Genotype by Environment Interaction and Grain Yield Stability of Food Barley (*Hordeum vulgare* L.) Genotypes in East Shewa

Abstract

The study was carried out at Adami Tulu Agricultural Research Center (ATARC) in Lume and Dugda Districts during the 2021 and 2022 main cropping seasons to identify stable, high-yielding food barley genotypes suitable for East Shewa Zone and similar agro-ecologies. Fourteen food barley genotypes were tested in a Randomized Complete Block Design (RCBD) with three replications. Each plot measured 2.5m × 1.2m (3 m^2*) with 6 rows, spaced 0.20m apart, and 0.50m between replications, with 1m between blocks. Data on yield and related factors were collected and analyzed, showing significant effects of genotype, environment, and their interaction on food barley performance. The AMMI model indicated that the environment contributed 54.55%, GXE 16.15%, and genotype 9.08% to the total variation. The higher influence of the environment suggests its crucial role in determining food barley yields. The first two IPCAs, IPCA-I (44.6%) and IPCA-II (27.7%), were found to be the most accurate models predicting genotype stability within GEI. Based on stability parameters (ASV and GGE-Biplot) and mean yield outcomes, G-5 and G-6 emerged as the most consistent genotypes across test sites. Hence, G-5 and G-6 are recommended as potential candidates for release.*

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Keywords: *Food Barley, Genotype by Environment Interaction, Stability, AMMI, GGE-Biplot*

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Introduction

Barley (*Hordeum vulgare* L.) plays a significant role in Ethiopian cereal production, contributing to food security (Berhanu et al., 2017). Ethiopia is a key player, accounting for about a quarter of the total barley production in Africa (FAO, 2021). Barley thrives at high altitudes (> 2000 m a.s.l.) and Ethiopia stands out as a hub for barley diversity worldwide, attributed to its valuable traits such as disease resistance (Bekele et al., 2000). Both food and malt barley varieties are grown in Ethiopia, with food barley dominating production at 90%, while malt barley makes up the remaining 10% (Alemu et al., 2016). In Ethiopia, barley grains are primarily used for animal feed, malting, and human consumption. Traditionally, barley features prominently in local cuisines, beverages, and various dishes. Its straw serves as quality fodder for animals and is also utilized for thatching purposes (Yosef et al., 2013).

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In Ethiopia, numerous food barley varieties have been introduced in Bale Highland and parts of Eastern Arsi in recent decades. However, there remains a scarcity of barley types suitable for low moisture stress regions like the mid Rift Valley. Consequently, farmers in drought-prone areas resort to cultivating their traditional landraces, which often yield poorly.

Assessing crop performance across various environments is crucial for understanding their adaptation and stability (Crossa, 1990; Ceccarelli, 1996). The performance of a trait is influenced by the genotype (G) of the variety, the environment (E), and the interaction between the genotype and environment (GE). GE interactions occur when the responses of different genotypes to varying environmental conditions are not consistent. A deeper comprehension of GE interactions and stability in crops serves as a valuable decision-making tool, especially during the final stages of introducing new varieties. It helps in gathering crucial insights into the adaptation patterns of breeding lines, screening new releases, and defining the recommended domains for released varieties (Yan and Kang, 2003). Among the various statistical models, the most commonly used approaches for analyzing GEI include the Additive Main Effects and Multiplicative Interaction (AMMI) model (Gauch, 2006) and the Genotype Main Effect and Genotype x Environment Interaction Effect (GGE).

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The primary factor influencing variability among genotypes (varieties) in terms of production stability is the genotype-environment (GE) interaction, meaning that the performance of genotypes is influenced by the particular environmental conditions in which they are cultivated. Therefore, the current research aimed to determine food barley genotypes that are both high-yielding and consistent across the study areas.

Materials and Methods

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at ATARC, Lume and Dugda Districts. Fourteen food barley genotypes were used as a planting material (Table 1). Plot sizes were ~~ill~~1.2 m x 2.5 m (3m^2). Each plot had six rows~~andwithin eachrow and~~of 0.2 m between rows with a row length of 2.5 m. The distance between adjacent blockswas 1 m. NPS was applied at the rate of 100 kg/ha respectively and with seed rate of 125kg/ha. The two outer rows were considered border rows. Weeding and all other recommended agronomic practice was followed for all locations.

