IMAM KHOMEINI INTERNATIONAL UNIVERSITY
IJGPB
Iranian Journal of Genetics and Plant Breeding
Print ISSN : 2251-9610
Online ISSN : 2676-346X

Evaluating AMMI and BLUP models for the identification of high-yielding barley genotypes adapted to cold rainfed regions in Iran

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ABSTRACT INFO

Research Paper

Received: 29 Jun 2024

Accepted: 22 Dec 2024

ABSTRACT

In this study, various statistical methodologies, including Additive Main effects and Multiplicative Interaction (AMMI) and Best Linear Unbiased Prediction (BLUP), were employed to identify high-yielding rainfed barley genotypes that are suitable for the cold and rainy regions of Iran. The experimental design comprised 25 barley cultivars and lines, along with three check cultivars, arranged in a randomized complete block design with four replications over three crop years (2017-2020). The AMMI analysis revealed that certain genotypes, specifically G15 and G21, demonstrated stability and adaptability across diverse environments, consistently yielding higher than other genotypes. Following the estimation of best linear unbiased predictions and conducting a stability analysis via the AMMI method, it was found that the highest yields were recorded in genotypes G6, G7, G15, G21, and G22, whereas the lowest yields were associated with genotypes G12, G25, G26, G27, and G28. According to the BLUP indices, genotypes G6, G15, G21, G20, G22, G17, G7, G9, and G19 were identified as superior in terms of grain stability and yield relative to the other genotypes. In the stability assessment utilizing a third-type biplot (yield versus WAASB (Weighted Average of Absolute Scores of the Best) index), it was noted that genotypes G2, G9, G10, G14, G16, G17, G19, G20, and G22 exhibited both high yield and stability. Furthermore, genotypes G4, G62, G7, G9, G10, G15, G16, G17, G19, G20, G21, and G22, which demonstrated the highest WAASBY (Weighted Average of Absolute Scores of the Best Yield) values, were classified as stable and high-yielding. Ultimately, when the first principal components in the AMMI analysis or GGE Biplot account for a lower percentage of genotype-environment interaction, it is advisable to employ methodologies that incorporate all significant principal components to effectively identify superior genotypes.

Key words: *Hordeum vulgare*, Interaction effect, Multi-location, Rainfed, Stability.

How to cite this article:
Ahakpaz F., and Asadi A. A. (2024). Evaluating AMMI and BLUP models for the identification of high-yielding barley genotypes adapted to cold rainfed regions in Iran. *Iranian Journal of Genetics and Plant Breeding,* 13(1): 33-49.
DOI: 10.30479/ijgpb.2024.20572.1372

INTRODUCTION

Barley (*Hordeum vulgare* L.) is recognized as one of the most significant cereal crops, ranking fourth in terms of economic importance, following wheat, rice, and corn (Ferreira *et al.,* 2016). Globally, the area allocated for barley cultivation encompasses 47.6 million hectares, resulting in a production volume of 156.8 million tons. In Iran, the area under barley cultivation is approximately 1.65 million hectares, yielding an output of 3 million tons (FAO, 2022). Although barley is characterized by its wide adaptability, it is often associated with a lower economic value. Nevertheless, it presents a viable alternative to wheat in arid regions where rainfall is insufficient for wheat production (Zali and Barati, 2020).

The rate of breeding processes for quantitative traits in agricultural plants is significantly influenced by genotype×environment interaction effects. The more pronounced these effects are, the more difficult it becomes to select genotypes based solely on phenotypic characteristics. Genotype×environment interaction (GEI) effects are particularly critical for grain yield, which is recognized as a complex trait (Sharifi *et al.,* 2021). The yield of barley, for instance, is affected by the differential responses of barley genotypes across various environments, which can be attributed to these interaction effects. The interaction between genotype and environment is a vital consideration in the development and dissemination of improved crop cultivars and lines (Farshadfar *et al.,* 2012). Furthermore, this interaction presents a significant challenge in the selection of appropriate genotypes for specific traits. GEI effects can manifest in two forms: crossed, which arises from the incomplete correlation between traits in paired environments, and non-crossed, which results from the heterogeneity of genetic variance. Both forms can be assessed using Mixed Models (MM) (Yang, 2002), as direct testing is not feasible due to their lack of a Chi-square distribution. The application of mixed models facilitates the analysis of unbalanced data and data pertaining to different temporal stages of an organism, as well as the estimation of variance and covariance components (Yang, 2010). A method that has been introduced for the analysis of multi-environment data is the Restricted Maximum Likelihood (REML) approach, which is grounded in Henderson's theoretical framework (Henderson, 1984). This method addresses the limitations associated with variance analysis using the Least Squares (LS) method, particularly for unbalanced and heterogeneous data (Holland, 2006). The REML method offers several advantages over classical methods for estimating variance components, including the direct estimation of genetic correlations and their standard errors with enhanced accuracy, flexibility in linear models for analyzing both balanced and unbalanced data such as multi-environment experiments, high efficiency for experimental designs such as alpha lattice and augmented designs with a single replication, and a reduction in the occurrence of negative estimates of genetic parameters that may arise from inadequate experimental design in classical methodologies (Searle *et al.,* 1992; Liu *et al.,* 1997; Holland, 2006).

Numerous methodologies have been proposed for the analysis of yield stability, encompassing both parametric (univariate and multivariate) and non-parametric approaches. Notable examples of multivariate methods include the Additive Main Effect and Multiplicative Interactions (AMMI) method (Gauch and Zobel, 1997) and the GGE Biplot (Genotype+Genotype×Environment) method (Yan *et al.,* 2000). Furthermore, the Best Linear Unbiased Predictors (BLUP) method has been recommended for the evaluation of data derived from multi-environment trials (MET). The BLUP method is particularly effective in estimating the average of random effects with high precision, especially within mixed models such as linear mixed-effects models (LMM) (Olivoto *et al.,* 2019a).

The AMMI analysis is a widely utilized method for interpreting genotype×environment interaction effects in multi-environment uniform experiments. This analytical approach facilitates the graphical representation of interactions, thereby rendering it more effective than traditional variance analysis (Van Eeuwijk *et al.,* 2016). It has been extensively applied in research focused on evaluating GEI effects and yield stability across various crops (Rahayu, 2020; Hasani *et al.,* 2021; Namdari *et al.,* 2022). Furthermore, the best linear unbiased predictions (BLUP) method is employed to estimate the average yield of genotypes in multi-environment experiments (Nardino *et al.,* 2016; Olivoto *et al.,* 2017). The AMMI analysis captures the majority of GEI effects on the first axis of the principal component interaction effects (IPCA1), while the primary source of random error is linked to the final IPCAs (Mofidian and Moghaddam, 2013). To mitigate the limitations associated with the AMMI method, researchers have proposed the integration of AMMI and BLUP methodologies (Olivoto *et al.,* 2019a). This integration introduces an index known as the stability index of the weighted average of absolute scores of the best unbiased (WAASB) linear

predictions (Olivoto *et al.,* 2019a). The calculation of WAASB involves conducting the AMMI analysis on the best linear unbiased predictions rather than on the original multi-environment test data. From a practical perspective, BLUP and AMMI can be regarded as two distinct methodologies that pursue the same objective: differentiating the patterns of GEI (Olivoto *et al.,* 2019a). The WAASB index offers several advantages over the AMMI decomposition indices. It is based on absolute deviations rather than the squared deviations employed in AMMI analysis, making it less sensitive to outlier data. Additionally, the calculation of WAASB incorporates all principal components (Olivoto *et al.,* 2019a). In contemporary agricultural crop breeding, researchers strive to combine stability with yield to develop genotypes that are both stable and high-yielding. They evaluate both yield and stability traits concurrently to select high-yielding genotypes while minimizing GEI effects. Following the computation of the WAASB index, another index, referred to as weighted average of absolute scores of the best yield (WAASBY), can be derived, which simultaneously considers grain yield and genotype stability. Depending on the objectives of the breeding program, breeders may assign varying weights to the WAASB stability index and yield (Olivoto *et al.,* 2019a). The introduction and application of the WAASB index for assessing seed yield stability in genotypes across diverse environments have recently garnered significant interest among researchers (Hossain *et al.,* 2023; Behera *et al.,* 2023; Pour-Aboughadareh *et al.,* 2024). Consequently, numerous studies have been conducted utilizing this index to investigate the effects of GEI (Karimizadeh *et al.,* 2021; Sharifi *et al.,* 2021; Mousavi *et al.,* 2023).

