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Stability Analysis and Selection of Maize (*Zea mays* L.) Genotypes Using AMMI and GGE Biplot

Gemechu Asefa[1], Temesgen Chibsa[2], Desalegn Chalchisa[3], Beyene Abebe[4], Tolera Keno[5], Sara Oli[6], Lemi Yadessa[7], Bitew Tilahun[8], Belay Garoma[9], Yaregal Damtie[10], Yednekachew Marid[11], Mamud Aman[12], Megersa Mengesha[13], Zenebech Teshome[14] and Bedilu Goben[15]

[1-9,15]Bako National Maize Research Center, Bako, P.O.Box 03, Ethiopian Institute of Agricultural Research (EIAR), Ethiopia.
[10]Pawe Agricultural Research Center, Pawe, Ethiopian Institute of Agricultural Research (EIAR) , Ethiopia.
[11,12]Hawassa Agricultura Research Center, Hawassa, Ethiopian Institute of Agricultural Research (EIAR) , Ethiopia.
[13]Asosa Agricultural Research Center, Asosa, Ethiopian Institute of Agricultural Research (EIAR) , Ethiopia.
[14]Jimma Agricultura Research Center, Jimma, Ethiopian Institute of Agricultural Research (EIAR) , Ethiopia.

[1]E-mail: gameasefa12@gmail.com

Abstract. Genotype evaluation for stability and high yielding in maize is an important factor for boosting productivity and sustainability of maize production. A total of 25 maize genotypes were evaluated over six environments namely Bako (BK), Asosa (AS), Hawasa (HW), Pawe (PW), Jimma (JM) and Arsi-Negele (AN) using randomized complete block design with three replications during 2022 for the objective to identify superior and stable maize genotypes through stability analysis. Combined ANOVA revealed highly significant ($p<0.01$) difference among genotypes, environments, and genotype by environment interaction (GEI) for studied traits including grain yield (GY). The environment and GEI were found to be the most significant causes of the grain yield (GY) accounted 60.3% and 21.4 % of overall variation, respectively. The sum of the first two principal components of AMMI and GGE biplot explained the GEI variation for GY 74.5% and 78.1%, respectively. The AMMI and GGE biplot analysis depicted some genotypes G20, G25,G2, G17, G21, G13, G9 and G16 gave GY above the mean and less affected by GEI. The polygon view of the GGE biplot showed that the first mega-environment contains four environments BK, PW, AS, and HW with G20, the second and third environment contains JM and AN with G11 and G13 as winner genotypes (vertex), respectively. Environments AS, PW and BK identified as best environments based on its yield, discriminating and representativeness which were close to ideal environments. Genotypes G20 (3XM2110426) identified as ideal and G25 (BH520), G2 (3XM2110423), G17 (BH549), G21 (3XM2110422), G9 (3XM1900467) and G18 (3XM2110424) considered as desirable genotypes based on proximity to ideal genotypes. Therefore, G20 (3XM2110426) and G2 (3XM2110423) are recommended for verification and release after confirming the reliable performance of these genotypes through conducting multiyear evaluation and determining mega-environments for maize production in similar agro-ecologies of Ethiopia.

Keywords. Discriminative, Environment, Genotypes, Selection, Stability.

1. Introduction

Maize (*Zea mays* L., 2n=20) is an important cereal crop belonging to the tribe *Maydeae*, of the grass family, *Poaceae*, Genus *Zea*, and Species *mays* [1]. In terms of wide adaptation, productivity, and total production maize is the main food and feed crop in worldwide and Africa including Ethiopia. Maize is cultivated annually on an estimated area of land 197 million and 41.2 million hectares globally and in Africa, respectively making it the second most widely grown crop in the world after wheat [2]. In 2020, maize production was 1,162 million tonnes which is markedly higher 52.9% and 53.6% than both rice (760.9 million tons) and wheat (756.7 million tons), respectively [2].

