

AMMI Analysis of Yield Stability and Adaptability in Barley: A Case Study of Afghanistan

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Abstract: Barley, an important cereal crop in Afghanistan, has low productivity. To identify high yielding and stable genotypes, an evaluation of nine barley inbred lines and a national check was conducted for yield and its stability at 6 diverse environments in Afghanistan. Experiments were designed to determine genotype (G) × environment (E) interaction (GEI) effect on grain yield using AMMI model and to identify the high yielding and stable barley genotypes. The main effect of G and GEI were highly significant ($P < 0.01$) on grain yield. The E, G, and GEI accounted for 75.0%, 7.5% and 8.2% of variation in grain yield. Based on the AMMI stability parameters, line G9 was the most stable lines across environments with above average grain yield and will be recommended as a candidate for the consideration of the Varietal Release Committee in Afghanistan.

Keywords: Barley, GE interaction, AMMI model, Grain yield, Stability

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1. Introduction

Barley (*Hordeum vulgare*) is a major cereal crop cultivated under diversified agroclimatic conditions, from temperate to arid and semi-arid regions of the world, including Afghanistan (Kaur et al., 2022). Globally it is ranked fourth in the cereal production, after maize, rice and wheat (Yirgu et al., 2022). Barley belongs to cereal family Poaceae and three types of cultivated barley are *Hordeum vulgare* (a six-rowed type), *Hordeum distichum* (a two-rowed type) and *Hordeum irregulare* (the least cultivated type) (Bedada et al., 2014; Russell et al., 2016). Barley was domesticated 10,000 years ago from wild relative *Hordeum spontaneum* in Israel-Jordan region (Badada et al., 2014; Badr et al. 2000; Zohary, 2017). As it is a cool-season crop, it can also be successfully grown from an altitude of sea level to more than 3000 MSL and well adopted in stressed environment where soil erosion, drought and frost are the main problems for several crops (Fana et al., 2018). Barley is a

multipurpose crop with several economic value and utilization (Newman et al., 2019; Sharma et al., 2022; Zhou, 2010) and have nutritive components, comparable with maize and other cereals (Lyu et al., 2022; Meints et al., 2021; Obadi et al., 2021). Barely has been used primary for animal feed (Perera et al., 2022; Raud et al., 2021; Sakellariou and Mylona, 2020), hay and ethanol production (Diaz et al., 2022; Soufan and Al-Suhaibani, 2021; Tse et al., 2021).

Russian Federation, Germany, France, Ukraine, Australia, Canada, Spain, Turkey, United Kingdom and USA are top barely-growing countries of the world (Ullrich, 2014; Mittal, 2022) with total production of 157.0 million tons from 51.1 million hectares with an average yield of 3.31 t/ha, while in Afghanistan, a total of 127.7 thousand Mt barley produced in the area of 86.0 thousand hectares with productive of 1.48 t/ha (FAO, 2020; Tricase et al., 2018). The barely production showed negative trend (from 514 down to 301.8 thousand Mt) including area of production and

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productivity (by 58.7 thousand ha and 0.47 t/ha) between 2013 and 2016, respectively. The low production and productivity are strictly associated with the unavailability of improved barley variety with wide adaptability and stability across the country and negative effect of several biotic and abiotic factors as drought, frost, diseases and poor soil (Alasti, et al., 2020; Chapagain and Good, 2015; Cossani et al., 2010; Schils et al., 2018). USDA (2018) reported that import (barley grain) has been increased since 2014 to meet the domestic demand due to decreasing in production.

Crop production, in drier regions of the world, including Afghanistan, is highly dependent on utilization of improved variety and adaptation of improved crop production practices, efficient soil and water management and agrochemical practices (Akbarzai et al., 2021a; Belachew et al., 2022; UnNisa et al., 2022; Zhang et al., 2016). Hence, there is need for the development of improved and high yielding cultivars, with absolute stability and wide adaptation, to fill the current production gape and farmers requirement in Afghanistan (Akbarzai et al., 2021b). Therefore, multi-environment trials (MET) were conducted in plant breeding program to identify high yielding and widely or specifically adapted genotypes for different environments. MET ensure the evaluation of number of genotypes across the years and locations and has two main goals (i) to identify the favorable environments and (ii) to identify the high yielding genotypes (Vaezi et al., 2017). The selection of superior genotypes in METs generally results in genotype-by-environment interactions that frequently make difficult the interpretation of results obtained and reduce efficiency of selection (Annicchiarico and Perenzin, 1994).