The objective of this research was to identify high-yielding barley genotypes that are adapted to the climatic conditions of the cold dryland regions of Iran. This was achieved through the application of the AMMI method, as well as a combination of the AMMI and BLUP methods, utilizing the WAASB and WAASBY indices, along with other BLUP-based indices. Additionally, the study aimed to evaluate the efficacy of these two models in enhancing the understanding of genotype×environment interaction effects.

MATERIALS AND METHODS

In this study, twenty-five advanced and promising cultivars and lines of barley, selected from advanced common yield comparison experiments, were evaluated alongside the check cultivars Ansar, Abider, and Sararoud 1 (Table 1). The research was conducted under rainfed conditions utilizing a completely randomized block design with four replications across various rainfed research stations located in the cold and temperate regions of Maragheh, Kurdistan (Qamlo), Zanjan (Qidar), Ardabil, Kermanshah (Sararood), Shirvan, and Hamadan over a three-year period from 2017 to 2020 (Table 2). The specifications and meteorological data for the testing stations are presented in Tables 3 and 4, respectively. Field preparation operations were executed at the study sites to the extent feasible. The fields were plowed to a depth of 20-25 cm during the autumn of the preceding year. In the spring, prior to the flowering of weeds, a cultivator was employed, and a disk was utilized before planting in the fall. The requirement for fertilizer elements was determined based on soil tests conducted at each station. The experimental plots consisted of six lines, each measuring six meters in length, with a spacing of 20 cm between lines. The seeding rate was established at 400 seeds per square meter, in accordance with the weight of 1,000 seeds for the respective genotypes. Herbicides were applied to manage broadleaf weed populations. The remaining agricultural practices across the different stations were largely consistent.

After determining the seed yield of each genotype, a simple variance analysis was conducted for each year and location. The homogeneity of the error variance was assessed using Bartlett's test and Hartley's F-max test. Subsequently, a combined variance analysis was performed to examine the main effects of genotype and environment, as well as the interaction effect of genotype×environment. The F-test for sources of variation was executed based on mathematical expectations, assuming the randomness of years and locations, along with the constancy of genotypes. To evaluate the stability of the genotypes, the Additive Main effects and Multiplicative Interaction (AMMI) method was employed. During the AMMI variance analysis, the values of the principal components were calculated for each genotype and environment, and the corresponding biplots were generated (Rodriguez *et al.,* 2007). To quantify the stability of the genotypes, singular value decomposition (SVD) was applied to the matrix of the best unbiased predictions of genotype×environment interactions, utilizing a linear mixed effects model. Variance components were estimated using REML. The significance of random effects was assessed through the likelihood ratio test (LRT). Variance components were identified with the aid of a scree plot. Ultimately, in pursuit of simultaneously selecting a stable and productive

Table 1. Pedigree of promising barley varieties and lines in the studied environments.

Code	Genotype pedigree	Genotype origin
G1	Ansar	DARI
G2	Abider	DARI
G3	Sararood-1	DARI
G4	B-c-74-2/Abidar	DARI
G5	VA92-44-275//Tokak/Demir-2	DARI
G6	BAŞGÜL	DARI
G7	EFES30	DARI
G8	GkOmega/CWB117-5-9-5//Sararood	DARI
G9	Roho/Masurka//ICB-103020/3/Kc/MullersHeydla//Sls/4/Sararood/5/GaraArpa/6/1142/Gumhuriyet//Radical IRB-008-54-0MH-0MH-0MH-0MH-2MH	DARI
G10	Obruk-86/3/Alpha//Sul/Nacta/4/Sadik-05/5/Icb-100059	DARI
G11	Reihan-03//Tokak/Demir-2	DARI
G12	MB-90-3(Beecher/1-BC-80411//1-BC-80593)	DARI
G13	Beecher-Sel//Gloria"S"/Copal"S"/4/Deir Alla 106//Hem/Bc/3/Rihane"S"	DARI
G14	Unknown	DARI
G15	GkOmega/4/Arr/Esp//Alger/Ceres362-1-1/3/ICB-100175	DARI
G16	ChiCm/An57//Albert/3/ICB-102379/4/GkOmega	DARI
G17	AYDANHANIM	DARI
G18	ZEYNELAGA	DARI
G19	G.B.71530	DARI
G20	G.B.71530	DARI
G21	G.B.71538	DARI
G22	G.B.71557	DARI
G23	G.B.72566	DARI
G24	G.B.72581	DARI
G25	G.B.72650	DARI
G26	G.B.72655	DARI
G27	G.B.72665	DARI
G28	G.B.72680	DARI

DARI: Dryland Agricultural Research Institute.

Table 2. Environments examined in the nationwide uniform test.

Code	Environment	Code	Environment	Code	Environment	Code	Environment
Mara1	Maragheh-1st year	Shir2	Shirvan-2nd year	Sara1	Sararood-1st year	Hame3	Hamedan -3rd year
Mara2	Maragheh-2nd year	Shir3	Shirvan-3rd year	Sara2	Sararood -2nd year	Arde1	Ardebil-1st year
Qam1	Qamlu-1st year	Zan1	Zanjan-1st year	Sara3	Sararood -3rd year	Arde2	Ardebil -2nd year
Qam2	Qamlu-2nd year	Zan2	Zanjan-2nd year	Hame1	Hamedan-1nd year	Arde3	Ardebil -3rd year
Qam3	Qamlu-3rd year	Zan3	Zanjan-3rd year	Hame2	Hamedan -2nd year		

genotype, the $WAASB_i$ and $WAASBY_i$ stability metrics were employed to quantify stability, as described by the following equations (Olivoto *et al.,* 2019a).

In the context of the presented equations, $WAASB_i$ represents the weighted average of the absolute scores for the i-th genotype, while IPCAik denotes the score of

$$WAASB_i = \frac{\sum_{k=1}^{P}|IPCA_{ik} \times EP_k|}{\sum_{k=1}^{P} EP_k}$$

$$WAASBY_i = \frac{\left\{W_Y \times \left[\left(\frac{GY_i}{GY_{max}}\right) \times 100\right]\right\} + \left\{W_s \times \left(100 - \frac{WAASB_i}{WAASB_{min}}\right)\right\}}{W_Y + W_S} \quad (1)$$

Table 3. Geographical characteristics and soil types of the investigated agricultural research stations.

Station	Longitude (degrees east)	latitude (degree north)	Height above sea level (meters)	Soil texture
Maragheh	46 ', 15 °	37 ', 15 °	1720	Clay-Loam
Qamlu	47 ', 00 °	35 ', 20 °	1500	Clay-Loam
Zanjan	48 ', 49 °	36 ', 58 °	1875	Loam-Silt
Ardabil	48 ', 17 °	38 ', 15 °	1342	Clay-Loam
Sararod	57 ', 55 °	37 ', 23 °	1351	Silt-Clay-Loam
Hamedan	48 ', 32 °	34 ', 53 °	1733	Sand-Loam
Shirvan	58 ', 07 °	37 ', 19 °	1086	Clay-Loam

Table 4. Comparative analysis of the average annual rainfall and temperature recorded at the agricultural research stations examined in this study over the three-year period under investigation.

