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Genotype by Environment Interaction and Stability Analysis of Barley Grain Yield in South Ethiopia

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Abstract

The objective of this study was to assess how GEI affected the grain yield of barley genotypes' and to utilize AMMI and GGE biplot analysis to understand this effect. Field experiment was conducted with an objective to assess how GEI affected the grain yield of barley genotypes' and to utilize AMMI and GGE biplot analysis to understand this effect. This experiment was conducted in randomized complete block design with three replications at six locations during 2021 main cropping season. The analysis of variance demonstrated that genotypes differed significantly (P≤0.001) from one another for the studied traits. In the AMMI analysis of variance, it was revealed that the environment (E), genotype (G), and G×E interaction accounted for 60.42, 8.56, and 31.13% of the treatment sum of squares, respectively. Moreover, Bule offers the highest yield and stability simultaneously among the test environments. The AMMI stability value and yield stability index recognized genotypes G3, G9, G7, and G11 as high yielding with stable performance across environments. In contrast, GGE biplot analysis *revealed G3, G6, G5, and G9 as stable and high yielding genotypes throughout the environments. Based on the results of the GGE biplot and AMMI analysis, genotypes G3 and G9 were* found *to be stable and high yielding. Therefore, G9 is ideal for release, while G3 would be best suited for wider-scale cultivation and promotion.*

Keywords: AMMI analysis; Barley, Genotype by environment interaction; Stability.

Introduction

Barley ranks fourth in terms of total production in the world among cereals after maize, wheat, and rice (FAOSTAT, 2022). Globally the major utilization of barley is for feed, and malting purposes, because of its nutritional value barley is consumed as a staple food in North and Sub- Saharan Africa, Central Asia and South -West Asia (Verma, 2018).Barley (*Hordeum vulgare* L.) is an important cereal crop in Ethiopia grown in diverse agro-ecologies mainly for human consumption and is the major staple food in the highlands. Besides, the straw is used for animal feed during the dry season and it is also a useful material for thatching roofs of houses and use as bedding (Berhanu *et al*., 2005). It ranks fifth next to tef, maize, wheat and sorghum in area and total production (CSA, 2021). Barley production constraints in Ethiopia are biotic (diseases, insect pests and weeds) and abiotic stresses such as poor soil fertility, soil acidity, drought, water logging and frost (Berhanu *et al*., 2005; Wondimu *et al*., 2022). The aim of barley

breeding in Ethiopia is to boost up productivity of grain yield. However, the grain yield is a complex trait in which its expression relies on genetics, environment and their interaction (Singh *et al*., 2019; Roostaei *et al*., 2022). Genotype × environment interaction (GEI) reduces the correlation between the genotype and the phenotype, hindering evaluation of the genetic potential of the cultivars (Farshadfar *et al*., 2013; Hebbache, 2021). Both yield and stability of performance should be considered simultaneously, to reduce the effect of GEI and to make selection of genotype more precise and refined. Hence, GE interaction must be either exploited by selecting superior genotypes for each specific target environment or avoid by selecting a wide adapted and stable genotype across a wide range of environments (Ceccarelli, 1996).

The GE interaction can reduce trait heritability and the ability to predict statistically superior genotypes under contrasting environments (Roostaei *et al*., 2022). Therefore, the GE interaction needs to be evaluated before introducing new cultivars to new environmental conditions. Understanding GEI to assess association between phenotypes and genotypic values as well as improve selection of superior and stable genotypes requires an understanding of the genetic basis for adaptation, its physiological and environmental causes (Crossa *et al*., 1999).

The use of multi-environment trials for testing genotype adaptation becomes a necessary tool (Rodrigues *et al*., 2016). There are several methods for GEI analysis, in which all aim at the identification of genotypes suitable for certain growing environments. Interactions are usually explained in more complex methods based on analysis of variance, regression analysis, principal component analysis and cluster analysis. Additive main effects and multiplicative interaction (AMMI) is a powerful model to analyze the GEI as suggested by (Zobel *et al*., 1988; Gauch *et al*., 2008), and the genotype main effects plus genotype by environment interaction effect (GGE-Biplot) as suggested by (Yan and Hunt, 2002; Yan, 2002) are the two most frequently used tools for multi-environment trials data analysis and are considered as an effective graphical tool to diagnose genotype by environment interaction patterns. In addition, cultivar superiority measures proposed by (Lin and Binns, 1988), AMMI stability value (Purchase, 2000), and yield stability index (Rao *et al*., 2004) are the commonly used methods for quantifying GEI and stability. Also, regression model suggested by Eberhart and Russel (1966) could be used to identify stable, high yielding and adaptable genotypes for varied or specific environments.

In Ethiopia G×E interaction studies have been conducted on different small cereals such as barley (Muluken *et al*., 2010; Wosene *et al.*, 2015; Girma *et al*., 2018; Wondimu *et al*., 2023) Wheat (Hintsa and Fetin, 2013; Temesgen *et al*.,

2015; Melkamu *et al.*, 2015; Mizan, *et al*., 2019; Gadisa *et al*., 2019; Agegnehu *et al*., 2019; Alemayehu, 2020a) finger millet (Alemayehu, 2023) and Tef (Alemayehu, 2020b) but these studies deals with different plant materials, locations and environments. Therefore, this experiment was initiated with an objective to assess GEI using AMMI and GGE biplot analysis on selected food barley genotypes under optimum environments for barley production in South Ethiopia.

Materials and Methods

Descriptions of the experimental site

The experiment was conducted at six test locations, with varying environmental factor (Table 1), these locations are Abera Gelede, Bule, Bursa, Gedeb, Kemba and Albazar and they are the main variety testing sites for barley improvement program and representative of different barley agro-ecologies of Southern Ethiopia. Barley prefers low temperature as it is a temperate crop but potentially grown in tropical and sub-tropical highlands. Similarly, in this study Bule and Kemba receives 6.46 and 13.2 ^{0}C minimum temperature and 19.04 and 25.22 ^{0}C maximum temperature respectively. The two locations Kemba and Bule received precipitation of 703.5 mm and 657 mm respectively in the growing season from mid-July to January 2021.

Table 1. Experimental site, geographical position, long term precipitation and temperature

Experimental site	Code of sites	Geographical position			Rainfall (mm)	Temperature	
		Altitude (m.a.s.l)	Latitude (N)	Longitude (E)		Min T (^{0}C)	Max T (^{0}C)
Abera Gelede	E1	2732	6^{0}28'41"	38^{0}29'98"	1148.4	4.8	22.2
Bule	E2	2803	6^0 16'54"	38^{0}24'49"	1367.9	8.4	16.3
Bursa	E3	2587	6^{0}35'18"	38^{0}36'51"	na	13.1	23.9
Gedeb	E4	2302	5^{0}55'13"	38^0 15'38"	917.5	10.2	22.4
Kemba	E5	1895	06^{0}03'34"	37^{0}10'13"	1596.2	14.6	26.9
Albazar	E6	2284	7^{0}86'49"	38^{0}14'33"	1013.4	11.6	25.0

na- not available

Experimental materials

The multi-location trial was conducting using 18 genotypes including four food barley varieties. Three released varieties and two landrace lines totally five genotypes commonly performed under both P and N use efficiency were obtained from the previous two seasons screening experiments including 144 food barley genotypes for nitrogen (2019) and phosphorous (2020) use efficiency. The rest 13 landrace lines from the phosphorous use efficiency experiment were considered for the trial and the material list is indicated in Table 2.