The performance of genotypes arises from the interaction of genotype and environment (GEI). The environmental factors may be characterized by biotic and abiotic stresses. Statistical techniques have been developed for the analysis and interpretation of GEI from MET where the commonly used statistical methods for analyzing GEI are the additive main effects and multiplicative interaction (AMMI) model (Ebdon and Gauch, 2002). The AMMI is an effective model for analysis of multi-environment yield trials (MEYTs) where it describes a large portion of the GE sum of squares uniquely partitioning into interpretable principal components (IPC) (Adil et al., 2022; Ebrahimnejad and Sabouri, 2018; Kebede and Getahun, 2017; Zhang et al., 2020). The main objectives of this study were (i) to apply AMMI to analyze the GE interaction effect on grain yield (ii) to identify the high

yielding and stable barley genotypes within test environments.

2. Materials and Methods

2.1. Experimental Conditions and Genetic Material

This study is based on the experiments conducted in six environments—three locations (Mazar, Baghlan and Bamyán) over three years (2016-17, 2017-18, 2018-19). The genetic materials (Table 1) used in this experiment to determine the yield performance of barley inbred lines including one national check (improved variety) at Dahdadi research farm in Mazar ($36^{\circ} 39' 25.4''$ N, $66^{\circ} 57' 39.9''$ E, 398 m asl, average annual precipitation 282 mm), Posi-Shan research farm in Baghlan ($36^{\circ} 09' N$, $68^{\circ} 64' E$, 564.9 m asl, average annual precipitation is 268.4 mm) and at Molaghalam research farm in Bamyán (at $34^{\circ} 43' N$, $67^{\circ} 49' E$, 2550 m asl, the average annual precipitation is 321 mm) during 2016, 2017 and 2018 cropping season.

The experimental design was a randomized complete block design with three replications at each site across three years. A plot consisted of four 5-m rows with 0.20 m row-to-row distance and 6 rows per plot, using the four central rows for evaluation. Weed management and pest and disease control were carried out according to the recommended cultural practices for Barely production by the Agricultural Research Institute of Afghanistan (ARIA). Sowing was done during November - December, and the crop was harvested during June - July. The grain yield was obtained from the central four rows (3.2m²) plot area for all the trials to remove the border effects. The yield was converted to ton per hectare for statistical analysis.

2.2. Statistical analyses

AMMI model was used to assess the genotype by environment interaction (GEI), adaptability and stability of genotypes in the tested environments. The AMMI model integrates the standard ANOVA with principal components (PC) analysis as described by Zobel et al., 1988. The AMMI model was applied to determine the effect of genotype (G), environment (E) and genotype by environment interaction (GEI).

During analyses, the combined among one to three locations and the three years were considered as an environment giving rise to six environments: Mazar, 2016 (E1), Mazar, 2017 (E2), Baghlan, 2017 (E3), Mazar, 2018 (E4), Baghlan, 2018 (E5), Bamyán, 2018 (E6). All obtained data were subjected to analysis using GenStat software (VSN Inc. 2015).

Table 1. The names and pedigree of nine tested barely lines including check and the environments

Symbol	Genotypes Pedigree	ORIGIN
G1	PETUNIA1/3/LEGACY//PENCO/CHEVRON-BAR CBSS05Y00208S-33Y-0M-0Y-0M-1AP	ICARDA
G2	Alanda-01/4/Alanda//Lignee527/Arar/3/BF891M-612 ICB02-0487-57AP-0AP-0AP-0AP	ICARDA
G3	Alanda-01/4/Alanda//Lignee527/Arar/3/BF891M-612 ICB02-0487-97AP-0AP-0AP-0AP	ICARDA
G4	Alanda-01/4/Alanda//Lignee527/Arar/3/BF891M-617 ICB02-0488-16AP-0AP-0AP-0AP	ICARDA
G5	TOCTE/PETUNIA 2//PETUNIA CBSS01Y00830T-E-0Y-1M-1M-1Y-0M-0AP	1 ICARDA
G6	6B95.2482//PENCO/CHEVRON-BAR/3/LEGACY CBSS01Y00890T-A-0Y-1M-1M-2Y-0M-0AP	ICARDA
G7	AGER/2*PETUNIA CBSW01WM00121T-0TOPY-4M-1Y-1M-1Y-0M-0AP	1 ICARDA
G8	CABUYA/MJA//PETUNIA 1/5/PENCO/CHEVRON-BAR/3/ ATACO/BERMEJO//HIGO/4/PETUNIA CBSS04B00030S-17M-0Y-0M-2Y-0M-0AP	1 ICARDA
G9	LACEY/9/MOLA/BERMEJO//NISPERO/5/CM67-B/RYE// CAM-B/3/ROW906.73/4/GLORIA-BAR/COME/6/LINO/7/ PINON/8/PETUNIA CBSS04B00140S-1M-0Y-0M-2Y-0M-0AP	1 ICARDA
G10	National check (improved variety)	Afghanistan