Cropping years	Variables	Ardebil	Maragheh	Sararod	Shirvan	Zanjan	Qamlu	Hamedan
2017-2018	Rain	226.4	326.8	518.8	252.7	426.3	396.3	389.2
	Temperature	8.06	5.2	11.7	9.3	7.5	6.9	8.4
2018-2019	Rain	274.2	494.6	782.5	337.8	430	444.5	506.8
	Temperature	8.1	5.6	11.1	9.8	7.6	7.4	8.4
2019-2020	Rain	255.4	423.3	521.2	141.3	390	339.5	307.9
	Temperature	8.3	5.1	11	9.1	7.4	7.1	8.2
Long-term	Rain	251.9	356.1	413.9	247.1	349.2	339.4	285.3
	Temperature	7.5	5.3	11.4	10	7.5	6.5	8.5

the i-th genotype along the k-th axis of the Interaction Principal Component Analysis (IPCA). Additionally, EPk signifies the proportion of variance accounted for by the k-th IPCA. The genotype exhibiting the lowest WAASB value is deemed stable, as indicated by Yan *et al.* (2000). The simultaneous selection for both mean yield and stability is facilitated through the WAASBY index, which allocates weights to mean yield (Y) and the stability index (WAASB). Specifically, $WAASBY_i$ is defined as the weighted average of WAASB and grain yield (GY) for the i-th genotype. Here, WY represents the weight assigned to the response variable, which, in this instance, is grain yield; GY_i refers to the average seed yield of the genotype across all environments; GY_{max} indicates the highest average grain yield recorded; WS is the weight attributed to the stability index (in this case, the WAASB index); $WAASB_i$ is the weighted average of the absolute scores for the i-th genotype; and $WAASB_{min}$ denotes the minimum WAASB value observed among the genotypes. In addition to the WAASB and WAASBY indices, statistical measures derived from the BLUP/REML mixed model, including the harmonic mean of genotypic values (HMGV), the relative performance of genotypic values (RPGV), and the harmonic mean of relative performance of genotypic values (HMRPGV), were also employed (Resende, 2004).

$$(2) \qquad HMGV_i = \frac{E}{\sum_{j=1}^{E}\left(\frac{1}{CV_{ij}}\right)}$$

$$(3) \qquad RPGV_i = \frac{1}{E}\left(\frac{\sum_{j=1}^{E} GV_{ij}}{\mu_i}\right)$$

$$(4) \qquad HMRPGV_i = \left(\frac{E}{\sum_{j=1}^{E}\frac{1}{RPGV_i}}\right)$$

In the equations presented, E denotes the number of environments, while GV_{ij} represents the genotypic value of the i-th genotype in the j-th environment, expressed as the average ratio across these environments. Additionally, μ_i signifies the average seed yield in the j-th environment. The harmonic mean of the relative performance of genotypic values is employed for the simultaneous selection of yield, stability, and compatibility among genotypes. In all methodologies utilized, the highest value indicates the most stable genotype. All statistical analyses were conducted using the Metan (Multi-Environment Trial Analysis) package (Olivoto, 2019) within R Studio software.

RESULTS AND DISCUSSION

The uniformity of the variance of experimental errors was evaluated using Bartlett's test and the F max Hartley test (Table 5). These statistical analyses were based on the variance of experimental errors calculated for yield data collected over multiple years and across different stations. The significant result obtained from Bartlett's test, in conjunction with the non-significant result from the F max Hartley test, suggests that the within-treatment variances are consistent. It is noteworthy that when assessing the uniformity of error variances, it is prudent to employ multiple testing methods. If any one of these methods yields a non-significant result, the uniformity of the experimental error variances may be accepted (Valizadeh and Moghadam, 2010).

Variance analysis was performed on data collected from seven locations over a three-year period (Table 6). Data from Shirvan in the first year and Maragheh in the third year were excluded due to distortion. The analysis, including the F-test, was based on the mean square and assumed randomness concerning both year and location, as well as the constancy of genotypes. The interaction effects of year×location and genotype×year×location were found to be significant at $p<0.01$, while the year effect was significant at $p<0.05$, and the effects of location and genotype were significant at $p<0.1$. These results indicate variability in environmental conditions across the different regions and years (Table 6). The significant interaction effect of year×location suggests a substantial influence on the triple interaction effect. The significance of the triple interaction of genotype×location×year (environment) implies that genotypes exhibit varying responses across different environments, thereby allowing for the assessment of grain yield stability. Variations in genotype responses are typically attributed to differences in gene expression or their distinct manifestations in varying environmental contexts (Jafari and Farshadfar, 2018). The main effect of the environment (comprising both main and interaction effects) and the interaction effect of genotype×environment (encompassing both double and triple interaction effects) accounted for the largest proportions of the total variance observed in the

Table 5. The variance of experimental errors across various distinct locations during three crop seasons, along with the results of the Fmax Hartley and Bartlett's tests utilized to assess the uniformity of variances.

Croping season	Mean of squares						
	Ardebil	Maragheh	Sararod	Zanjan	Hamedan	Qamlu	Shirvan
2017-2018	0.1206	0.1725	0.1706	0.1478	0.1796	0.1801	-
2018-2019	0.1761	0.1129	0.1377	0.1043	0.2006	0.1380	0.130
2019-2020	0.1222	-	0.1119	0.1404	0.1760	0.17	0.1459
Fmax Hartley=1.92^{ns}							
Bartlets test=141.4**							

** and *: Significant at the probability level of 1 and 5%, respectively.

Table 6. The results of a combined variance analysis of the yield of promising barley lines across the studied locations over a three-year period in a cold climate.

Source	df	Sum of square	Mean of square	Percentage of sum of square
Year	2	370.03	185.01**	22.50
Location	6	466.61	77.77*	28.38
Year×location	10	314.1	31.41***	19.10
Block (year×location)	57	70.3	1.23	4.28
Genotype	27	15.32	0.57*	0.93
Year×genotype	54	19.87	0.37	1.21
Location×genotype	162	56.28	0.35	3.42
Year×location×genotype	270	101.93	0.38***	6.20
Error	588	229.79	0.149	13.98
Total	2127	1644.24		
Coefficient of variation (%)	13.2			

***, ** and *: Significant at the probability level of 1, 5 and 10%, respectively.

experiments, with contributions of 69.98% and 10.83%, respectively (Table 6). Generally, a high impact of the environment coupled with a low interaction effect of genotype×environment suggests that the studied genotypes exhibit good stability (Ehyaei *et al.,* 2022). Some researchers have noted that the environment contributes the largest sum of squares, indicating the presence of diverse testing environments (Kanouni *et al.,* 2007; Ehyaei *et al.,* 2022). Despite the significance of the main effect of genotype, the relatively small contribution of genotype to the total sum of squares (approximately 1%) can be attributed to the effective selection of these genotypes in preliminary breeding program experiments (Golkari *et al.,* 2021). Among the genotypes studied, G6, G7, G15, G21, and G22 exhibited the highest grain yields, while G12, G25, and G28 recorded the lowest yields. Variations in climate, soil conditions, and crop management practices across different years and experimental locations during the growth period may explain the observed differences between environments. Furthermore, the significance of double and triple interaction effects, along with genetic diversity among genotypes and their responses to geographical and climatic factors, must be taken into account. Consequently, identifying the genotype with the highest yield alone may be insufficient. A stability analysis that considers both high grain yield and minimal yield fluctuation across different years is essential for identifying genotypes that are well-suited for the region. To facilitate this, stability analysis was conducted using AMMI methods and best linear unbiased predictions to identify stable genotypes with high grain yield.

AMMI analysis

The AMMI analysis presented in Table 7 indicates that the first eight principal components are statistically significant, collectively accounting for nearly 85% of the variation in the GEI effect. Notably, the first and second components exert the most substantial influence, contributing 37.6% to the expression of this interaction effect, while the subsequent components follow in terms of their relative importance. The variance attributed to each component is essential for effectively differentiating genotypes and validating the observed relationships. In principal components analysis, the objective is to utilize a linear combination of variables to elucidate the majority of their variance. The first component captures the highest amount of variance, whereas the second component addresses the largest portion of the residual variance that

Table 7. AMMI analysis for the grain yield of promising rainfed barley varieties in cold climate conditions.