Table 2. List of genotypes used for genotype by environment experiments

Genotypic code	Genotypes name	Type	Remark
G1	16739-D	Landrace line	
G2	HB -1966	Food barley variety	Standard check
G3	HB-1307	Food barley variety	Standard check
G4	17257	Landrace line	
G5	3514-B	Landrace line	
G6	242093-A	Landrace line	
G7	208905-A	Landrace line	
G8	1773-B	Landrace line	
G9	17252-C	Landrace line	
G10	18330-A	Landrace line	
G11	24965-C	Landrace line	
G12	17688-A	Landrace line	
G13	HB 1964	Food barley variety	Standard check
G14	64165-A	Landrace line	
G15	18302-A	Landrace line	
G16	64116-A	Landrace line	
G17	17148	Landrace line	
G18	Cross 41/98	Food barley variety	Standard check

Experimental design and crop management

Field trial was carried out at six test locations in 2021 main growing season, in randomized complete block design with three replications. Each plot had six rows with 2.5 m length and spaced 0.2m apart. Fertilizer was applied at a rate of 38 kg P_2O_5 and 46 kg N per hectare in the form of NPS and urea, respectively. All phosphorous source and $1/3^{rd}$ of urea was applied at sowing while the remaining $2/3^{rd}$ urea was applied 35 days after planting when the crop reached at full tillering stage. Weed management in all the experiments was performed as per the recommended practices by hand weeding.

Data collection

Data were collected on plot basis and on plant base. For each plant base data five randomly selected plants were taken from the middle four rows. Grain yield per plot, thousand seed weight, days to maturity, and days to heading were the data captured on plots bases while plant height, spike length, and seeds per spike were measured on plant base.

Statistical analysis

Following the standard procedure suggested by Gomez and Gomez (1984), a mixed linear model was used to analyze the variance for each location as well as the aggregate data across locations to assess genotype performance differences in yield and yield-related traits. GenStat (2014) was used to carry out AMMI, and GGE biplot analysis and SAS (2022) used for combined analysis over locations. Genotype means were compared using the least significant difference (LSD) test.

The GEA-R (Genotypic by Environment Analysis with R Widows) Version 4.1 (Angela *et al*., 2016) was used for AMMI visualizations and GGE biplots.

The Additive Main Effects and Multiplicative Interaction (AMMI) Model Analysis

AMMI combines ANOVA and principal component analysis (PCA) into a single study with additive and multiplicative parameters. Additive effects were obtained by applying the AMMI model with six growing environments (E), eighteen barley genotypes (G), and the multiplicative term is about G×E interactions. Following the fitting of multiplicative effects for the genotype by environment interaction using principal component analysis, AMMI analysis is used to fit the additive effects of genotypes and environments (Zobel *et al*., 1988) and is analyzed using the model below (Gauch, 1992):

$$Y_{ij} = \mu + G_i + E_j + (\sum K_n V_{ni} S_{ni}) + Q_{ij} + e_{ij}$$

Where, Y_{ij}- is the observed yield of genotype i in environment j, μ - is the grand mean, G_i - the additive effect of the i^{th} genotype (genotype means minus the grand mean), E_j - is the additive effect of the j^{th} environment (environment mean deviation), K_n - is the eigenvalue of the PCA axis n, V_{ni} and S_{ni} - are scores for the genotype **i** and environment **j** for the PCA axis **n** Q_{ij} = is the residual for the first n multiplicative components, e_{ij} - is the error

Stability analyses

The AMMI stability parameters (Gauch and Zobel, 1988; Zobel *et al*., 1988) and GGE biplot were computed for grain yield and GEI analysis of variance using GenStat Software (GenStat, 2014). Accordingly, interaction principal component axis (IPCA) scores of genotype and environment and AMMI stability value from the AMMI model were computed as the standard procedure set by each model.

AMMI stability value

The relative contributions of IPCA1 and IPCA2 principal component analysis scores to the interaction sum of squares were used to calculate each genotype's AMMI Stability Value (ASV). Purchase et al. (2000) state that the ASV was calculated using the following formula:

$$\text{ASV}=\sqrt{\left[\left[\frac{SSIPCA1}{SSIPCA2}\left(IPCA1\ score\right)\right]^2 + \left[IPCA2\ scores\right]^2\right]}$$

Where ASV= AMMI stability value, SSIPCA1/ SSIPCA2= the weight given to the IPCA1 value, by dividing the IPCA1 sum of square by the IPCA2 sum of square.

After obtaining the IPCA1 and IPCA2 data using GenStat software, Microsoft Excel was used to compute the ASV using the provided formula. The greater the adaptability of a certain genotype for a given environment, the higher the IPCA scores whether positive or negative. However, smaller ASV values signify more environmental stability (Farshadfar *et al*., 2011).

Yield stability index (YSI)

The Yield Stability Index (YSI) combines stability and mean yield into a single criterion; genotypes with high yield and stability are desired when both parameters have low values (Bose *et al*., 2014). The yield stability is calculated as follows:

$$YSI = RASV + RY$$

Where RASV is the ranking of AMMI stability value and R is the rank of barley genotypes based on grain yield across environments. This index is the rank of ASV and yield (Farshadfar *et al*., 2011).

$$Pi = \frac{n(x-mi-Mm)^2+\sum_{j=1}^{n}(xij-xmi-Mj+Mm)^2}{2n}$$

Where: X_{ij}= is the response of the i^{th} genotype in the j^{th} environment, Xm= is the mean of genotype i in the overall environments, M= is the genotype with maximum response among all genotypes in the jth environment, Mm= the mean of the genotypes with the maximum response overall environments and n is the number of environments.

GGE biplot analysis

The GGE biplot is a graphical tool which displays, interprets and explores two important sources of variation, namely genotype main effect and GE interaction of MET data (Yan *et al*., 2000) by using GEA-R (Genotypic by Environment Analysis with R Widows) Version 4.1 (Angela *et al*., 2016). For this study, the GGE biplot method outlined by Yan (2002) was used to display the G and GE interaction patterns in the data. GGE biplot analysis considers that only the G and GE effects are relevant and that they need to be considered simultaneously when evaluating genotypes. The model for the GGE biplot based on singular value decomposition (SVD) of the first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda\_1\, \xi\_i1\, \eta\_j2 + \varepsilon\_ij$$

Where Y_ij is the measured mean of genotype i in environment j, μ is the grand mean, β_i is the main effect of the environment j, $\mu - \beta\_j$ being the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values (SV) for the first and the second principal component (PCA1 and PCA2) respectively, ξ_i1 and ξ_i2 are eigenvectors of the genotype 1 for PCA1 and PCA2 respectively,

η_1j and η_2j are eigenvectors of environment j, for PCA1and PCA2 respectively, ε_ij is the residual associated with genotype i in environment j.