Maize Production in Ethiopia has shown a considerable increment from 1.67 million tonnes (on 1.1mil ha) in 1995 to 10.75 million tonnes (on 2.56 mil. ha) in 2022. In 2021/22, cereal crops in Ethiopia covered 81.97% (9.99 mil. ha) out of the total crop area, maize took up (21.02%) which is the second position after Teff (24.05%). In terms of production, maize made up 32.79% (about 107,513,689.44 qt) followed by wheat (17.71%) and Teff (17.1%) with an average yield of 4.2 t/ha which represents an increment of 177.8% from 1.51 t/ha in 1995 to 4.2 t/ha in 2022 [3]. This indicates that maize breeders have been very fruitful in developing or releasing improved technologies/ varieties with full packages and are still striving to enhance the maize yield and further improve productivity.

Identifying the most stable and widely adapted genotype under multiplications is important in many plant-breeding programs for all crops, including maize. However, significant fluctuations of genotype performance to different growing conditions or locations occurred due to the genotype-by-environment interaction (GEI) phenomenon [4]. This phenomenon has been and still, is a major factor limiting the success of germplasm selection and identification of superior genotypes for use in plant breeding programs. It also minimizes the usefulness of the genotype means across locations or environments for selecting and advancing superior genotypes to the next stage of selection [5].

Different scholars [6-12], have been reported the presence significant genotype-environmental interactions(GEI) for maize grain yield in their studies conducted on different materials, in different locations and years.

Among different methods of measuring the stability of genotypes, the most commonly used to identify the stable genotype(s) are the .additive main effects and multiplicative interaction (AMMI) model [13] and genotype main effects in addition to genotype by environment interaction (GGE) biplot [14]. The Additive Main Effects and Multiplicative Interaction (AMMI) model has been used extensively for analysis of multi-environment yield trials for two main purposes: understanding complex genotype by environment interactions and increasing accuracy to improve recommendations, repeatability, the selections, and genetic gains [13].

Genotype main effects in addition to genotype by environment interaction (GGE) biplot GGE bi-plot analysis considers both genotype and GEI effects and graphically displays GEI in a two-way table [15]. It is an effective method based on principal component analysis (PCA) to fully explore multi-environment trial (MET) data. The GGE biplot is superior to the AMMI1 graph in mega-environment analysis and genotype evaluation because it explains more G+GE and has the inner-product property of the biplot, the discriminating power vs. representativeness view of the GGE biplot is effective in evaluating test environments, which is not possible in AMMI analysis [16].

Both GGE biplot analysis and AMMI analysis combine rather than separate G and GE in mega environment analysis and genotype evaluation [16]. Therefore, the objective of this study was to identify superior or high-yielding and stable genotypes from a pool of advanced maize genotypes and to identify ideal test environments based on their discrimination ability and representativeness.

2. Materials and Methods

2.1. Germplasm

The germplasm used for the study was maize germplasm generated, organized, and tested under advanced variety trials (AVT) in 2022 (indicated in *Table*). A total of 25 germplasm including both commercial and genetic checks were included in the materials.

Table 1. Summary of experimental materials for the study.

S.No.	Genotype Name	Designate	Type of cross
1	SXM2111375	G1	SCH
2	3XM2110423	G2	3WCH
3	3XM1900243	G3	3WCH
4	SXM2111373	G4	SCH
5	SXM2111378	G5	SCH
6	BH546	G6	3WCH (Commercial Check)
7	SXM2111372	G7	SCH
8	3XM2110425	G8	3WCH
9	3XM1900467	G9	3WCH
10	SXM2111377	G10	SCH
11	BH5211	G11	3WCH (Genetic Check)
12	3XM1900453	G12	3WCH
13	SXM2111374	G13	SCH
14	3XM1900302	G14	3WCH
15	SXM2111369	G15	SCH
16	3XM2110425	G16	3WCH
17	BH549	G17	SCH (Commercial Check)
18	3XM2110424	G18	3WCH
19	Limu	G19	3WCH (Commercial Check)
20	3XM2110426	G20	3WCH
21	3XM2110422	G21	3WCH
22	SXM2111371	G22	SCH
23	SXM2111370	G23	SCH
24	BH661	G24	3WCH(Commercial Check)
25	BH520	G25	SCH (Genetic Check)

Note: SCH = Single Cross Hybrid, 3WCH = Three Way Cross Hybrid.