Source	df	Sum of square	Mean of square	Percentage of sum of square	Acumulative percentage of sum of square
ENV	18	1152.62	64.03**		
REP(ENV)	57	69.84	1.22		
GEN	27	12.48	0.46**		
GEN: ENV	486	159.63	0.328**		
PC1	44	30.72	0.698**	19.2	19.2
PC2	42	29.37	0.699**	18.4	37.6
PC3	40	22.06	0.551**	13.8	51.5
PC4	38	14.6	0.384**	9.1	60.6
PC5	36	12.67	0.352**	7.9	68.6
PC6	34	10.46	0.308**	6.6	75.1
PC7	32	9.28	0.29**	5.8	80.9
PC8	30	7.43	0.248**	4.7	85.6
PC9	28	5.11	0.182	3.2	88.8
PC10	26	3.96	0.152	2.5	91.3
PC11	24	3.35	0.149	2.1	93.4
PC12	22	3.14	0.143	2	95.3
PC13	20	2.25	0.112	1.4	96.7
PC14	18	2.12	0.118	1.3	98.1
PC15	16	1.17	0.073	0.8	98.8
PC16	14	1.11	0.079	0.7	99.5
PC17	12	0.56	0.047	0.4	99.9
PC18	10	0.23	0.023	0.1	100
Residuals	1539	225.09	0.14		
Total	2127	1779.27	0.68		

** and *: Significant at the level of 1 and 5%, respectively.

remains unexplained by the first component (Sharifi, 2021; Karimizadeh *et al.,* 2021). Additionally, other researchers have acknowledged the limited role of the two primary components in elucidating variations in the GEI effect (Aghaee Sarbezeh *et al.,* 2012; Karimizadeh *et al.,* 2020; Amini *et al.,* 2023).

Genotypes exhibiting extreme values (both positive and negative) of the IPC1 demonstrate a significant interaction effect with their environment, whereas genotypes with values approaching zero exhibit a minimal interaction effect. Among the evaluated genotypes, G4, G5, G9, G11, G14, G15, G18, G19, G20, G21, and G26 were identified as having the lowest IPC1 values. Notably, only G15 and G21 surpassed the mean total yield of 2.92 tons per hectare, thereby qualifying as stable genotypes with high general stability (Table 8). Figure 1 illustrates the biplot of the first principal component of the interaction effect plotted against the average yield of AMMI1. In this biplot, the horizontal axis represents the cumulative main effects (average yields), while the vertical axis denotes the multiplicative interaction effects (the values of the first principal component of the interaction effect). The central vertical line of the biplot indicates the total average yield. Genotypes and locations positioned to the right of this line yield higher than the total average. The horizontal axis at the center of the biplot (IPCA1) signifies the absence of GEI effects; thus, the proximity of genotypes and environments to this horizontal line correlates with reduced interaction effects (Yan and Hunt, 2001). As previously noted, genotypes and environments exhibiting a pronounced interaction effect are characterized by substantial values (either positive or negative) for the first principal component of the interaction effect. Consequently, genotypes G3, G12, G13, G24, G25, and G28 were determined to be more unstable compared to their counterparts. It was also observed that the environments Mara1, Qam1, Sara1, Arde1, and Hame3 yielded above-average results; however, they did not exhibit a consistent trend in the first principal component of the interaction effect. Conversely, Arde2, Zan3, and Shir3 recorded the lowest IPC1 values, while Sara2 and Zan1 exhibited the highest IPC1 values (Figure 1).

Genotypes G4, G9, G10, G19, and G21 were identified as the most stable genotypes, as evidenced by their low values for the first and second interaction principal component axes (IPCA1 and IPCA2), and their positioning near the center of the AMMI2 biplot (Figure 2). The AMMI2 biplot serves as a tool for evaluating the discriminatory capacity of various environments and for understanding the interrelationships among them. According to the biplot analysis, the environments Hame1, Sar2, and Arde1, characterized by long vectors, exhibited a high degree of separation and are thus deemed suitable for assessing the relative efficiency of genotypes and for distinguishing among them. These environments are particularly valuable for the selection of specific genotypes, especially when considering the categorization of target environments into mega-environments. In contrast, environments situated near the origin of the biplot demonstrate limited differentiation capability and provide minimal

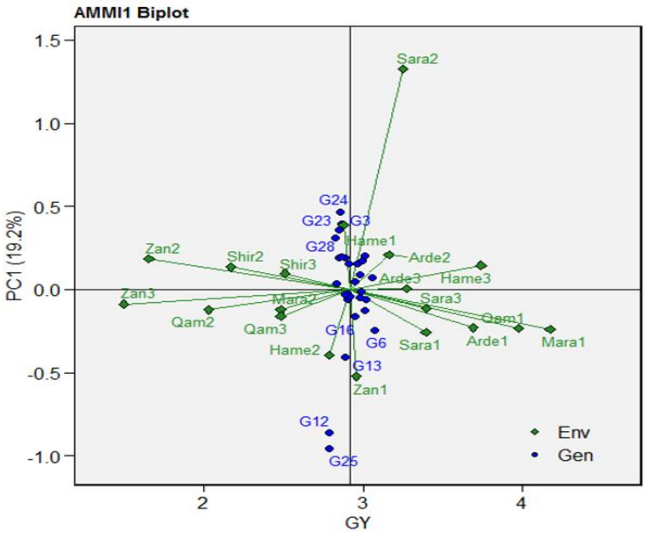

Figure 1. AMMI1 biplot for 28 barley genotypes across 18 different environments.

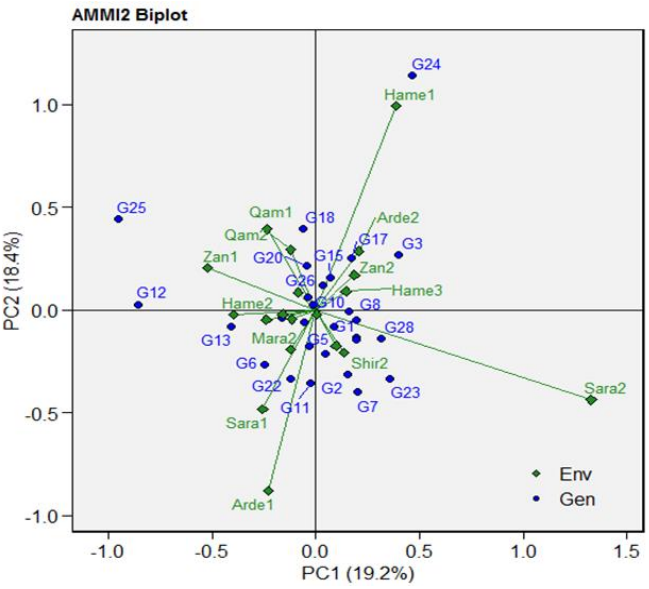

Figure 2. Biplot of the AMMI2 analysis, which is utilized to identify superior genotypes and differentiate environments based on the first and second principal components.

Table 8. First to tenth principal components for promising barley genotypes and investigated environments.