3. Results and Discussion

3.1 AMMI Model Analysis

The result of AMMI analysis for grain yield of 10 barely inbred lines and 6 environments are given in Table 2. The main effect of genotypes and genotype × environment interaction (GEI) was highly significant ($p < 0.01$). The result further indicated that environments (E), genotypes (G) and genotype × environment interaction (GEI) accounted for 75.01%, 7.5% and 8.16% of the total variation, respectively. Furthermore, results showed that the environment is

the predominant source of variation and grouping the environments may provide a clearer understanding of the GEI. There were significant variations in environmental conditions. Moreover, the performance of genotypes significantly differed across the tested environments as indicated by a higher GEI component than the genotype component (Shukla et al. 2015). Other researchers also reported a higher percentage of G×E relative to the genotype and recommended the stability analysis and partitioning of GEI into its component (Amiri et al., 2013; Homma 2015; Erdemci 2018).

Table 2. AMMI analysis of variance for grain yield (t/ha) of the 10 barely genotypes tested over six environments (combination of three locations and three years)

Source	DF	SS	MS	% TSS	% GE
Treatments	59	332.4	5.63**	90.67	
Genotypes	9	27.5	3.05**	7.50	
Environments	5	275	54.99**	75.01	
Block	11	10.3	0.93**		
Interactions	45	29.9	0.66**	8.16	
IPCA 1	13	13.7	1.05**		48.66
IPCA 2	11	7.8	0.70*		32.79
Residuals	21	8.4	0.40		18.55
Error	99	23.9	0.24		
Total	179	366.6	2.05		

*, ** Significance at 5 and 1 percent probability levels, respectively.

Table 3. Mean Grain yield (t/ha), first and second Interaction Principal Components Analysis (IPCA), AMMI stability Value (ASV) of the 10 barley genotypes over the six environments (combination of three locations and three years)

G/E	E1	E2	E3	E4	E5	E6	Mean	IPCA1	IPCA2	ASV
G1	6.18	4.90	4.91	2.45	2.10	3.98	4.09	0.39	-0.36	0.77
G2	5.10	5.80	4.99	3.62	2.45	4.45	4.40	-0.72	0.20	1.27
G3	5.91	4.82	4.74	2.30	1.89	3.99	3.94	0.26	-0.44	0.63
G4	5.48	3.74	4.03	1.73	1.45	2.25	3.11	0.78	0.21	1.39
G5	5.42	5.48	4.99	3.49	2.52	3.91	4.30	-0.28	0.41	0.64
G6	5.64	5.45	4.91	2.57	1.90	5.06	4.25	-0.37	-0.86	1.08
G7	5.69	4.85	4.72	2.68	2.09	3.55	3.93	0.21	0.07	0.37
G8	5.68	4.74	4.66	2.62	2.06	3.37	3.85	0.28	0.13	0.51
G9	5.73	5.17	4.96	3.29	2.53	3.46	4.19	0.12	0.51	0.55
G10	5.40	6.00	5.23	3.78	2.65	4.72	4.63	-0.67	0.13	1.17
Mean	5.62	5.10	4.81	2.85	2.16	3.87	4.07			

G: genotype; E: environment

The AMMI estimates the main effect of genotypes and multiplicative interaction as principal components, IPCA1 and IPCA2, found suitable to model to predict the GEI in grain yield (Gauch and Zobel, 1996). In our study, the IPCA1 and IPCA2 were significant and explained 48.66% and 32.79% of the total variation in G×E interaction. Therefore, the two PCAs axes presented 81.45% of the interaction sum of squares (GEI) with 18.55% residual contribution. The result was consistent with the findings of other researchers (Mortazavian et al., 2014; Fana et al., 2018) from the study on barley.

