G5 genotypes were identified as stable genotypes, and G23, G16, G15 and G18 genotypes as unstable genotypes. According to the first, second and average two years, it can be concluded that G2 and G21 genotypes are high yielding genotypes, and G13 genotype is a low yielding genotype, while G21 genotype is a stable genotype. G23, G18, G17 and G15 genotypes were identified as unstable genotypes. De Vita et al. [24] evaluated the yield stability of wheat cultivars and lines and selected high-yielding cultivars. Stability analysis was performed by different methods, and the results of the evaluated methods are somewhat similar. In most methods, Gascogne and Line C-81-14 had a more stable grain yield with an average grain yield of 7851 and 8522 Kg/ha. Based on the obtained results, Damavand and Varamin environments were identified as superior, and the Qazvin regions as unfavourable regions. According to the results of the experimental years, G12 and G21 genotypes were identified as superior genotypes and G13 genotype as undesirable genotypes. According to the AMMI biplot, the G18 genotype in Damavand region, the G19 genotype in Qazvin region, the G16 genotype in Isfahan region, and the G21 and G20 genotypes in Varamin region had high yields. G10 and G22 genotypes were identified as stable genotypes in this biplot. Tekdal and Kendal [25] examined 122 different durum wheat genotypes in two different environments using the AMMI model. They stated that 59.8, 3.5, and 36.7% of the total squares were allocated to the effect of genotype, environment, and GEI, respectively. Advanced lines were more stable than older cultivars and native lines. The G24 genotype was the most stable among the genotypes in the two places of stable yield. Other crops have been studied by other researchers such as maize [26–28], rice [29], and soybean [30] in recent years by the AMMI method. The AMMI model is suitable for introducing potential cultivars stable for different environments with variable climatic conditions. Farshadfar et al., 2006, evaluated the stability of 22 wheat genotypes in Iran using the AMMI method and graphic biplot analysis. The results showed that 92.5% of the changes relating to the sum of squares were explained using AMMI1, AMMI2, and AMMI3 methods, 4.5 times more than the linear regression analysis method. The yield and stability of 88 advanced wheat genotypes in 188 environments were evaluated using the AMMI method. The results showed that none of the studied genotypes showed significant superiority over other genotypes [31]. Sharma et al. [32] used the GGE biplot model to find winter wheat genotypes with high yield and stability, among 25 genotypes obtained from the international program of Simit in Central Asia and West Asia (IWWIP) for winter wheat breeding, and five genotypes were identified with high yield and stability.

#### 5. Conclusions

Accordingly, ABC Lombardia and Riana genotypes were identified as high-yielding, and Riana genotypes as stable genotypes. Based on the results of the polyhedral diagram, A 47/415 and Aneta genotypes were selected as superior genotypes in all three experimental periods. The results of the ideal genotype diagram were Ogniana and Riana genotypes, and based on the exemplary environment diagram results, Damavand and Varamin environments were identified as ideal environments.

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