Genotype	Yield	IPCA1	IPCA2	IPCA3	IPCA4	IPCA5	IPCA6	IPCA7	IPCA8	IPCA9	IPCA10
G1	2.89	0.19	-0.13	-0.08	0.13	-0.09	-0.25	-0.22	0.43	0.03	0.13
G2	2.91	0.15	-0.31	-0.05	-0.31	-0.03	-0.32	-0.16	-0.38	-0.18	-0.23
G3	2.86	0.4	0.27	-0.49	0.11	0.16	0.43	-0.54	-0.13	-0.28	0.09
G4	2.92	-0.04	0.06	-0.31	-0.05	0.19	0.07	0.06	0.32	-0.14	0.24
G5	2.87	-0.03	-0.18	-0.01	0	-0.16	-0.53	-0.01	-0.42	-0.17	-0.19
G6	3.07	-0.25	-0.26	-0.43	-0.33	0.61	0.05	0.05	0.04	-0.08	-0.24
G7	3.01	0.2	-0.4	-0.12	0.022	0.17	-0.28	0.38	-0.12	0.14	0.19
G8	2.87	0.19	-0.04	0.11	-0.03	0.09	0	-0.19	0.07	0.16	0.17
G9	2.98	0.09	-0.08	0.16	0.027	-0.04	-0.05	0.39	-0.01	0.01	0.33
G10	2.96	0.15	0	0.09	0.06	-0.21	-0.06	-0.26	0.18	-0.09	-0.2
G11	2.9	-0.02	-0.35	-0.29	0.35	-0.1	-0.23	-0.05	0.04	-0.11	0.21
G12	2.78	-0.86	0.03	0.18	-0.17	0.02	0.25	-0.31	-0.25	0.28	0.11
G13	2.88	-0.41	-0.08	0.35	-0.1	-0.21	0.14	-0.03	0.32	-0.13	0.06
G14	2.95	0.04	-0.21	0.107	0.53	-0.16	0.05	-0.18	0.17	0.03	-0.43
G15	3.05	0.07	0.16	-0.61	-0.2	-0.16	0.08	0.14	0.32	-0.09	-0.13
G16	2.95	-0.16	-0.04	-0.03	0.45	-0.26	-0.03	-0.11	-0.04	0.25	-0.17
G17	2.99	0.17	0.26	-0.38	-0.75	-0.53	-0.02	0	-0.05	0.4	-0.04
G18	2.9	-0.06	0.39	-0.07	0.34	-0.41	0.18	0.01	-0.31	-0.06	0.18
G19	2.99	-0.01	0.02	-0.11	0.19	0.12	0.19	0.15	-0.09	0.45	-0.08
G20	2.98	-0.04	0.21	-0.11	0.046	-0.09	0.1	0.17	-0.25	-0.07	0.24
G21	3.02	-0.06	-0.06	-0.12	0.17	0.23	0.3	0.48	-0.18	-0.19	-0.18
G22	3.01	-0.12	-0.33	0.15	0.13	0.059	0.12	0.12	-0.17	-0.6	0.09
G23	2.85	0.36	-0.33	0.3	-0.07	0.43	-0.15	-0.24	0.08	0.38	0.16
G24	2.86	0.46	1.14	0.36	0.1	0.37	-0.34	0.06	-0.06	0.01	-0.09
G25	2.79	-0.95	0.44	0.11	-0.07	0.23	-0.37	-0.09	0.15	-0.16	0.01
G26	2.84	0.03	0.12	0.15	0.047	-0.04	0.13	0.36	0.29	0.17	-0.34
G27	2.85	0.19	-0.14	0.58	-0.3	-0.34	0.03	0.19	0.13	-0.35	0.01
G28	2.83	0.31	-0.13	0.57	-0.24	0.15	0.52	-0.16	-0.13	-0.09	-0.08
Arde1	3.69	-0.23	-0.88	-0.13	0.077	-0.38	0.52	-0.01	0.39	-0.07	0.09
Arede2	3.16	0.21	0.29	0.4	-0.49	0.22	0.15	0.28	0.25	0.15	0.07
Arde3	3.27	0.004	-0.02	-0.01	0.89	0.77	0.01	-0.1	0.29	0.01	-0.24
Hame1	2.88	0.39	0.99	-0.69	-0.11	-0.23	0.24	-0.14	0.39	0.2	-0.09
Hame2	2.77	-0.39	-0.02	-0.84	-0.26	0.51	0.27	0.28	-0.37	-0.31	0
Hame3	3.74	0.14	0.09	0.1	0.43	0.43	-0.19	0.25	-0.34	0.24	0.61
Mara1	4.17	-0.23	-0.05	-0.35	0.26	-0.59	-0.23	0.19	-0.34	0.09	-0.25
Mara2	2.48	-0.12	-0.19	-0.04	-0.19	0.09	-0.18	-0.37	0.23	-0.9	0.06
Qam1	3.98	-0.23	0.39	0.12	0.14	-0.11	-0.14	0.08	-0.38	-0.27	-0.03
Qam2	2.03	-0.12	0.29	0.49	-0.09	-0.32	0.29	-0.31	0.02	-0.47	-0.3
Qam3	2.48	-0.16	-0.02	0.09	-0.06	-0.11	-0.16	-0.14	0.08	0.14	-0.14
Sara1	3.94	-0.26	-0.48	-0.27	-0.12	-0.09	-0.19	-0.26	0.06	0.35	-0.18
Sara2	3.25	1.32	-0.44	-0.02	0.13	0.12	-0.1	0.33	-0.1	-0.2	-0.16
Sara3	3.4	-0.11	-0.04	0.57	-0.21	0.21	0.31	0.2	-0.34	0.52	-0.34
Shir2	2.17	0.13	-0.21	0.12	-0.46	0.24	0.08	-0.12	-0.02	-0.3	0.09
Shir3	2.51	0.096	-0.17	-0.17	-0.33	0.13	-0.49	0.1	0.04	0.19	0.27
Zan1	2.96	-0.52	0.21	0.29	0.22	-0.16	-0.25	0.74	0.42	-0.14	0.19
Zan2	1.65	0.18	0.17	0.08	0.11	-0.01	-0.39	-0.24	-0.12	0.02	0.18
Zan3	1.49	-0.08	0.08	0.24	0.08	0.07	-0.28	-0.41	-0.14	-0.11	0.18

information regarding the genotypes. Consequently, these environments should not be employed as reference experimental settings (Karimizadeh *et al.,* 2020). Furthermore, the biplot can facilitate the examination of correlations between environments. Hame1, Arde2, Zan2, and Hame3 exhibited a high correlation with one another, while Arde1, Sara1, and Mara2 displayed a similar pattern based on the vector lengths and the angles between them. Additionally, Qam1, Qam2, and Zan1 also demonstrated a strong correlation.

Therefore, it can be inferred that these environments may be regarded as similar in future studies aimed at evaluating the yield stability of cultivars.

Best linear unbiased predictions

The Scree test was performed to ascertain the optimal number of components that could elucidate the GEI effect. The results indicated that the first ten principal components significantly contributed to the explanation of the interaction within the GEI matrix derived from BLUP (Figure 3). Specifically, the first and second principal components accounted for only 19.2% and 18.4% of the variance, respectively. Therefore, relying solely on the first and second principal components for interpreting stability analysis results may lead to misleading conclusions. Given that a mixed model was utilized in the data analysis of this study, the likelihood ratio test was employed to evaluate the significance of the experimental factors. The findings revealed that both the genotype and GEI had a significant impact on grain yield (Table 9). The significance of the GEI effect suggests that the seed yield of a genotype may fluctuate across different environments. Consequently, the application of BLUP analysis is deemed appropriate for the examination of such data (Olivoto *et al.,* 2019a). As a result, the best linear unbiased predictions were estimated, and stability analysis was conducted on these BLUPs using the AMMI method.

Various genetic parameters, including genotypic variance, genotype×environment variance, variance of residual values, and phenotypic variance, were estimated utilizing the restricted maximum likelihood method. The ratios of these parameters to the phenotypic variance were found to be 1.28%, 26.74%, and 71.99%, respectively (Table 9). The selection of genotypes, recommendations for genotypes, and the identification of optimal environments in plant breeding programs frequently depend on multi-environment experiments. Consequently, accurate predictions are essential. In this study, the broad-sense heritability for seed yield was determined to be low, approximately 1.2%, primarily due to the significant influence of genotype×environment interaction in comparison to the effect of genotype alone. The coefficient of determination for genotype×environment interaction and the mean genotypic heritability rate were calculated to be 0.26 and 0.356%, respectively. The accuracy of genotype selection and the correlation between genotypic values across environments were measured at 0.5968 and 0.267, respectively. The genotypic coefficient of variation, residual coefficient of variation, and the ratio of the two were recorded as 1.766%, 13.206%, and 0.1337%, respectively. The effect of GEI on genotype effect was quantified at 20.75. To enhance the accuracy of predictions, breeders may consider employing statistical models with superior predictive capabilities, such as the best linear unbiased predictors. Furthermore, stability analysis utilizing the AMMI method can be conducted on these predictions (Olivoto *et al.,* 2019a).