Table 1. List and description of food barley genotypes were used in the experiment

SN	**Code**	**Genotypes/Pedigree**	**Source**
1	G-1	CABUYA/M111/7/TRADITION/6/P.STO/3/ LBIRAN/UNA80//LIGNEE40/4/BLLU/5/PETUNIA	ICARDA
2	G-2	CANELA/C14196	ICARDA
3	G-3	FRES/M1004	ICARDA
4	G-4	SHEMIAL NO.3/MSEL	ICARDA
5	G-5	PUEBLA/CORDO//TOCTE/3/FALCON-BAR	ICARDA
6	G-6	P.STO/3/LBIRAN/UNA80//LIGNEE640/4/BLLU/5/ PETUNIA 1/6/LEGACY//PENCO/CHEVRON-BAR	ICARDA
7	G-7	VMORALES	ICARDA
8	G-8	CHAMICOO/M111	ICARDA
9	G-9	FRES/LEGACY	ICARDA
10	G-10	Bentu	SARC
11	G-11	LIGNEE 27/ GERBEL /3/BOY-B*2/SURB //C12225.2 D/4/ GLORIA-BAR/COM	ICARDA
12	G-12	SVANHALSBAR/MSEL//AZAF/GOB24DH/3/ DEFERA/DESCONNCIDA-BAR	ICARDA
13	G-13	5th GSBON-LI-71	ICARDA
14	G-14	5th GSBON-LI-3	ICARDA

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Data collection

Data were collected for the following trait accordingly;Plant height (cm), Peduncle length (cm), Spike length (cm), Kernel number per spike, Days to heading, Days to maturity, Grain yield (kg/ha) and Thousand kernel weights (g).

Statistical Analysis

AMMI Model: AMMI is applied to analyze GEI for pattern identification and noise reduction. Integrating traditional ANOVA with principal component analysis yields more dependable genotype performance estimates than site mean values. Its role is to pinpoint key breeding environments and select relevant test sites within them to find genotypes best suited for targeted adaptation (Angela et al., 2016).

$$\boldsymbol{Y_{ij}} = \mu + \mathrm{g}_{\boldsymbol{i}} + \boldsymbol{e_j} + \sum_{\boldsymbol{1}}^{\boldsymbol{N}} ʎ_{\boldsymbol{k}} \Upsilon_{\boldsymbol{ik}} \boldsymbol{\delta_{jk}} + \mathcal{E}_{\boldsymbol{ij}}$$

Where Yij is the grain yield of the i^{-th} genotype in the j^{-th} environment, μ is the grand mean, gi and ej are the genotype and environment deviation from the grand mean, respectively, ʎk is the eigenvalue of the principal component analysis (PCA) axis k, Yik and δjk are the genotype and environment principal component scores for axis k, N is the number of principal components retained in the model, and Ɛij is the residual term.

GGE- biplot

The GGE-bi-plot method, incorporating the biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000), was applied to visually examine the METs data. This method utilizes a biplot to illustrate the crucial factors (G and GE) for genotype assessment and their role in the variation of GEI analysis in METs data (Yan, 2001). The GGE-bi-plot reveals the initial two principal components extracted through singular value decomposition of environment-centered yield data (yield variation attributed to GGE) (Yan et al., 2000).

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AMMI Stability Value (ASV):ASV represents the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Due to the IPCA1 score's greater impact on the GxE interaction sum of squares, a weighted value is required. This value was computed for each genotype and environment based on the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows:

$$\textbf{ASV}=\sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1_{Score})]^2 + (IPCA2_{Score})^2}$$

Where SSIPCA1/SSIPCA2is the weight given to the IPCA1-value by dividing the IPCA1 sum ofsquares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments (Purchase, 1997).

Genotype SelectionIndex (GSI): Stability is one of many factors for selection since the most stable genotypes might not always yield the best performance. Hence, the genotype selection index (GSI) was determined for each genotype by considering the rank of mean grain yield of genotypes (RYi) and the rank of AMMI stability value (RASVi) across different environments.