Results and Discussion

Combined analysis of variance across environments

Analysis of variance revealed that there were significant differences (P≤0.001) among the genotypes for all traits (Table 3), indicating the presence of genetic variability in genotypes for traits studied. This finding is in agreement with Zerihun (2011) who reported significant environmental variations for grain yield among 18 barley genotypes evaluated at 11 environments. The analysis of variance for phenology, agronomic, yield and yield components showed that there was significant variation among genotype, environments and G×E interaction indicating that the environment had an impact on grain yield performance of the tested genotypes. In line with this study Mirosavljevic *et al.* (2016) reported that agronomic traits such as heading date, plant height, spike length, thousand grain weight and grain yield of 12 Serbian barley genotypes were significantly affected by the influence of cultivar (C), year (Y) and cultivar- by -year interaction (C×Y). In line with this study Teshome (2017), in South Western Ethiopia, Melese *et al*. (2022) and Shegaw (2023) in South Ethiopia, Wondimu *et al.* (2022) in Central Ethiopia found significant differences in agronomic and yield components of barley genotypes across the test environments.

Table 3. Mean square of combined ANOVA for eight traits of 18 barley genotypes selected from Phosphorous Use Efficiency Experiment

Trait	Source of variation				
	Genotype (G)	Environment (E)	GEI	Rep(env)	Error
	Df= 17	Df= 5	Df= 85	Df= 12	Df= 214
DH	609.20***	1876.75***	60.22***	1.08	1.47
DM	510.13***	5506.78***	89.78***	3.02	2.10
GFP	167.37***	2377.70***	121.05***	3.35	2.52
PH	1033.80***	19792.56***	331.02***	38.82	33.84
SL	9.73***	18.91***	1.21***	0.02	0.02
NSP	1394.92***	781.75***	100.95***	90.44	28.06
TKW	302.80***	545.63***	35.44***	38.37	17.85
GY	2360852.50***	57410508.00***	1740048.90***	91106.00	56879.40

***= Significant at (P ≤ 0.001) probability level, respectively, Df= degree of freedom, DH= Days to heading, DM= Days to maturity, GFP= Grain feeling period, PH= Plant height, SL= Spike length, NSP= Number of seeds per spike, TKW= Thousand kernel weight, GY= Grain yield

Mean performance of genotypes across environments

The average grain yield varied from 76 kg ha^{-1} for G4 (E4) to 5029 kg ha^{-1} for G1 (E2). Between E4 (Gedeb) and E2 (Bule), the average environmental grain yield ranged from 1224 kg ha^{-1} to 3855 kg ha^{-1} (Table 4). Environments Bule (E2), Kemba (E5), and Albazar (E6) had the highest mean grain yields of 3855, 2724, and 1914 kg ha^{-1} respectively. For the genotypes those were evaluated, there were

extremely significant (P≤0.001) variations in the mean grain yield among the six environments (Table 4). Variations in the environment lead to variations in the quantitative traits of the genotypes under test. The genotypes' mean features showed that G8 was late to head, requiring 95 days, whereas G15 and G4 were early to head, requiring 75 and 77 days, respectively (Table 5). In terms of days to maturity, genotypes G8 and G6 mature later, taking 145 and 146 days, respectively, whereas genotypes G15 and G4 matured early, taking 127 and 129 days, respectively. G2 and G7 were the genotypes with the largest spike lengths, measuring 9.9 cm each. For G15 and G6, the number of seeds per spike varied from 23 to 50.

Overall, the results show that environmental influences impacted the phenological, yield, and yield components of the barley genotypes under study. They also showed that there is genetic variability among the genotypes tested. Regarding days to heading four genotypes (G4, G9, G15 and G17) were early to head than four released varieties whereas 12 of the genotypes were late to head (Table 5). Among the four early heading genotypes only the three were matured earlier (G4, G9 and G15) than the standard check G2 (HB 1966) and two genotypes (G7 and G10) had equal maturity time and the rest 11 genotypes took longer maturity time. In relation to grain filling period only three genotypes *viz* G3, G17 and G18 had extended grain filling period for dry mater accumulation than the standard check G2 (Table 5). Corroborate to this finding, Muluken *et al*. (2010), who carried out an experiment in seven locations in northwest Ethiopia and noticed significant difference among genotypes for agronomic traits including days to heading, maturity, plant height, and thousand kernel weights. This result is consistent with the findings of Mirosavljevic *et al*. (2016), who found considerable variability in agronomic and yield component traits, including heading date, plant height, spike length, thousand grain weight, and grain yield. This study is in line with earlier investigation by a number of researchers who discovered that a significant genotype by environment interaction as well as genotype and environment variance brought variation in the quantitative traits of cereals (Girma *et al*., 2018; Gadisa *et al*., 2019; Agegnehu *et al*., 2019; Alemayehu, 2020a; Alemayehu, 2023). The overall conclusion is that there is genetic variability among the genotypes and environmental conditions had an impact on the phenological, yield, and yield components of the barley genotypes under study. This indicates that there was significant variation in the environment, genotype, and genotype by environment interaction. Good grain yield of barley genotypes was obtained in the two locations (Bule and Kemba) having suitable temperature and precipitation than the other locations.

Table 4. The average yield (kg ha^{-1}) performance of 18 barley genotypes across six environments

Genotype	E1	E2	E3	E4	E5	E6	Mean
16739-D	1021	5029	2194	1512	668	2252	2113
HB -1966	767	3941	2968	2337	1975	1317	2218
HB-1307	1902	4559	2313	996	4200	2782	2792
17257	419	2821	861	376	3170	2184	1638
3514-B	829	4820	4222	1765	3173	2108	2819
242093-A	1235	4669	2886	1200	2327	1818	2356
208905-A	1216	2770	1469	2182	2560	2086	2047
1773-B	1385	3866	1641	919	1135	980	1654
17252-C	2009	3753	1119	2200	2903	3193	2530
18330-A	1355	3000	821	1397	2773	1433	1797
24965-C	960	4026	1686	597	2352	2059	1947
17688-A	909	3764	430	454	4592	1556	1951
HB 1964	808	3541	843	1303	2823	1506	1804
64165-A	1890	3884	849	584	3237	1576	2003
18302-A	840	2474	657	2012	2475	2781	1873
64116-A	1844	3665	623	540	3630	1705	2001
17148	2091	4575	801	695	3778	1971	2318
Cross 41/98	696	4232	1218	1258	1258	1149	1635
Mean	1232	3855	1533	1240	2724	1914	
CV(%)	14.8	11.3	11.3	18.4	10.3	15.0	