The predicted average seed yields obtained through the BLUP method are illustrated in Figure 4. The genotypes G6, G15, G21, G7, and G22 exhibited the highest predicted yields, surpassing the overall mean. Conversely, the genotypes G12, G25, G28, G26, and G27 demonstrated the lowest yields, which were below the mean yield of all genotypes.

To evaluate the stability of the genotypes, a biplot diagram was employed, illustrating the relationship

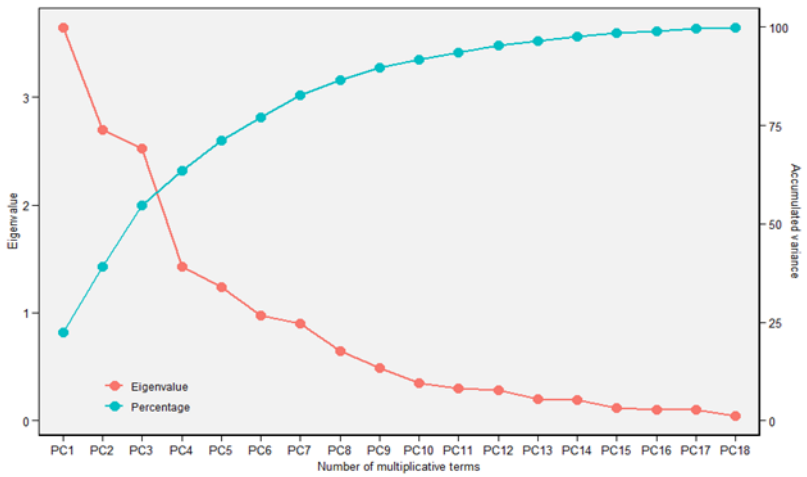

Figure 3. Eigenvalues of the Best Linear Unbiased Prediction for Genotype-Environment Interaction (BLUP_GEI) matrix concerning grain yield.

Table 9. Evaluation significance of factors using the Likelihood Ratio Test (LRT) denoted by χ^2, as well as the estimation of variance components through Restricted Maximum Likelihood (REML) for seed yield.

Statistics	Likelihood statistics	
	Genotype	Genotype×environment
Chi square X^2	2.83	170.44
p-Value	9.2×10-2	5.92×10-39

Parameters estimated by the restricted likelihood method		Variance components, estimates (percent)
Genotypic variance	σ^2g	0.00266 (1.28%)
Genotype×environment variance	σ^2i	0.0552 (26.74%)
Variance of residual values	σ^2e	0.1486 (71.99%)
Phenotypic variance	σ^2P	0.2064
Broad-sence heritability	h^2g	0.012
coefficient of explanation of genotype×environment interaction effect	R^2gei	0.26
Mean genotypic heritability	h^2mg	0.356
Genotype selection accuracy and	As	0.5968
Correlation between genotypic values across environments	rge	0.267
Genotypic coefficient of variation	CVg (%)	1.766
Residual coefficient of variation	CVe (%)	13.206
Ratio of genotypic coefficient of variation to residual coefficient of variation	CVg/CVe ratio	0.1337
Ratio of genotype×environment interaction to genotype effect	σ^2i/σ^2g ratio	20.75

Values in parentheses are percentages of observed variance relative to phenotypic variance.

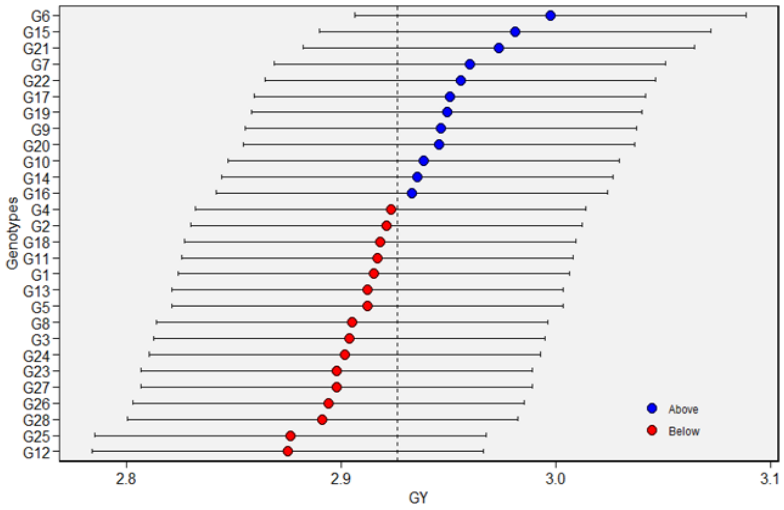

Figure 4. Predicted seed yield, as determined by the best linear unbiased prediction (BLUP), for 28 barley genotypes. The blue circles denote genotypes with BLUP values above the mean, while the red circles indicate those with BLUP values below the mean. The horizontal error bars represent the 95% confidence interval of the predictions, calculated using a two-tailed t-test.

between the first principal component of the environment and the nominal yield. This diagram, commonly referred to as a polygonal biplot or "which-won-where," displays the score of the first principal component of the environment on the X-axis and the nominal yield of the genotypes on the Y-axis (see Figure 5). Each genotype is represented by a line described by the equation y=a+bx, where x denotes the axis score of the IPCA1, a represents the mean yield of each genotype, and b signifies the IPCA1 for each

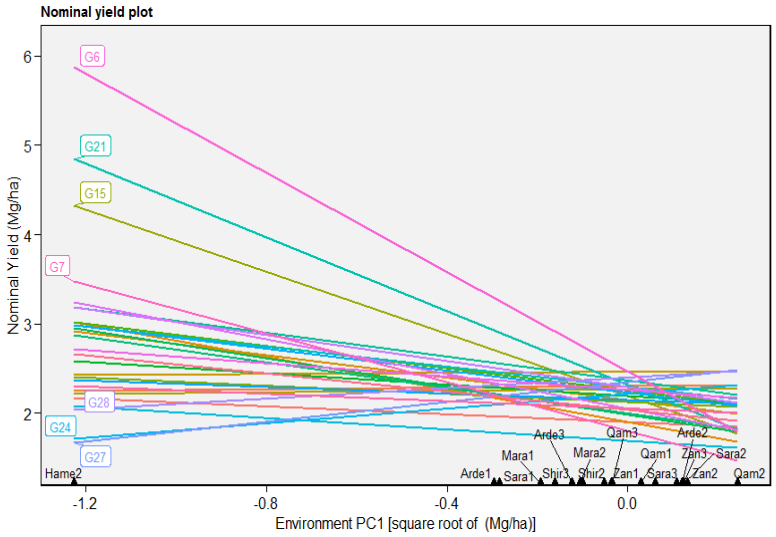

Figure 5. Yield evaluation diagram for 28 barley genotypes across 19 environments, illustrating the relationship between nominal seed yield and the scores of the first axis of the principal environmental component of interaction (IPCA1).

genotype (Olivoto *et al.,* 2019b). The equations of these lines suggest that, with the exception of genotypes G6, G21, G7, G15, G24, and G27, the remaining genotypes exhibited a minimal contribution to the GEI effect, as indicated by their low (b) coefficients (slopes of the lines), thereby rendering them more stable. Conversely, the aforementioned genotypes (G6, G21, G7, G15, G24, and G27) demonstrated higher principal component scores, indicating variable yields across different environments, and were thus classified as unstable, particularly in Hamedan during the second year. According to this diagram, which is derived from the first axis of the principal component analysis, among the high-yielding genotypes identified through the BLUP method (Figure 5), genotypes G6, G21, G7, and G15 were recognized as unstable due to the steepness of their corresponding lines. In contrast, the remaining genotypes, including G22, G17, G19, G9, G20, G16, G14, and G10, were deemed more stable. It is important to note that the interpretation of this diagram should be approached with caution, as it is based solely on the first principal component, which accounts for only 19.2% of the variability in the GEI. Consequently, additional analyses incorporating other principal components may provide more robust insights.