2.2. Description of Site and Experimental Design

A total of 25 maize germplasm (19 experimental hybrids, four commercial checks, and two genetic checks) were evaluated across six environments in 2022. The experimental sites were representative of sub humid mid-altitude agro ecology of Ethiopia. The description of study areas with some climatic and soil characteristics is presented in Table . The experiments were laid down by randomized completely block design with three replications. The entries were hand-planted in two-row plots of 5.0m in length at each location. The spacing used was 0.75 m between rows and 0.25 m between plants was used following the agronomic recommendations of the respective environments. Initially, two seeds were planted per hill and later thinned to one plant to achieve the target plant densities of 53,333 plants ha^{-1} at each location.

Table 2. Summary of ecological description of the study sites.

Location	Altitude(m.a.s.l)	RF (mm)	Temperature (^{0}c)		Latitude	Longitude	RH	Soil type
			Min.	Max.				
Bako (BK)	1650	1598	14.36	27.1	09^{0}06'00"N	37^{0} 09'E	63.55	Nitosol
Asosa(AS)	1545m	1166	15.70	28.30	10^{0}02'24"N	34^{0} 34'E	-	Nitosol
Jimma(JM)	1753	1572	11.6	26.3	7040’00’’N	36^{0}47’E	67	Redish/Nitosol
Pawe(PW)	1120	1000-	17.1	33.2	11^{0}09'03"N	36^{0} 03'E	74.5	Nitosol

Location	Altitude(m.a.s.l)	RF (mm)	Temperature (^{0}c)		Latitude	Longitude	RH	Soil type
			Min.	Max.				
		1500						
Arsi-Negele(AN)	1960	866	9.1	26	7°20’00"N	38°09’E		Nitosol
Hawassa(HW)	1689	797	12.6	27.3		38°30’ E		

2.3. Data Collected

Data were collected on grain yield (GY) (adjusted to 12.5-grain moisture and expressed as tons ha^{-1}), plant (PH) and ear height (EH) (cm), days to 50% anthesis (DA), and silking (DS) on plot basis at each of the six locations.

2.4. Statistical Analysis

Combined statistical analysis for genotype-environment interaction across six environments was done by R software v 4.4.2 software in a joint-ANOVA and a mixed model with interaction effect was performed to analyze data from multi-environment trials using the following model stated by [17].

$$yijk = \mu + \alpha i + \tau j + (\alpha\tau\ ) ij + \gamma jk + \varepsilon ijk$$

where yijk is the response variable (e.g., grain yield) observed in the kth block of the ith genotype in the jth environment (i = 1, 2, . . . , g; j = 1, 2, . . . , e; k = 1, 2, . . . , b); μ is the grand mean; αi is the effect of the ith genotype; τj is the effect of the jth environment; (ατ) ij is the interaction effect of the ith genotype with the jth environment; γjk is the effect of the kth block within the jth environment; and εijk is the random error.

The Additive Main Effect and Multiplicative Interaction (AMMI) model, which combines standard analysis of variance with principal component analysis (PCA) analysis was used to investigate genotype x environment interaction. The AMMI analysis was done using R software according to the model suggested by[17] stated that the response variable of genotype i in environment j using the Additive Main Effect and Multiplicative interaction (AMMI) model, is estimated by

$$yij = \mu + \alpha i + \tau j + X\ p\ k{=}1\ \lambda kaiktjk + \rho ij + \varepsilon ij$$

where λk is the singular value for the k-th interaction principal component axis (IPCA); aik is the i-th element of the k-th eigenvector; tjk is the jth element of the kth eigenvector. A residual ρij remains if not all p IPCA are used, where $p \le \min(g - 1; e - 1)$.