E1= Abera Gelede, 2=Bule, 3= Bursa, 4= Gedeb, 5= Kemba 6= Albazar

Table 5. Mean values of agronomic traits and grain yield of 18 barley genotypes

Genotypes	DH	DM	GFP	PH	SL	NSP	TKW	GY
G1	90	139	49	83.4	7.4	42	43.4	2112.82
G2	82	137	55	97.4	9.9	28	55.3	2217.54
G3	85	142	57	89.0	7.8	45	45.1	2792.02
G4	77	129	52	93.0	8.8	24	47.0	1638.41
G5	86	141	55	92.0	7.6	44	46.3	2819.45
G6	92	146	54	100.1	8.5	50	42.9	2355.67
G7	90	137	47	106.7	9.9	28	50.1	2047.15
G8	95	145	50	96.4	8.2	45	40.5	1654.20
G9	79	130	51	102.3	8.8	42	42.5	2529.50
G10	83	137	54	85.2	8.2	38	40.6	1796.57
G11	92	143	51	94.5	8.5	42	44.5	1946.58
G12	91	143	52	91.1	8.8	26	48.1	1950.74
G13	82	136	54	95.6	8.0	26	45.8	1804.08
G14	84	139	55	92.0	8.9	43	38.2	2003.41
G15	75	127	52	92.5	8.5	23	46.8	1873.11
G16	91	142	51	96.9	8.7	37	40.8	2001.38
G17	86	142	56	88.0	7.5	41	44.0	2318.49
G18	79	139	60	73.1	7.7	27	49.2	1635.04
Mean	85.45	138.61	53.15	92.70	8.40	36.00	45.10	2083.12
F- test	***	***	***	***	***	***	***	***
CV%	1.4	1.1	3.0	6.3	1.4	14.7	9.4	11.5
LSD (0.05)	0.79	0.97	1.06	3.81	0.29	3.65	2.82	159.72

***= Significant at ($P \leq 0.001$) probability level, DH= Days to heading, DM= Days to maturity, GFP= Grain feeling period (days), PH= Plant height (cm), SL= Spike length (cm) NSP= Number of seeds per spike, TKW= Thousand kernel weight (g) GY= Grain yield (Kg ha^{-1})

Additive main effects and multiplicative interaction (AMMI) analysis

Table 6 displays the AMMI analysis of variance for grain yield (kg ha^{-1}) of 18 barley genotypes that were tested in the six different environments. Both environment and genotype exhibited a substantial ($P \leq 0.001$) impact on grain yield when the additive component of the study was taken into account. In this study, the environment explained 60.42 percent of the variation in grain yield, while genotype accounting for 8.45% and the G×E interaction accounting for 31.12%. This finding is corroborated by earlier research on barley (Vaezi *et al*., 2017; Girma *et al*., 2018; Kendal *et al*., 2019) and wheat (Temesgen *et al*., 2015; Agegnehu *et al*., 2019; Alemayehu, 2020a), which showed that the environment was the main factor influencing variation in grain yield, followed by G×E interaction.

The current study found that environment account for the majority of the difference in grain yield. This suggests that there are many settings that can be further subdivided into mega environments. This finding is consistent with the findings of Kendal *et al*. (2019), who observed that the variation in grain yield among environments suggests a high degree of environmental variability. Grain yield was considerably ($P \leq 0.001$) influenced by the genotype by environment interaction in the multiplicative component. The variance in the treatment sum of squares, as determined by AMMI (31.13%), was explained by GEI effects (Table 6). This study confirms the findings of Girma *et al*. (2018), Alemayehu (2020a), Kaya and Turkoz (2016), Khanzadeh *et al*. (2018), and Ozturk (2021) who discovered that the GE interaction explained 25.84, 25.52, 20.6, 22.7, and 14.39 percent of the variance, respectively greater than the variance observed from genotypic effect. Because the environment contributed more to GEI than to genotype influence, there was a bigger variation in GEI for the observed yield variation. Two significant IPCAs were retrieved from the interaction component by the AMMI model (Table 6). Additionally, the AMMI's multiplicative component showed that the mean squares for IPCA1 and IPCA2 were very highly significant ($P \leq 0.001$). Therefore, IPCA1 and IPCA2 accounted for 76.83% of the total GEI sum of squares, capturing 54.16% and 22.67% of the interaction sum of squares, respectively. This suggests that a substantial influence on the variance in GEI had been exercised by the former two IPCAs. Moreover, the IPCA1 mean square was higher than the IPCA2 mean square, suggesting that GEI caused variations in the genotypes' grain yields.

Table 6. AMMI ANOVA for grain yield (kg ha^{-1}) of 18 barley genotypes

Source	D.f.	SS	MS	Sum of squares explained (%)	G×E Interaction Explained (%)
Treatments	107	475091191	4440105***		
Genotypes	17	40134493	2360853***	8.45	
Environments	5	287052545	57410509***	60.42	
Block	12	1093272	91106		
Interactions	85	147904154	1740049***	31.13	
IPCA 1	21	80111111	3814815***		54.16
IPCA 2	19	33531331	1764807***		22.67
Residuals	45	34261712	773363***		23.17
Error	204	11603409	56879		
Total	323	487787872	1510179		

This result is consistent with previous findings on barley from Vaezi *et al*. (2017), Girma *et al*. (2018), and Kendal *et al*. (2019). As a result, the AMMI model with the first and second multiplicative terms was sufficient for cross-validation of the GEI-explained variation in grain yield, which can be shown using a biplot. The outcome was consistent with the findings of multiple authors (Hintsa and Fetin, 2013; Dogan *et al*., 2016; Vaezi *et al*., 2017; Girma *et al*., 2018; Gadisa *et al*., 2019; Gupta *et al*., 2022) who used the first two IPCAs for GGE biplot analysis of various crops. These authors reported that the best predictive model was AMMI with the first two multiplicative terms, which revealed a similar magnitude of GEI variance revealed by the first two principal components of GEI.

AMMI stability value (ASV) and yield stability index (YSI)

Genotypes G11, G13, and G10 in the AMMI stability value model had reduced ASV, indicating good stability but lower yielding, while genotypes G3, G9, G7, and G11 displayed moderate ASV and lower YSI values. Compared to other genotypes, these genotypes exhibit comparatively higher yield performance and stability (Table 7). Genotypes with high grain yield and the lowest YSI values are thought to be the most stable (Bose *et al*., 2014; Hebbache *et al*., 2021; Alemayehu, 2023). Consequently, these genotypes with great adaptation and high grain production were distinguished by the stability index. Similarly, Roostaei *et al*. (2022) discovered that the genotypes with the highest mean yield were also the most stable. Farshadfar *et al*. (2013) in chickpea, Alemayehu (2023) in finger millet, and Hebbache *et al*. (2021) in barley all in agreement with the current finding. However, the most unstable genotypes with significant ASV were G1, G12, and G2. Even though these genotypes were not stable across the environments but they are adapted to specific niches. Similarly, Roostaei *et al*. (2022) observed that unstable genotypes exhibiting distinct environmental responses were those with a higher IPCA1 score. Because the most stable genotypes would not always produce the finest performance, the principles of stability alone might not be the only selection criteria. According to Farshadfar *et al*. (2011) and Alemayehu (2023), stability should not be the sole criterion for selection, as the genotypes with the highest levels of stability may not always