To achieve a more precise evaluation of stability, a third-type biplot was employed. In this biplot, grain yield is represented on the horizontal axis, while the weighted average of the absolute scores is depicted on the vertical axis (Figure 6). The genotypes and environments are categorized into four quadrants based on their yield and stability. Quadrant I includes

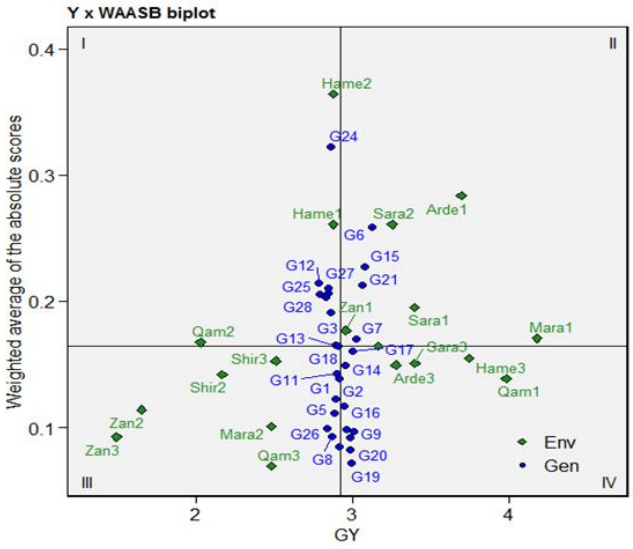

Figure 6. Biplot of yield versus weighted mean absolute scores for the best linear unbiased predictions of the genotypes×environment interaction effect (WAASB).

genotypes G24, G12, G28, G27, G3, and G25, along with environments Hame1, Hame2, and Qam2. These genotypes and environments are classified as unstable due to their significant contribution to the genotype-environment interaction effect, resulting in yields that are below the overall average. They are specifically suited for these environments (Olivoto *et al.,* 2019b). Quadrant II comprises genotypes G6, G15, G21, and G7, which exhibit yields above the mean but are considered unstable due to their elevated values on the WAASB index. The environments in

this quadrant, including Arde1, Sara1, Sara2, Zan1, and Mara1, warrant special attention due to their high yield and effective detection capability. In quadrant III, genotypes G11, G1, G5, G8, G26, and G18, along with environments Shir2, Shir3, Zan2, Zan3, Mara2, and Qam3, are identified as stable, characterized by low WAASB values and yields that are below average, indicating limited detection capability and suboptimal yield. Finally, quadrant IV consists of genotypes G19, G20, G22, G10, G9, G16, G2, G14, and G17, which are recognized for their high yield and stability, as evidenced by their low WAASB values and superior yield performance. These genotypes exhibit greater stability compared to others (Donoso-Nanculao *et al.,* 2016; Mohammadi *et al.,* 2016; Dos Santos *et al.,* 2019; De Abreu *et al.,* 2019).

Ranking of genotypes based on stability index weighting and grain yield dependent variable

In Figure 7, genotypes were identified utilizing the WAASBY values, which serve as a simultaneous selection criterion that incorporates both mean seed yield and the WAASB stability index. The calculation of WAASBY values involved assigning different weights to grain yield and the WAASB index. The graph illustrates that both indices hold equal significance in the selection of genotypes, as an identical weighting was applied to both the grain yield index and the WAASB stability index. Utilizing a 50:50 ratio for weighting, the genotypes exhibiting the highest WAASBY values, and thus deemed stable with high grain yield, include G19, G22, G20, G9, G10, G4, G7, G16, G17, G6, G15, G21, G14, G8, G5, G1, and G2. These genotypes are distributed across various quadrants of the graph, reflecting their stability and performance in terms of grain yield. It is crucial to conduct a comprehensive evaluation of genotype stability by comparing the two diagrams, while considering the weights assigned to the stability indices and the mean yield. Some genotypes that exhibit low scores in the first and second IPCA may yield misleading conclusions if selected or excluded based solely on the first and second principal components. In such instances, the WAASB index derived from the BLUP matrix may prove beneficial. However, caution is warranted in the interpretation of results, as only the simple component of GEI is observable in the first principal components, while the complex aspects of GEI may have been omitted in these biplots. In scenarios where the contribution of these components to the GEI is minimal, enhanced identification of high-yielding genotypes with extended stability can be achieved through the biplot of seed yield versus the weighted average of absolute

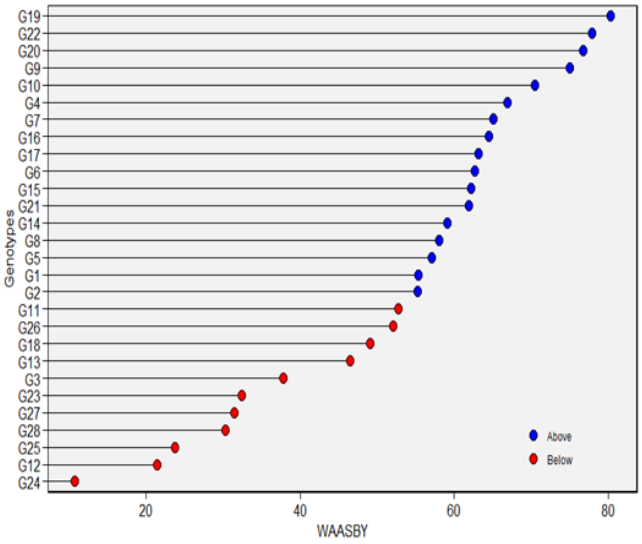

Figure 7. Estimated values of the weighted average of the Weighted Average of Agricultural Stability and Mean Yield (WAASBY) for 28 barley genotypes, utilizing an equal weighting of 50% for both yield and stability.

scores (Figure 6) or the WAASBY diagram (Figure 7).

In Figure 8, varying weights are assigned to two dependent variable indices: grain yield and the WAASB stability index. The chart presents rankings based solely on the WAASB stability index in the leftmost column, where a weight of 100% is allocated to the WAASB stability index and a weight of 0% to the grain yield variable on the X-axis. Progressing from left to right in each subsequent column, the weight assigned to the grain yield variable is incrementally increased by 5%, while the weight of the WAASB stability index is correspondingly decreased by 5%. The ranking in the rightmost column is exclusively based on grain yield, which receives a weight of 100%. The results of the ranking with a 50:50 weight ratio are illustrated in Figure 7, where both the WAASB stability index and grain yield are assigned equal weight. In the leftmost column, genotypes G20, G19, G4, G22, and G9 exhibited the highest stability, whereas G24, G6, G12, and G15 demonstrated the lowest stability. However, it is crucial to acknowledge that this ranking may lack reliability, as it does not account for the seed yield of the genotypes. In the rightmost column, where the ranking is determined solely by yield, irrespective of genotype stability, genotypes G6, G15, G7, G21, and G22 achieved the highest yields, while G12, G25, and G28 recorded the lowest yields. These findings are consistent with those presented in Figure 6. Genotypes are categorized by color to facilitate the identification of genotypic groups exhibiting similar stability and

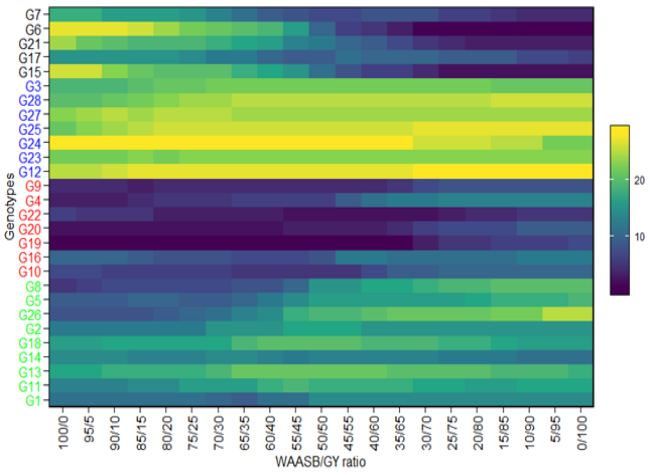

Figure 8. Rankings of 28 barley genotypes based on varying weights assigned to stability and yield performance.

yield characteristics. Specifically, genotypes G3, G28, G27, G25, G24, G23, and G12 (indicated in blue) are characterized as low-yielding but unstable, while G7, G6, G21, G17, and G15 (indicated in black) are classified as high-yielding but unstable. Genotypes G8, G5, G26, G2, G18, G14, G13, G11, and G1 (indicated in green) are identified as stable yet low-yielding. Finally, genotypes G9, G4, G22, G20, G19, G16, and G10 (indicated in red) are recognized as high-yielding and stable, and as depicted in Figure 8, they rank among the top selections based on both stability and yield, with equal weighting assigned to these two indicators.