The GGE biplot is a biplot that displays the GGE part of MET data. GGE biplot analysis was used to carry out the usage of the genotype via environment analysis in R software v 4.4.2 [18]. The GGE biplot was built according to the formula given by Yan et al.[14]:

$$Yij - \mu - bj = I1ci1hj1 + I2ci2hj2 + eij$$

Where, Yij= the performance of the ith genotype in the jth environment; μ= the grand mean; bj=the main effect of the environment j; l1and l2= singular value for IPCA1 and IPCA2, respectively; ci1 and ci2= eigen vectors of genotype i for IPCA 1 and IPCA2, respectively; hj1andhj2= eigen vectors of environment j for IPCA1 and IPCA2, respectively; eij = residual associated with genotype i and environment j.

3. Results and Discussion

3.1. Analysis of variance (ANOVA)

Analysis of variance (ANOVA) within individual locations for all traits showed significant differences for genotypes which directed us to perform combined analysis of variance (result of individual location analysis not presented). The combined analysis of variance and AMMI analysis are shown below in Table and *Table* .

The combined ANOVA indicated there were highly significant differences ($p < 0.01$) among environments (E), genotypes(G), and interactions(GEI) for maize grain yield (GY)and other important traits like days to anthesis (DA), days to silking(DS), plant height(PH) and ear height(EH),. The environmental effect accounted for most of the total variation (G+E+GEI) for all studied traits including GY (60.3%). This indicated that there is wide variation in testing conditions under materials evaluated. In line with this, different scientists [7-12,19] reported highly significant and larger contribution of environment effect from the total variation for grain yield in maize in their studies in different materials, locations and years. Maize flowering characters, namely DA and DS, were also significantly affected by the environment, accounting for 89.9% and 85.6% of the total variation (G+E+GEI), respectively (Table). This indicates different environmental factors among locations causing differential flowering dates among maize genotypes.

Table 3. Combined ANOVA for grain yield and other traits of maize genotypes across locations during 2022.

SOV	DF	GY		DA		DS		PH		EH	
		MS	Exp (%)	MS	Exp (%)	MS	Exp (%)	MS	Exp (%)	MS	Exp (%)
Environment(E)	5	163.0**	60.3	2975.0**	89.9	2511.76**	85.6	12947.0**	39.6	12959.0**	49.6
Rep within E	12	15.26**	9.7	33.32**	2.2	53.44**	3.7	3488.0**	14.8	1615.0**	9.5
Genotype(G)	24	10.28**	18.3	31.17**	4.5	38.74**	6.3	2249.0**	33.0	1491.0**	27.4
G x E	120	2.41**	21.4	7.68**	5.6	9.90**	8.1	372.0**	27.3	251.0**	23.1
Residuals	288	1.25		4.89		6.18		266		184.0	
Total	569										
CV (%)		16.19		2.69		2.94		7.06		11.6	
Mean		6.91		82.29		84.49		231.1		116.9	

Note Value with ** indicated highly significant difference at 0.01 probability level, ns= non-significant, SOV = Source of variation, DF= degree of freedom, MS = mean square, Exp = Total variation explained (%), GY =Grain yield, DA = Days to anthesis, DS = Days to silking, PH = plant height, EH = Ear height, CV = Coefficient of variation (%).

3.2. Additive Main Effects and Multiplicative Interaction (AMMI) Analysis

Observing the decomposition of the GEI across environments through the AMMI model (Table), the first and second principal components (PCs) are highly significant ($p < 0.01$) for all traits including GY except DA and DS. This indicates that 25 maize genotypes vary and the environments are significant from each other. In the present study, the first two IPCA explained 74.4% of the total GEI variation, with contributions of 41.9% and 32.5%, respectively for grain yield (GY) in Table . For flowering characters, the contribution of the first and second IPCs was 71.7 and 71.3 of GEI variation for DA and DS, respectively. Each IPC captured 53.9, 17.9, and 50.0, 21.3% of GEI for DA and DS, respectively (Table).