produce the highest yields. The issue of utilizing yield stability as the only criterion for genotype selection is lessened by the yield stability (YSI) approach, which combines yield and stability into a single index. Temesgen *et al*. (2015) also suggested that in order to fully utilize the beneficial effects of GE interaction, yield and stability should be taken into account simultaneously. On the other hand, genotypes such as G12, G18, G8, G1, G4, and G16, exhibited high YSI values and yields below the grand mean, suggesting that their performance was unstable in all test environments. Additionally, the genotype and environment main effects are shown in the x axis of the AMMI PCA1 biplot, and the interaction effect is shown in the y axis (IPCA1 score vs mean yield). According to Dogan *et al*. (2016) and Hebbache *et al*. (2021) the genotype exhibits widespread adaptation of that trait to tested contexts when the IPCA1 score is closer to zero. As a result, G7 and G11 had IPCA1 scores of -0.2091 and -3.99154, respectively (Table 7). Due to their close proximity to the origin and mean grain yield that is comparable to the general average, these two genotypes are not sensitive to interaction effect. Conversely, genotypes G9 and G3 were rather stable and exhibited high adaptation to the studied environments (Figure 1).

The first two IPCAs were used to construct the AMMI 2 biplot (IPC1 vs. IPC2 scores), which captured 76.83% of the total variation in GE interactions. AMMI2 biplot illustrates good explanation of the data pattern of genotype and environments based on the first IPCAs scores, which helps effective means of visual interpretation of GE interaction patterns and identification of genotypes or environments that contribute to low, medium or high level of interaction (Figure 2). In terms of GE interaction and environment discrimination abilities, Kemba and Bursa, the environments with the longest vectors, tended to contribute the most. The environments Gedeb and Bule with moderate vectors tended to high contribution into GE interaction, while the other enivironments Abera Gelede and Albazar were not most informative in genotype descrimination due to short vectors. Regarding the AMMI2 biplots genotypes G13, G11 and G10 found to be highly stable with moderate grain yield performance (Figure 2). Genotype G13 and G10 more adapted to Abera Gelede and Albazar wheras G11 for Bule areas so can be recommended for production in these areas and similar agro-ecologies. Genotypes G3, G9, and G7 are very productive and relatively stable, making them more suited to the agro-ecologies of Kemba, Albazar, and Gedeb, respectively while genotypes G5, G17 and G2 are high yielding with least stable genotypes specifically adapted to Bule and Bursa (G5), Kemba (G17) and Gedeb (G2) these areas are more suited for production to these specific genotypes.

Table 7. Mean grain yield (kg ha^{-1}) and AMMI stabilty values for barley genotypes tested in six environments

Genotypes	IPCA1	IPCA2	ASV	R^a	MGY	R^y	YSI
G1	-30.2212	-1.40787	72.216	18	2113	7	25
G2	-24.9929	-3.95275	59.842	16	2218	6	22
G3	10.08222	13.77847	27.750	6	2792	2	8
G4	14.06312	-1.75903	33.645	7	1638	17	24
G5	-22.8698	17.02171	57.229	15	2819	1	16
G6	-17.564	13.04841	43.945	12	2356	4	16
G7	-0.2091	-22.5556	22.561	4	2047	8	12
G8	-16.8374	2.63591	40.313	11	1654	16	27
G9	6.94925	-21.945	27.518	5	2529	3	8
G10	8.03247	-9.54586	21.434	3	1797	15	18
G11	-3.99154	6.99756	11.828	1	1947	12	13
G12	28.55122	14.32422	69.701	17	1951	11	28
G13	5.52114	-3.40353	13.623	2	1804	14	16
G14	13.72462	8.57997	33.894	8	2003	9	17
G15	7.22792	-31.9816	36.346	9	1873	13	22
G16	20.37582	7.09441	49.195	14	2001	10	24
G17	18.14662	13.10575	45.292	13	2318	5	18
G18	-15.9885	-0.03522	38.199	10	1635	18	28
Grand mean					2083.12		

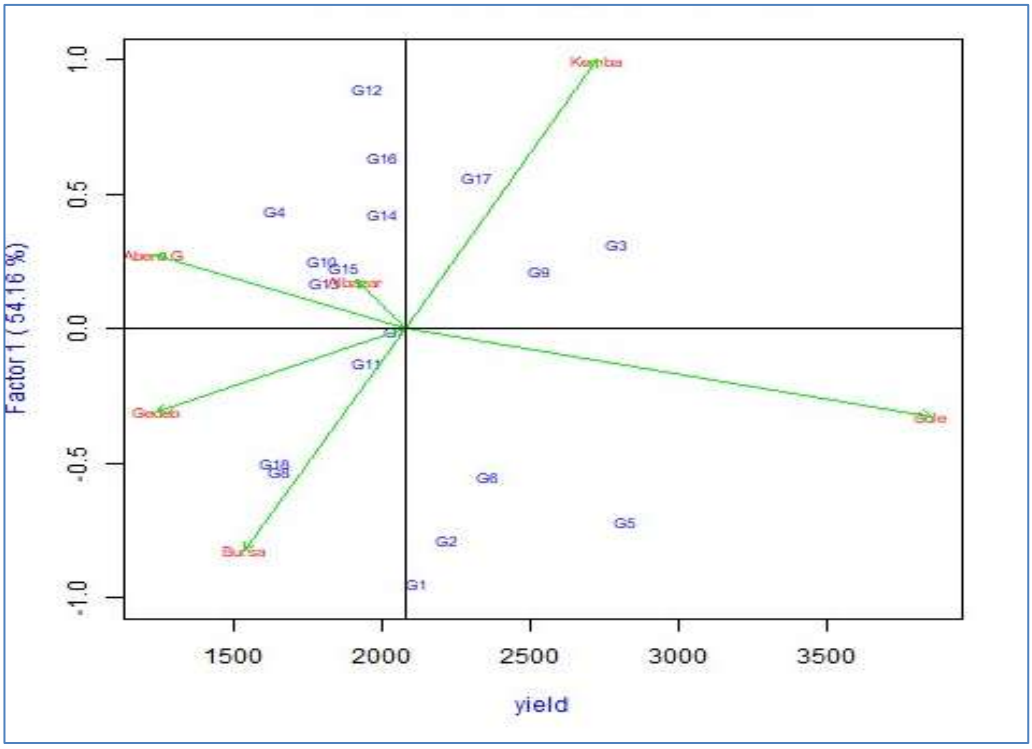


Figure 1. AMMI1 biplot for grain yield showing the plotting of mean yield and IPCA1 score of genotypes