GSIi = RASVi + RYi

A genotype with the least GSI is considered as the most stable (Farshadfar, 2008). Analysis of variance was carried out using statistical analysis system (SAS) version 9.2 software (SAS Institute Inc., 2008). Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE bi-plot analysis were performed using Gen Stat 15th edition statistical package VSN International (2012).

Results and Discussion

Combined analysis of variance

Statistically significant differences (P< 0.01) were observed among food barley genotypes, environments, and their interaction for grain yield (Table 2). This suggests the existence of genetic variation among the food barley genotypes and the potential to select high-yielding and

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stable genotype(s). The environments were diverse, and the responses of food barley genotypes across environments were also varied. Similar studies were conducted by Bedasa (2014), Wosene et al. (2015), Behailu et al. (2018), and Tashome (2017) on food barley.

Table 2: Combined analysis of variance for grain yield of fourteenfood barley genotypes

S.V	d.f.	Sum square	Mean square
Rep	2	1142836.21	571418.12
Env	5	207612040.23	41522408.32***
Geno	13	34562637.61	2658664.21***
Env*Geno	65	61489172.13	945987.33***
Total	251	380541698.4	

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AMMI analysis of variance for G, E and GxE Interactions

The AMMI analysis of variance for grain yield of food barley genotypes, evaluated across 6 environments (three locations and two years), is depicted in Table 3. Significantly different results ($p<0.01$) were observed for environments (E), genotypes (G), and a notable variation ($p<0.01$) was noted for the interaction between environments and genotypes (GEI), IPCA1, IPCA2, and IPCA3. Environments contributed 54.55% to the total variation in grain yield, while genotype variances accounted for only 9.08% of the total variation. The involvement of GEI in explaining yield performance variation stood at 16.15%, underscoring its importance in MET trials.

The extensive sum of squares for the environment indicated a diverse environment with significant differences among environmental means, leading to variation in the performance of the genotypes. This variability could potentially be attributed to differences in soil types and altitude ranges across locations. Previous studies have suggested that environmental factors account for 80% of the variation, with 10% attributed to genotype and genotype-environment interactions (Sabaghnia et al., 2013). Notably, Abay et al. (2009) and Gebremedhin et al. (2014) reported substantial environmental sum squares in food barley.

The AMMI analysis showed a significant interaction among principal components. The three multiplicative principal components were significant ($P<0.01$), while the other interaction principal component was not. According to Yan (2007), the AMMI model involving the first two IPCAs adequately predicts the genotype by environment interaction, assessing the fitness of the additive main effect and multiplicative interaction (AMMI). IPCA1 accounted for 44.6% explanation, IPCA2 for 27.7%, and IPCA3 for 17.7% of the total variation. Together, these three interaction principal components explained 90% of the genotype by location interaction (Table 3).

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Table 3. The Additive and multiplicative interaction Analysis of variance

Source variation	Df	Sum Sq	Mean Sq	Pr(>F)	Explained % SS
Total	112	380541697.9			
Environment (E)	5	207612039.8	41522408	0.00014	54.55
Replication/E	12	5550140	462511.7	0.44	
Genotype (G)	13	34562637	2658664	0.0030	9.082483
GxE	65	61489172	945987.3	0.0001	16.15833
PC1	17	27422324	1613078	0.00001	44.6
PC2	15	17034868	1135658	0.0027	27.7
PC3	13	10890427	837725.2	0.0328	17.7

Yield performance of Food Barley Genotypes Across Locations

Mean performance of the tested food barley was presented in (Table 4). It revealed that some genotypes continually performed best in some group of environments and some were inconsistent across the environments. The average grain yield ranged from the lowest 2274.32 kgha^{-1} at Lume in 2022 to the highest kgha^{-1}at Dugda in 2022 with grand mean of 3558.76 kgha^{-1}. The average grain yield across the environment ranged from the lowest of G-11533.3kgha^{-1}to the highest of 51000.0kgha^{-1} for G-5. This large portion of variation might be due to the genetic potential of the genotypes. G-5 and G-6 genotypes were the higher yielders than other genotypes through the studied environments. However, G-1 genotype~~s~~ had the lowest yield potential through the tested locations. Similarly,~~(~~(Mengistu et al., ((2013)) ~~were~~ reported differential yield response to different environment of sorghum varieties. The differential response of genotypes across environment indicated that the cross over types of interaction. The difference in yield ranks of genotypes across the locations showed the high cross over types of GxE interaction (Purchase et al., 2000; Yang et al.,2007).