Different authors also reported for various cross and self-pollinated crops that the first two PC scores explained a significant and greater percentage of GEI. As an example, on maize a significant PC1 and PC2 was reported by the authors like [7] 52.99% and 17.85%; [20] 23.4 and 16.6%;[21] 46% and 19% for maize inbred lines and 54% and 16% for single crosses; [11] 28.2% and 24.16%. Similarly [22] on Coffee arabica.

Table 4. AMMI model-based analysis of variance for grain yield and other traits of maize genotype locations during 2022.

SOV	DF	GY			DA			DS			PH			EH		
		MS	Pro.	Acc.	MS	Pro.	Acc.	MS	Pro.	Acc.	MS	Pro.	Acc.	MS	Exp.	Acc.
Environment (E)	5	163.0**	60.3	-	2975.0**	89.9	-	2511.76**	85.6	-	12947.0**	39.6	-	12959.0**	49.6	-
Rep within E	12	15.26**	9.7	-	33.32**	2.2	-	53.44**	3.7	-	3488.0**	14.8	-	1615.0**	9.5	-
Genotype	24	10.28*	18.3	-	31.17**	4.5	-	38.74**	6.3	-	2249.0**	33.0	-	1491.0**	27.4	-

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SOV	**DF**	**GY**			**DA**			**DS**			**PH**			**EH**		
		MS	**Pro.**	**Acc.**	**MS**	**Pro.**	**Acc.**	**MS**	**Pro.**	**Acc.**	**MS**	**Pro.**	**Acc.**	**MS**	**Exp.**	**Acc.**
(G)		*														
G x E	120	2.41**	21.4	-	7.68**	5.6	-	9.90**	8.1	-	372.0**	27.3	-	251.0**	23.1	-
PC1	28	4.33**	41.9	41.9	17.74**	53.9	53.9	21.21**	50.0	50.0	575**	36.0	36.0	365.6**	34.0	34.0
PC2	26	3.62**	32.5	74.4	6.33	17.9	71.7	9.76*	21.3	71.3	534**	31.1	67.1	356.3**	30.7	64.7
PC3	24	1.639	13.6	88.0	5.30	13.8	85.5	6.87	13.9	85.2	297	15.9	83.0	215.3**	17.1	81.8
PC4	22	1.084	8.2	96.3	3.87	9.2	94.7	5.40	10.0	95.2	216	10.6	93.7	179.9	13.1	95.0
PC5	20	0.538	3.7	100.0	2.42	5.3	100.0	2.86	4.8	100.0	142	6.3	100.0	75.8	5.0	100.0
Residuals	288	1.25			4.89			6.18			266			184.0		
Total	569	3.83			33.87			32.14			574			410.1		

Note Value with * and ** indicates significant difference at 0.05 and 0.01 probability level, respectively. SOV = Source of variation, DF= degree of freedom, MS = mean square, Pro: proportion variance (%); Acc: accumulated variance(%), GY =Grain yield, DA = Days to anthesis, DS = Days to silking, PH = plant height, EH = Ear height, CV = Coefficient of variation (%).

3.2.1. Additive Main Effects and Multiplicative Interaction1(AMMI 1)

The AMMI1 biplot shows genotype and environment means and the grand mean on the abscissa (x coordinate) and its PC1 scores for genotypes and environments on the ordinate (y-coordinate) [23] *Figure* . The biplots make up a range from high-yielding environments in the II quadrant (upper right) and III quadrant (low right) to low-yielding environments in sections I quadrant (upper left) and IV (low left). Genotypes or environments with large IPCA1 scores, either positive or negative had a large interaction effect, whereas genotypes with IPCA1 score of zero or nearly zero had a smaller interaction effect and were considered stable over a wide range of environments ([14, 24] . Accordingly, genotypes, G8 and G1 followed by G25, G16, G15, G2, and G20 showed PC1 scores approximately close to zero indicating that these genotypes were less influenced by the environment (least GE interaction) (*Figure*). However, for genotypes to be stable or generally adaptable to all environments, the genotypes should attain above-average mean performance and the IPCA score would be nearly zero. Therefore, among the genotypes, G25, G16, G20, G2 and G21 gave grain yield above the mean (located on the right side of the graph) and close to zero in terms of the PC1 axis. So, these are high-yielders and less influenced by environmental interaction. However, the most unstable genotypes and the lowest grain yield among the genotypes belonged to G4 and G14.