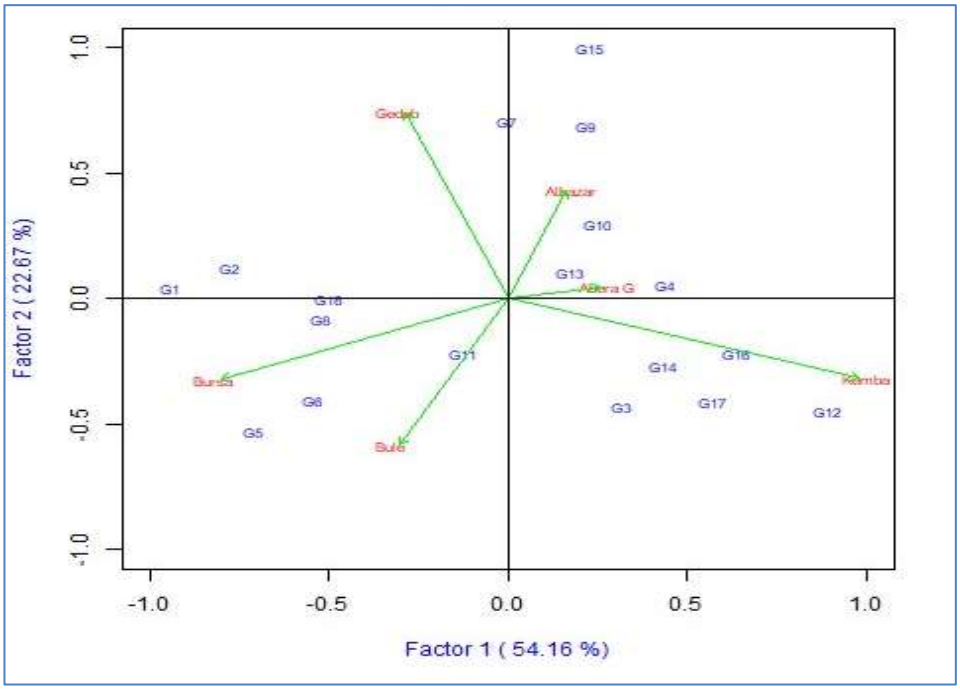


Figure 2. AMMI 2 biplot for grain yield showing the plotting of IPCA1 and IPCA2 of genotypes

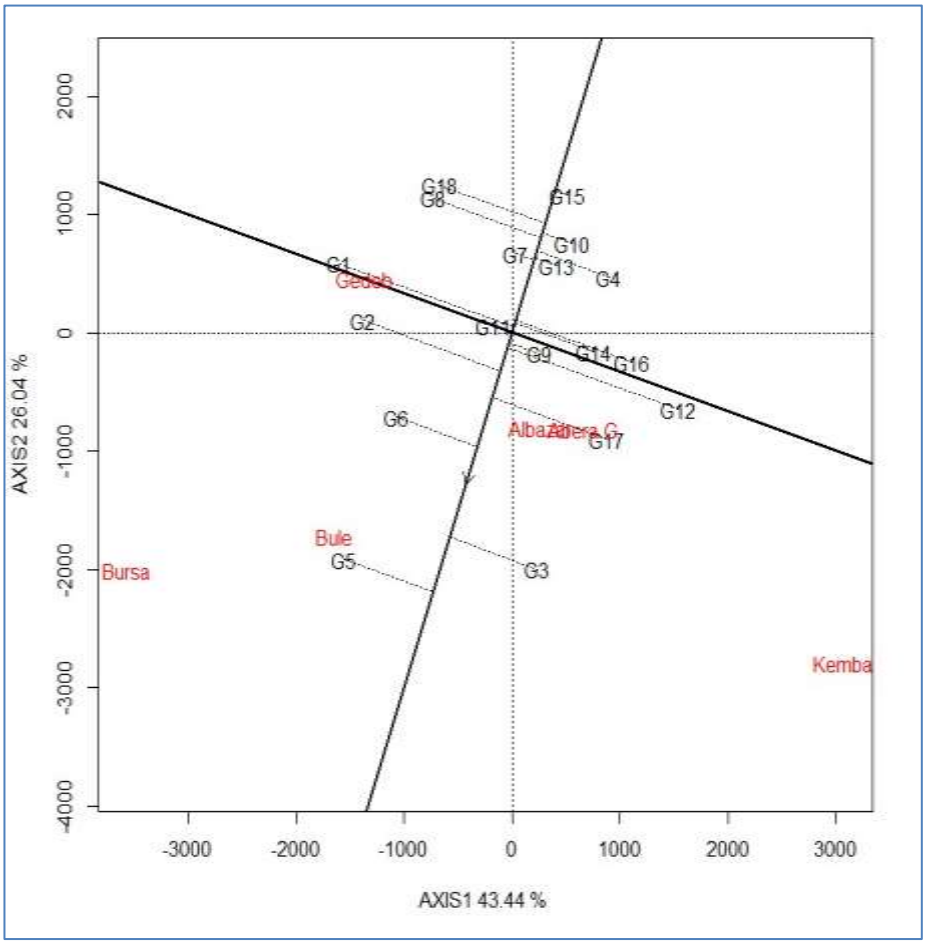
GGE biplot analysis

The biplot shows the genotypic main effect (G) and the genotype by environmental interaction (GEI) effect of the genotype for various environmental data sets (Yan *et al*., 2000). PCs 1 and 2 accounted for 43.44% and 26.04% of the GGE sum of squares, respectively, according to the use of the biplot for partitioning using GGE biplot analysis (Figure 3).

Mean grain yield and stability of barley genotypes

The barley genotypes were ranked along the average-tester axis (ATC abscissa) in the GGE biplot (Figure 3), with the horizontal line representing their average performance over the six locations and the single-arrowed line representing the average environment coordinate (AEC) abscissa (or AEA) and pointing to higher mean yield across environments. Consequently, the AEC coordinate separated genotypes that had below-average mean grain yield from those that showed higher grain yields than the average; genotypes G4 (17257), G18 (Cross 41/98), G8 (1773-B), G10 (18330-A), G13 (HB 1964), G15 (18302-A) and G11 (24965-C) showed below-average mean grain yield, while G5 (3514-B), G3 (HB-1307), G6 (242093-A), G9 (17252-C), G17 (17148), G2 (HB -1966) and G1 (16739-D) showed above-average mean. The genotypes with large distances in either direction from the AEA abscissa in Figure 3 indicate increased GE interaction and

decreased stability. As a result, the genotypes G1 (16739-D), G2 (HB -1966), and G17 (17148) yield more and are the most unstable, whereas the genotypes G11 (24965-C), G7 (208905-A), G13 (HB 1964), and G15 (18302-A) yield less and are extremely stable. The best genotypes for selection are those with high mean grain yield and good stability. Because they were stable and produced large yields, the genotypes G3, G6, G5, and G9 were chosen as the most highly adaptable to various environments. According to this study, a number of researchers (Yan *et al*., 2007; Wosene *et al*., 2015; Melkamu *et al*., 2015; Temesgen *et al*., 2015; Girma *et al*., 2018; Mizan *et al*., 2019; Gadisa *et al*., 2019; Wondimu *et al*., 2023) reported the relative contributions of stability and mean grain yield for the identification of desirable genotypes after the GGE bi-plot procedure.