Ranking based on BLUP based indicators

The application of a mixed model for the concurrent selection of yield and stability incorporates genotypic values, which enhances the accuracy of identifying optimal genotypes (Resende, 2004). In this context, BLUP model-based statistics, including HMGV, RPGV, and HMRPGV, were employed to discern superior genotypes with respect to yield and stability (Kolumbari and Filho, 2013). The analysis revealed that genotypes G6, G15, G21, G20, G22, G17, G7, G9, and G19 exhibited the highest numerical values, signifying their superiority in both stability and yield. In contrast, genotypes G12, G26, G25, G27, and G28 recorded the lowest values for HMGV, RPGV, and HMRPGV, categorizing them among the least effective in terms of grain yield and stability (Table 10.)

CONCLUSION

Based on the findings from the combined variance analysis, which indicated significant effects attributable to genotype, location, year, and the interaction effects of year×location and genotype×year×location, a stability analysis was performed utilizing AMMI and mixed model methodologies. The AMMI analysis revealed that the first and second principal components accounted for the most substantial contribution (37.6%) to the GEI effect, with subsequent components following in relative importance. Consequently, the genotypes G19, G11, G26, G5, G4, G14, G20, G18, G21, G15, and G9 exhibited the lowest values for the first principal component. Among these, only G15 and G21 demonstrated yields exceeding the mean yield, thereby categorizing them as stable genotypes with high general adaptability. In addition to the AMMI analysis, a mixed linear model was employed to analyze the trial data, and the likelihood ratio test was utilized to evaluate the significance of the experimental factors. The significance of the GEI effect underscored the variability in yield among genotypes across different environments. As a result, the BLUP were estimated, and stability analysis was conducted using the AMMI method. The evaluations indicated that the highest yields were recorded for genotypes G6, G15, G21, G7, and G22, while the lowest yields were associated with genotypes G12, G25, G28, G26, and G27. Based on the indices derived from BLUP, genotypes G6, G15, G21, G20, G22, G17, G7, G9, and G19 were identified as superior in terms of grain stability and yield relative to other genotypes. Furthermore, stability analysis employing a third-type biplot (yield vs. WAASB index) revealed that genotypes G19, G20, G22, G10, G9, G16, G2, G14, and G17 exhibited both high yield and stability. Given that the first two principal components contributed relatively low values to the GEI effect (19.2 and 18.4, respectively), the WAASBY genotypic stability index was utilized to assess genotype stability. This approach provided reliable estimates and facilitated the simultaneous interpretation of yield and stability within a two-dimensional graphical representation. The results indicated that genotypes G19, G22, G20, G9, G10, G4, G7, G16, G17, G6, G15, and G21, which exhibited the highest WAASBY values, were characterized as stable and high-yielding. By applying varying weights to both yield and stability indices, it was determined that the genotypes G9, G4, G22, G20, G19, G16, and G10 exhibited superior yields and stability compared to the other genotypes. Furthermore, when comparing traditional methods of stability analysis, such as AMMI and mixed models, it becomes evident that the application of these classical methods is not justifiable in instances where the homogeneity of variances across separate tests is not confirmed by various homogeneity of variances

Table 10. Yield stability statistics of barley genotypes across 18 environments, as determined by the REML/BLUP model.

Gen	GY	HMGV	HMGV_R	RPGV	RPGV_Y	RPGV_R	HMRPGV	HMRPGV_Y	HMRPGV_R
G1	2.89	2.68	17	0.993	2.9	19	0.992	2.9	18
G2	2.91	2.72	10	1	2.93	12	0.999	2.92	13
G3	2.86	2.67	23	0.988	2.89	22	0.984	2.87	21
G4	2.92	2.68	19	0.998	2.91	14	0.996	2.91	14
G5	2.89	2.7	13	0.996	2.91	15	0.994	2.9	15
G6	3.07	2.79	1	1.04	3.03	1	1.03	3.02	1
G7	3.01	2.73	8	1.02	2.97	4	1.01	2.96	5
G8	2.87	2.67	23	0.989	2.89	21	0.988	2.89	20
G9	2.98	2.74	7	1.01	2.96	8	1.01	2.96	7
G10	2.96	2.75	3	1.01	2.96	9	1.01	2.96	9
G11	2.9	2.68	18	0.994	2.9	17	0.992	2.9	17
G12	2.78	2.6	28	0.966	2.82	28	0.961	2.81	28
G13	2.89	2.7	14	0.995	2.91	16	0.993	2.9	16
G14	2.95	2.7	12	1	2.93	11	1	2.93	11
G15	3.05	2.77	2	1.03	3.01	2	1.03	3	2
G16	2.94	2.69	15	1	2.92	13	1	2.92	12
G17	3	2.74	6	1.02	2.97	6	1.01	2.96	8
G18	2.9	2.68	20	1.02	2.9	18	0.991	2.9	19
G19	2.99	2.71	11	0.994	2.95	10	1.01	2.95	10
G20	2.98	2.74	4	1.01	2.96	7	1.01	2.96	6
G21	3.02	2.73	9	1.02	2.98	3	1.02	2.97	3
G22	3.01	2.74	7	1.02	2.97	5	1.02	2.97	4
G23	2.85	2.67	22	0.987	2.88	23	0.983	2.87	23
G24	2.86	2.69	16	0.992	2.9	20	0.983	2.87	22
G25	2.79	2.63	26	0.972	2.84	27	0.965	2.82	27
G26	2.84	2.61	27	0.975	2.85	26	0.973	2.84	26
G27	2.85	2.64	24	0.982	2.87	24	0.978	2.86	24
G28	2.83	2.63	25	0.978	2.86	25	0.975	2.85	25
G3	2.86	2.67	23	0.988	2.89	22	0.984	2.87	21
G4	2.92	2.68	19	0.998	2.91	14	0.996	2.91	14
G5	2.89	2.7	13	0.996	2.91	15	0.994	2.9	15
G6	3.07	2.79	1	1.04	3.03	1	1.03	3.02	1
G7	3.01	2.73	8	1.02	2.97	4	1.01	2.96	5
G8	2.87	2.67	23	0.989	2.89	21	0.988	2.89	20
G9	2.98	2.74	7	1.01	2.96	8	1.01	2.96	7

GY: Grain yield (kg/ha), R: Rank of the given parameter, HMGV: Harmonic mean of genotypic values, RPGV: Relative performance of the genotypic values, HMRPGV: Harmonic mean of the relative performance of genotypic values.

tests. Conversely, when the first and second principal components in the AMMI analysis or GGE Biplot account for a minimal percentage of the GEI, the utilization of these two methods is not warranted. In such cases, it is advisable to employ methodologies that incorporate all significant principal components to effectively identify superior genotypes.

ACKNOWLEDGEMENTS

This article presents the findings of the research project entitled "Evaluation of Agricultural Characteristics, Compatibility, and Stability of Grain Yield of Barley Genotypes in Cold and Temperate Rainfed Regions, the Rainfed Agricultural Research Institute and various research stations situated in the cold climate regions of the country. The authors would like to express their gratitude and appreciation to the colleagues involved in this project at both the institute and provincial centers.

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