The environment scores from AMMI analysis relating to interaction, environments with large IPCA scores are more discriminating of genotypes while environments with IPCA scores near zero show little interaction across genotypes and low discrimination among genotypes ([14]. In the current study, Asosa (AS) followed by Hawassa (HW) and Pawe (PW) had a IPC1 score or vector closer to zero compared to other environments, indicating a lower interaction effect (stable) which almost ensures the better performance of all genotypes in those environments. However HW was lowest yield environment. Jimma (JM) was the most discriminating site (unstable) and low yielder. Bako (BK) and Asossa (AS) were above-average yields. In line with this, [25] reported high-yielder genotype and environment with stable and/or unstable performance in their studies.

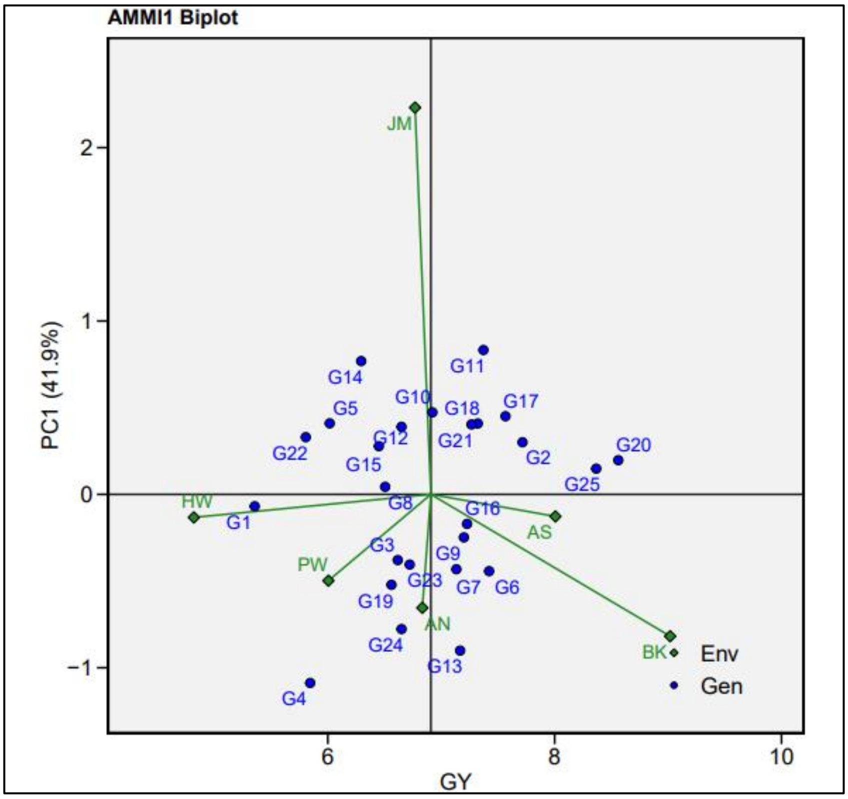

Figure 1. Biplot AMMI1 (Means vs PC1) for the productivity of maize (t/ha) with 25 genotypes (G) and six environments (E).

3.2.2. Additive Main Effects and Multiplicative Interaction1 (AMMI 2) for Grain Yield

The AMMI 2 biplot (*Figure* was generated using the genotype and environment scores of the first two AMMI components ([26]. The first and the second interaction principal components (IPCA) individually explained 41.9%, and 32.5% of the total GEI variation, respectively. The first two IPCAs cumulatively captured 74.4% of the GEI variation of tested maize genotypes. In maize, previous authors [25] reported the two IPCAs accounted for 60.9% (IPCA1 was 37.3% and IPCA2 was 23.6%) of the total interaction of variation and [7] reported that AMMI with the first two IPCAs explained 40% of the total GEI variation in maize.