Table .4 Mean Grain Yield (kg/ha) per location across years

Genotype	2021	2022	Over all

	ATARC	Dugda	Lume	ATARC	Dugda	Lume	Mean
Bentu	4444.44	4022.22	2277.78	4511.11	4005.56	2110.67	3561.96
G-5	5072.22	5100.00	3211.11	4188.89	5200.00	3368.44	4356.78
G-3	3161.11	2632.89	2577.78	2733.33	3672.22	2522.22	2883.26
G-4	2675.56	2958.89	2250.00	3193.33	5088.89	2244.44	3068.52
G-2	4061.11	4150.00	2094.44	5511.11	4925.56	1723.33	3744.26
G-8	4155.56	4122.22	2339.44	4083.33	4572.22	2466.67	3623.24
G-7	3744.44	4872.22	2411.11	4361.11	4038.89	2833.67	3710.24
G-6	4777.78	4727.78	2600.00	4661.11	4694.44	3236.56	4116.28
G-9	3544.44	5344.44	2222.24	3361.11	4611.11	2066.67	3525.00
G-1	3661.11	4377.78	1888.89	3688.89	4377.78	1533.33	3254.63
G-11	3294.44	4188.89	2169.89	4472.22	3950.00	1943.89	3336.56
G-12	3422.22	3283.33	2288.89	3650.00	5555.56	2186.67	3397.78
G-13	3650.00	4000.00	2800.00	4094.44	4300.00	2067.78	3485.37
G-14	3233.33	5027.78	2011.11	5322.22	5422.22	1536.11	3758.80
Mean	3778.41	4200.60	2367.33	4130.87	4601.03	2274.32	3558.76
LSD 0.05	858.45	1117.20	986.16	940.70	907.60	808.90	372.9
CV (%)	16.31	19.10	29.91	16.35	14.16	25.54	19.0
F-test	***	***	ns	**	**	**	***

CV = coefficient of variation, LSD = Least Significant Difference

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AMMI Analysis

In this study, mean grain yield, IPCA 1 and IPCA 2 scores, AMMI stability values (ASV) and GSI with their ranking orders of the 14 food barley genotypes tested at six environments are presented in Table 5. The AMMI analysis partitioned the sum of squares of GEI into four interaction principal component axes (IPCA), of which the first third IPCA were significant (Table 4). The results from the AMMI model showed that, the first IPCA captured 44.6% of the interaction sum of squares. Similarly, the second IPCA explained 27.7% of the GEI sum of squares. In line with this, Zobel *et al*. (1988) proposed that two interaction principal components axes for AMMI model were sufficient for a predictive model. Other interaction principal component axes captured were mostly non-predictive random variation and did not fit to predict validation observations.

AMMI Stability Value (ASV): The importance of AMMI model is in reduction of noises if the principal component did not cover much of the GE sum of squares (Gauch, 1992; Guach and Zobel 1996). It is the distance from zero in two-dimensional scatter of IPCA1 score against IPCA2 scores. Since the IPCA1 score more contributes more to the GEI sum of square, it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total GEI sum of square. According to stability parameter, a genotype with least ASV score is the most stable. The genotypes such as G-5, G-6 andG-7 genotypes had least ASV value and were the most stable respectively (Table5). The high interaction of genotypes with environment was confirmed by high ASV value and difference in ranking order, suggesting unstable yield across environment. The most unstable genotypes were G-1, G-12 and G-3 (Table 5).