The mean value of the genotype and the environment are given in Table 3. The environment means for grain yield (mean of genotypes) varied from 2.16 t/ha at E5 to 5.62 t/ha at E1. The E1, E2 and E3 environments had higher than average (4.07 t/ha). The mean of grain yield of tested genotypes varied from 3.11 t/ha for G4 to 4.63 t/ha for G10. G10 yielded higher than average in 4 out of 6 environments and 60 % of genotypes yielded higher than the overall genotypic mean with the contribution of 6 barley lines viz. G10, G2, G5, G6, G9 and G1 constantly yielded higher than average (4.07 t/ha). Ahmadi et al. (2012) reported four high-yielding genotypes (G1, G14, G11 and G2) out of 18 barley genotypes based on mean performance across tested environments; Vaezi et al. (2017) grouped the barley genotypes as high (G9, G2 and G5) and low (G6, G8 and G10) yielding in comparison to genotypes mean (2.09 t/ha) where the genotypes mean was in the range of 1.86 t/ha - 2.30 t/ha.

3.2. AMMI stability value (ASV)

Purchase et al. (2000) introduced, ASV, as a measure of stability of the genotype based on two principal components under AMMI Analysis. ASV is the distance of the varieties from point zero of the scatter diagram (IPCA1 vs. IPCA2). Therefore, lower score of ASV and IPCA1 presenting to high stability of genotypes. The genotypes G7, G8 and G9 are identified as three most stable genotypes due to their low value of ASV (0.37 – 0.55), where the G4, G2, G10 and G6 are recognized as unstable genotypes (ASV: 1.08 – 1.39) (Table 3). Amiri et al. (2013) also grouped the wheat genotypes based on ASV analysis as stable and unstable; Vaezi et al. (2017) reported and identified the 5 barely line as stable one with a small ASV score and less interaction with environments while the other 5 lines had high ASV score and detected as unstable lines.

3.3. AMMI biplot analysis

Based on the AMMI biplot which estimates the genotype stability and adaptability differences in related environments by using IPCA vs IPCA2. Therefore, the AMMI biplot is presenting the yield difference of 10 genotypes in 6 environments in Fig. 1. A stable genotype has a value closer to the origin of the axis (IPCA1) with a small contribution to the interaction (Gauch, 1992). The variation due to environment is higher than the genotype in both main effects and interactions (IPCA1).