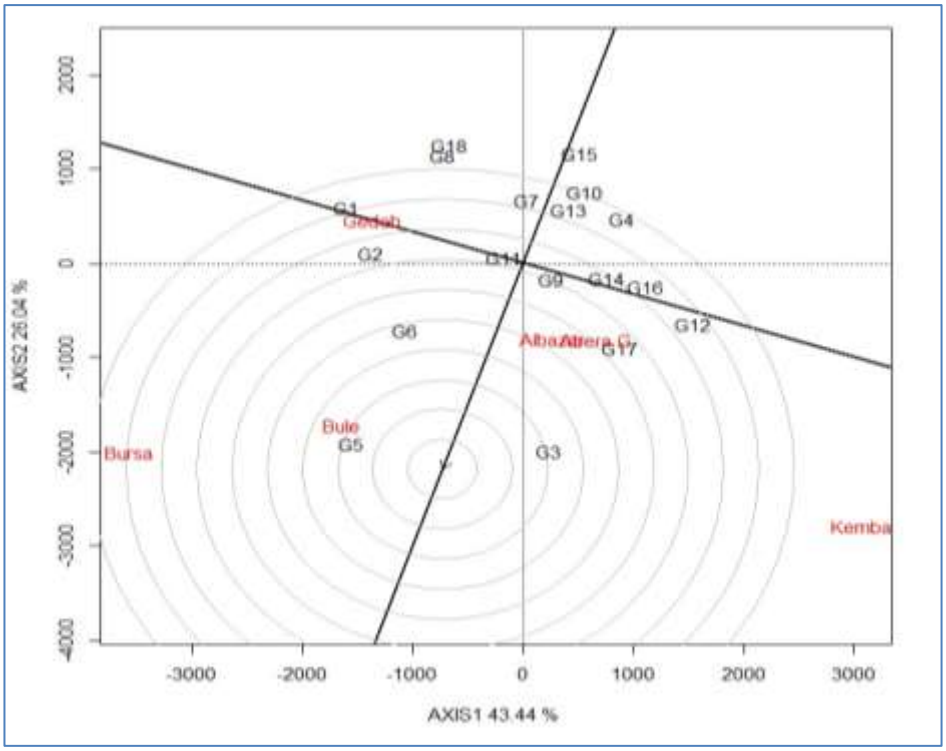


AXIS1= PC1, AXIS2= PC2

Figure 3. GGE biplot showing “mean vs. stability” of 18 barley genotypes across six environments

Comparison of genotypes relative to the ideal genotypes

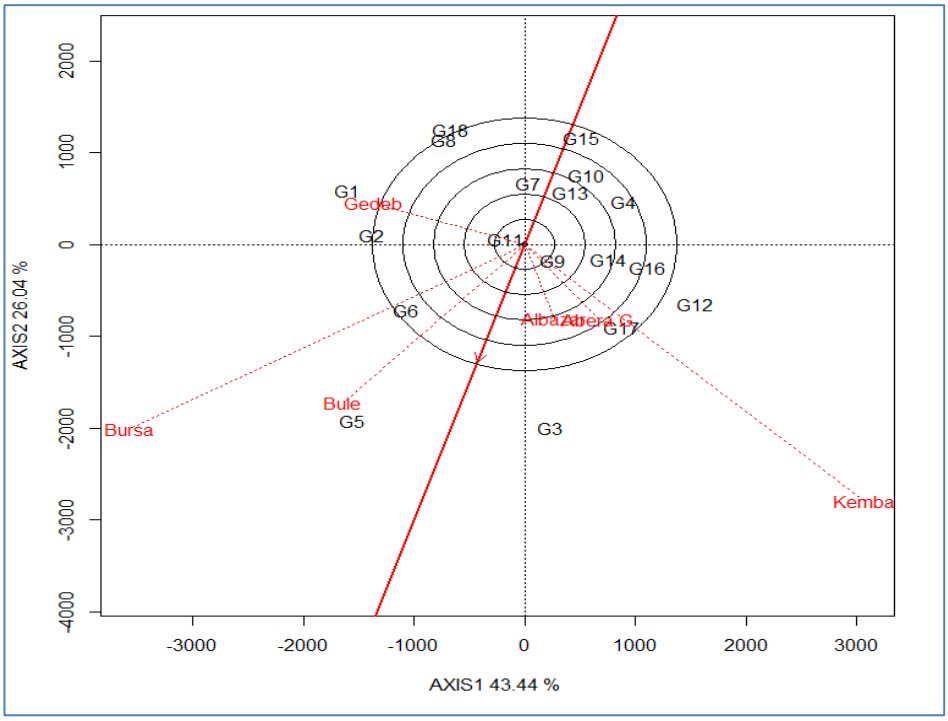
The average environmental coordinate (AEC) approach was used in the GGE biplot methodology to estimate genotype yield and stability (Yan and Hunt 2001). According to Yan and Tinker (2006), genotypes in the GGE biplot with high PC1 scores have high mean yields, while those with low PC2 scores have yields that are consistent across environments. The Average Environmental Coordinate (AEC) is the line that goes through the biplot origin and is determined as the mean of the PC1 and PC2 scores for all environments (Yan and Kang, 2003). According to Yan and Hunt (2001), the average environment coordinate is shown as a single arrow that points in the direction of the concentric circle for increased stability. Thus, to illustrate the difference between genotypes and the ideal genotype, concentric circles were created starting from the middle and pointed with an arrow (Yan and Tinker, 2006). According to Farshadfar *et al*. (2012) and Khanzadeh *et al*. (2018), the optimal genotype has the highest mean grain yield and is stable in all situations. Near the optimal genotype are the genotypes that are considered desirable. As a benchmark for selection, the optimal genotype is located close to the biplot's first concentric circle. G3 was the ideal genotype to plant in stable environment Bule sub center followed by G5, and G6 which are desirable genotypes. This finding is in agreement with work of (Farshadfar *et al*., 2012; Khanzadeh *et al*., 2018; Gadisa *et al.,* 2019; Kendal *et al.,* 2019). Because genotypes G15, G18, and G8 deviate greatly from the ideal genotype, they are considered undesirable based on the average environmental coordination (AEC) technique, which more variable and poorer in in yield performance (Figure 4). It is evident from Figure 4 that Bule has the maximum yield and stability at the same time when it comes to the settings. Kemba and Gedeb also had the most interaction as they are far from the concentric circle.