Table 5. IPCA1, IPCA2 scores, AMMI stability value and Genotype Selection Index of food barleygenotypes

Genotype	**Mean Yield**	**Ryi**	**IPCA1**	**IPCA2**	**ASVi**	**RASVi**	**GSI**
Bentu	3562	7	-3.78	4.06	5.38	8	15
G-5	4357	1	0.46	1.07	1.09	1	2
G-3	2883	14	2.25	0.98	5.27	7	21
G-4	3069	13	1.89	-2.93	3.17	3	16
G-2	3744	4	-2.44	-8.59	8.62	14	18
G-8	3623	6	3.56	3.61	5.04	5	11
G-7	3710	5	-2.14	1.72	3.17	4	9
G-6	4216	2	1.07	1.51	1.69	2	4
G-9	3525	8	-4.10	4.26	5.81	9	17
G-1	3255	12	-4.43	3.45	6.66	13	25
G-11	3337	11	-4.28	4.77	6.12	10	21
G-12	3398	10	3.53	-2.13	6.23	12.00	22
G-13	3485	9	2.65	1.15	6.21	11.00	20
G-14	3759	3	-3.24	-3.84	4.72	5.00	8

Key: RYi =Rank of grain yield, IPCA = Interaction principal component axis, ASV = AMMI Stability value, ASVi = Rank of AMMI Stability value, GSI= Genetic Selection index

Evaluation of Genotypes Based on GGE-bi-plot model

The estimation of stability of genotype were done by using the average coordinates of the environment (AEC) methods (Yan, 2001; Yan and Hunt, 2001). The average environment is defined by the average values of PC1 and PC2 for the all environments, and it is presented with a circle. The average ordinate environment (AOE) defines by the line which is perpendicular to the AEA (average environment axis) line and pass through the origin.

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This line divides thegenotypes in to those with higher yield than average and in to those lower yield than average. Byprojecting the genotypes on AEA axis, the genotypes are ranked by yield; where the yieldincreases in the direction of arrow. In this case the highest yield had genotypes G-5, G-6 and G-7but the lowers had G-3, G-4 and G-12 figure (1). Stability of the genotypes depends on theirdistance from the AE abscissa. Genotypes closer to or around the center of concentric circleindicated these genotypes are more stable than others. Therefore, the greatest stability in the highyielding group had genotypes G-5, G-6 and G-7. The genotype ranking is shown on the graph of genotype so-called “ideal” genotype (Fig 1). Anideal genotype is defined as one that is the highest yielding across test environments and it iscompletely stable in performance that ranks the highest in all test environments; such asgenotypes in this case were G-5 and G-6.

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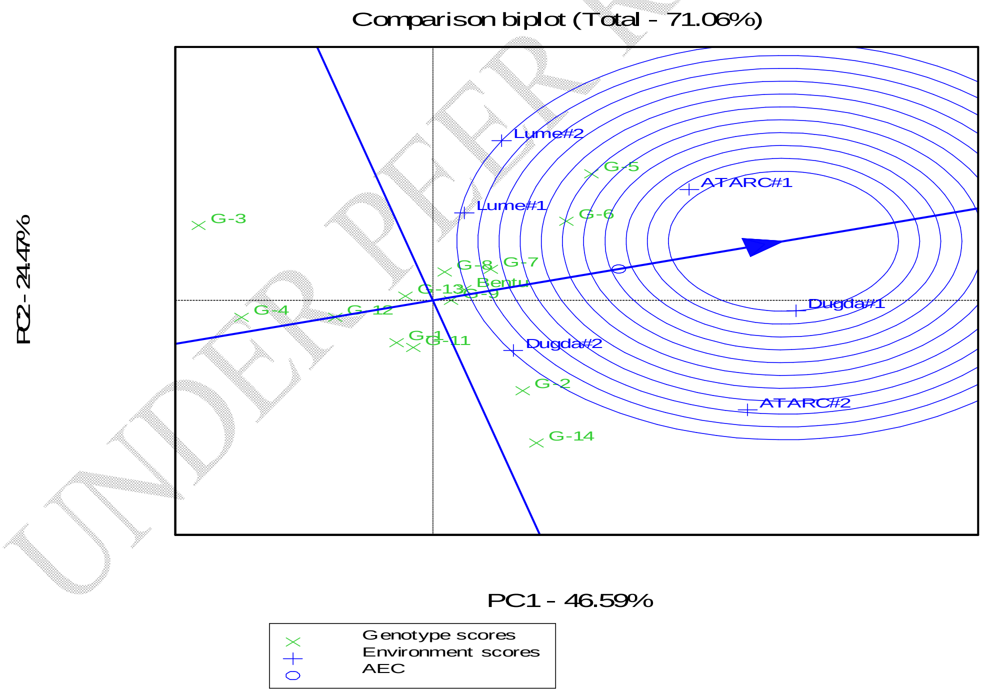

Figure 1: GGE biplot based on genotypes focused scaling for comparison for their pod yieldpotential and stability.