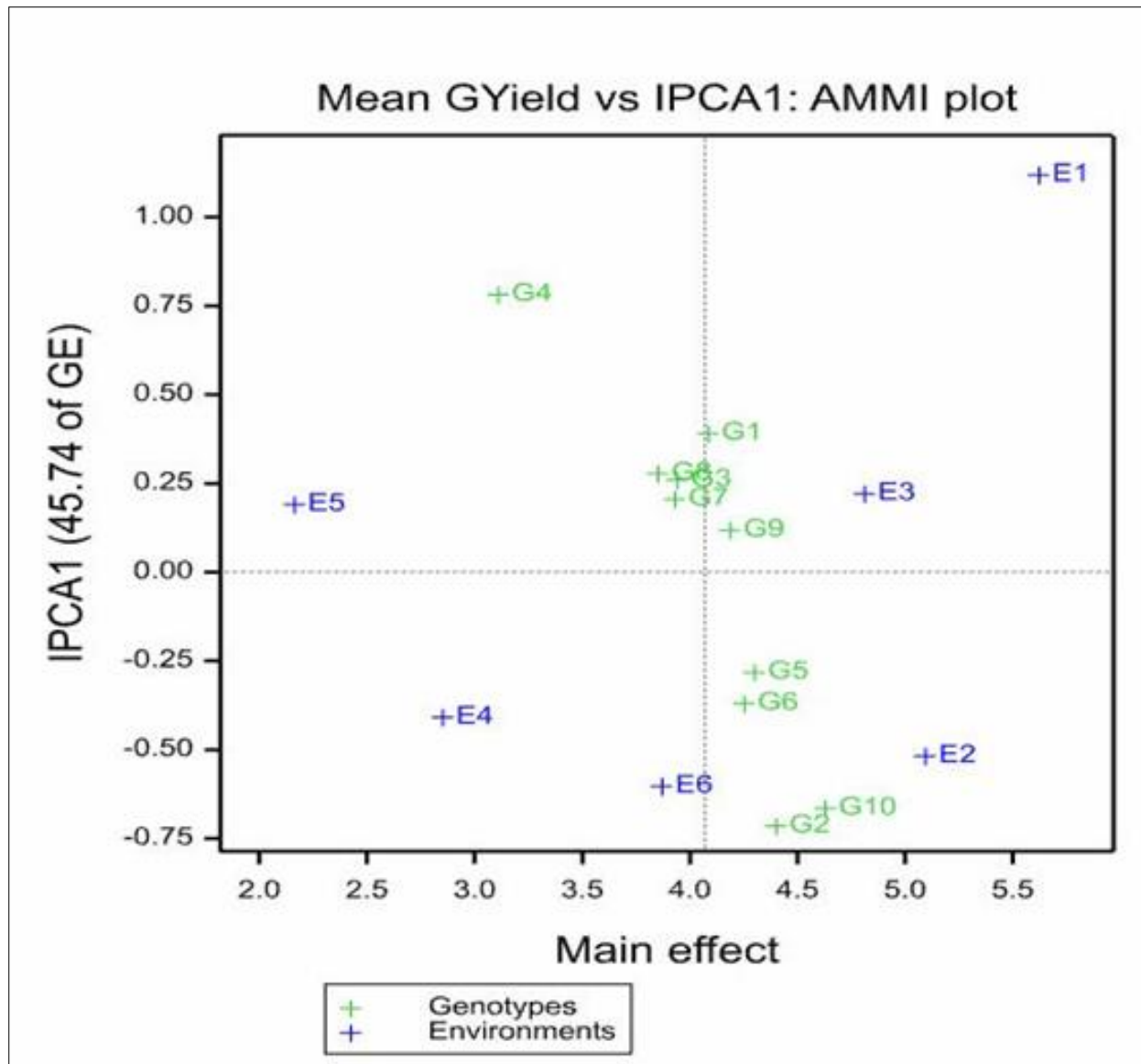


Fig. 1. The AMMI biplot (IPCA1 vs mean) for barley yield (t/ha) of 10 genotypes across six environments (combination of three locations and three years).

Among the genotypes, G9 is the most stable genotype with above average yield and wide adaptability while G4 and G2 were the unstable genotypes although G2 had mean over the average mean. In the biplot, the genotype G1, G2, G5, G6, G9 and G10 had higher average yields and adapted to favorable environments, while the genotypes G3, G4, G7 and G8 were adapted to poor environment. According to environmental index value (negative and positive), the environments were separated as rich (E3), medium (E1 and E2) and poor (E4, E5 and E5). These results are in agreement with the findings earlier reports for rice (Islam et al., 2014); wheat (Erdemci et al., 2018) and barley (Fana et al., 2018)

4. Conclusion

The result indicated that the AMMI analysis is the best statistical method for the identification of stable and wide and specific adapted genotypes in MET. The AMMI analyses indicated, the environment has a high effect on the grain yield of barley rather than the effect of GEI and genotype. Therefore, the stability analysis is necessary to determine the stable and wide adapted genotype in tested environments. According to AMMI biplot analysis, the G5 and G9 were the most stable and wide (G9) and specific (G5) adapted genotypes with grain yield mean of above average and could be considered for further release as variety.

Competing Interest Statement: Authors declare that there is no conflict of interests arising from this study.

List of Abbreviations: **AMMI:** the additive main effects and multiplicative interaction, **ANOVA:** Analysis of variance, **Asl:** Above sea level, **ASV:** AMMI Stability Value, **DF:** degree of freedom, **E:** environment, **FAO:** Food and Agriculture Organization of the United Nations, **G:** Genotype, **GEI:** Genotype by environment interaction, **ICARDA:** International Center for Agricultural Research in the Dry Areas, **IFAD:** International Fund for Agricultural Development, **MET:** Multi-environment trials, **PCA:** Principal Components Analysis, **USDA:** United States Department of Agriculture.

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