AXIS1=PC1, AXIS2= PC2
Figure 4. Comparison of genotypes relative to the ideal genotype

Discriminating ability of testing location

GGE biplot analysis of discriminating ability and representativeness result indicate that out of six test environments indicated that Bule, Bursa, and Kemba were the most discriminating barley genotypes, while Abera Gelede, Albazar, and Gedeb were consistently non-discriminating and provided little information on the genotypes due to their close proximity to the bi-plot origin and very short vector(Figure 5). Kemba and Bursa had long vectors and big angles with the AEC indicate that they might not be used to select superior genotypes, but rather to weed out unstable genotypes and choose environments that are specifically suited to them; making the environment discriminating but non-representative. Bule had relatively tiny angles and long vectors with the AEC in those situations. Bule is excellent for selecting genotypes that are both discriminating and representative of the test environments, as evidenced by here. Bule is also more effective at distinguishing between genotypes. Several writers (Vaezi *et al*., 2017; Khanzadeh *et al*., 2018; Girma *et al*., 2018; Kendal *et al*., 2019; Gadisa *et al*., 2019) employed GGE biplot to determine representativeness and discriminating test environments for various crop genotypes.



AXIS1=PC1, AXIS2= PC2

Figure 5. GGE biplot showing rank of test locations based on discriminating ability and representativeness

Which-won-where patterns of genotypes across the environments

The best barley genotypes for each environment were determined, and the stability of genotypes was evaluated, using the GGE biplot analysis, which is the most efficient method of summarizing genotype and genotype-by-environment interaction of the data set. The most visually appealing part of the GGE biplot is the polygon view feature, which tackles the "which-won-where" pattern of multi-environment data and offers a graphical depiction of crossover GE interaction, mega-environment distinction, and unique genotype adaptation. This polygon consisted of six sectors. G1 (16739-D), G18 (Cross 41/98), G15 (18302-A), G12 (17688-A), G3 (HB-1307), and G5 (3514-B), which were positioned at the corners of a polygon, were therefore the genotypes that were vertex genotypes with the longest vectors. The top yielding genotypes in the area included in each sector are represented by the vertex genotypes, and these genotypes were among the most responsive to the environments in their respective directions when compared to other genotypes. But the two vertex genotypes namely G18 (Cross 41/98), and G15 (3514-B) were low-yielding and located in Gedeb, reflecting poorly yielded at all location. The genotypes within the polygon were less responsive to location than the corner genotypes. As shown in Figure 6, the rays of the line graphs divided the graph into six sectors, and two environments each appearing in one

sector each (E2, E3, E4) and (E1,E5, E6) by identifying the existence of two mega-environments where G1 (16739-D) was in winning environments (Gedeb), G12 (17688-A) winning environment (Kemba), G3 (HB-1307) in winning environments (Albazar and Abera Gelede) and G5 (3514-B) in winning environments (Bule and Bursa). Numerous writers have documented and recognized mega-environments and the potential for employing GGE biplot models to choose stable genotypes (Yan *et al*., 2000; Yan *et.al*., 2007; Dogan *et al*., 2016; Vaezi *et al*., 2017; Kendal *et al*., 2019; Gadisa *et al*., 2019; Agegnehu *et al*., 2019).

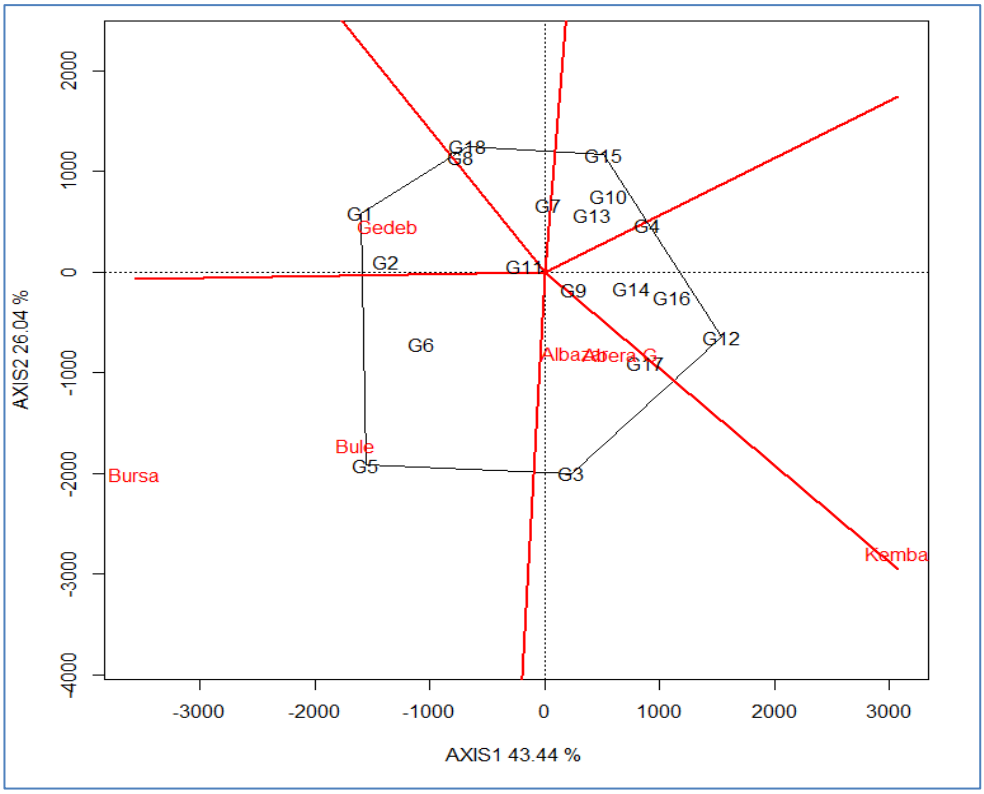


Figure 6. Which-won-where pattern of GGE biplot

Conclusion

A broad range of variation exists between genotype, environment, and G×E interaction, as demonstrated by the combined analysis of variance, which revealed that genotype, environment, and G×E interaction are highly significant among the genotypes for all traits. According to the AMMI analysis of variance the environment (E) and genotype (G) main effects accounted for 60.42% and 8.45% of the treatment sum of squares, respectively. Additionally, the G×E interaction contributed 31.13% to the treatment sum of squares. The genotypes G3 and G9

were found to be stable and high yielding in all situations by AMMI and GGE biplot techniques. Furthermore, genotypes G3, G9, G7, and G11 were highlighted by the yield stability index and AMMI stability value as having better yields and consistent performance in a variety of settings, making them suitable for recommendation in various environments. G5, which was positioned in the middle of the concentric circles in the genotype ranking, was the best genotype in terms of stability and high yield performance when compared to the other genotypes. Additionally, it is possible to view the genotypes G3, G6, and G17 as desirable because they are found next to the ideal genotype. As a benchmark for assessing the development of barley varieties in upcoming breeding programs, genotype G5, which was shown to have the highest producing ability in this study and fell into the first concentric circle, was the stable genotype. However, genotypes such as G12, G18, G8, and G1 were found to have the least consistent performance and could not be suggested for particular situations due to their high YSI and ASV values. The current study offers important insights into the genotype yield stability status of barley and the optimal settings for next Ethiopian improvement projects. Accordingly, Bule has the highest yield and stability simultaneously of all the environments. The genotypes G3 (HB-1307) and G9 (17252-C) were generally found to be stable and high yielding, making G9 acceptable for release and G3 suitable for cultivation in a larger environment.

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