GGE biplot analysis

GGE biplot pattern of ‘mean vs. stability’ analysis showed that PCA1 and PCA2 explained 44.6%and 27.7% of the GGE variance, respectively (Fig. 2). This figure helps to visualize grain yieldperformance and stability of the genotypes. The average environment coordinate (AEC) or average environment axes (AEA) line crosses through the biplot’s origin if SVP=1 (single value portioning). As reported by Yan and Rajcan (2002), the mean of PC1 and PC2 of theenvironmental scores is defined.The ‘mean vs stability’ view frequently stating as AEC andSVP that helps to simplify thegenotype evaluation based on the mean performance and stability under a wide range ofenvironment (Fig. 2). The arrow sign on the AEC abscissa linedirected the ranking of genotypes in increasing order with a greater value of grain yield. In thisstudy,genotype on horizontal line G-5 followed by G-6 showed high yielder and the most stableacross evaluated environments.

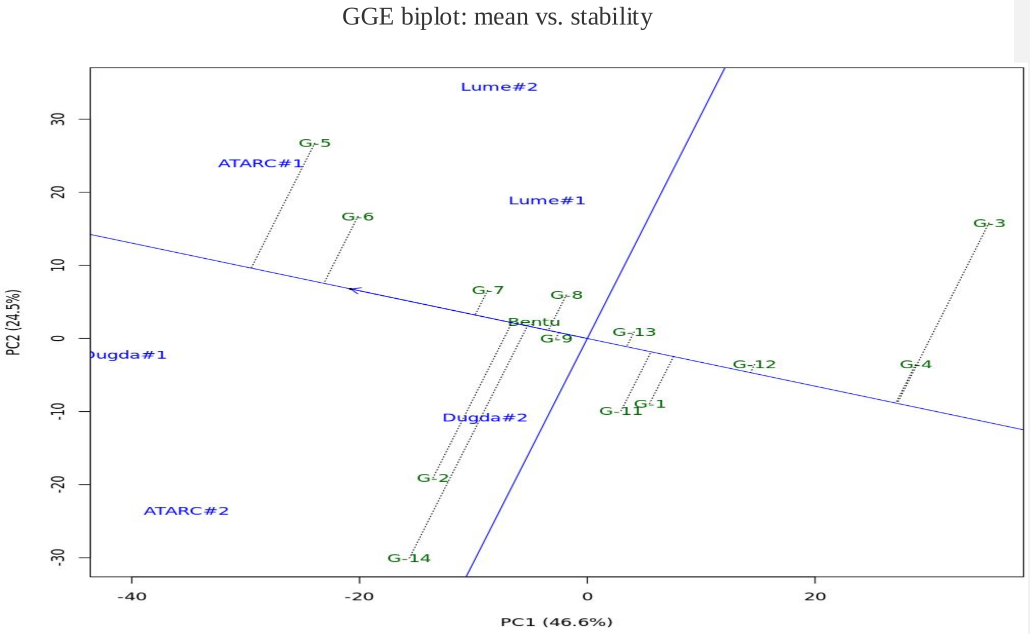

Figure 2: 'Mean vs stability' pattern of GGE biplot illustrating interaction effect of food barley genotypes

Conclusion

The genotype and environment main effects (genotype and environment) and genotype x environment interaction effect was significant on food barley genotypes. AMMI model shows the variation was largely due to environmental variation.The high percentage of environmental variation is an indication that the major factor that influence yield performance of food barley genotypes is the environment. G-5 and G-6 were plotted to the ideal genotypes considered as desirable genotypes based on GGE bi-plot graph and stable genotypes while G-1 and G-3 were far from the ideal genotypesconsidered as most unstable genotypes with poor performance across locations.G-5 and G-6genotypeshad the least AMMI stabilityand genotypic selection index value and were widely adaptable and stable high-yieldinggenotypes. Therefore, these two genotypes were selected as candidate varieties for possible release.

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