According to Purchase [27], the genotypes and environments that are located far away from the center are more responsive or unstable, while genotypes that are closer to the center of the biplot have higher stability performance. In the AMMI2 biplot graph, close genotypes and environments have positive associations and the place of stable genotypes is near the origin of the biplot [28-30]. In the present study, AMMI2 showed some of genotypes like G8, G15, G16 and G2 plotted relatively close to the center designating their minimum involvement in the total G x E interaction and considered as stable genotypes (Figure 2). However, for genotypes to be considered as stable, it should attain a high mean performance greater than the grand mean. Therefore, G2 and G16 could be considered as the most stable genotypes with their high grain yield performance and being closer to the origin as compared to the others. Whereas, genotypes G4, G13 and G23 were farthest from the center of the biplot having substantial involvement in G x E interaction sum squares. Therefore, these genotypes were considered as unstable genotypes.

Similarly, Bako (BK) can be considered as a stable environment due to the closeness of its vector endpoints to the center of the biplot. In contrast, the farther away from the center of the biplot for the environments, the more interaction the environment has with genotypes. As was already identified, JM was the most interactive environment on AMMI1 biplot, AMMI2 biplot also confirmed JM as the most interactive environment as it was farthest from the center of the biplot *Figure*).

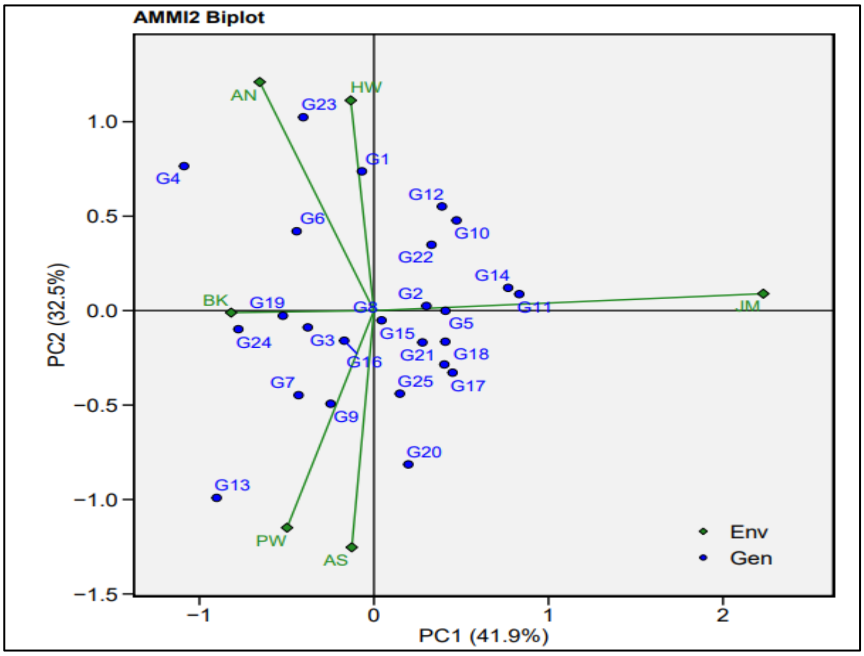

Figure 2. Biplot of IPCA1 versus IPCA2 for grain yield of 25 maize genotypes tested across six environments.

In *Figure* the association between the genotypes and the environments can be clearly seen. Genotypes with similar performance and those that are close to the environment indicate their better adaptation to that particular environment. For instance, G24 and G19 are strongly associated with BK, and G23 is particularly suitable at AN and HW. G13 is strongly associated with PW, and G11 and G14 JM. Genotypes and environments that fall into the same sector interact positively, and negatively if they fall into opposite sectors [31].

3.3. Genotype Evaluation Based on GGE biplot

3.3.1. Which-Won-Where Pattern for Grain Yield

Which-won-where view of the GGE bi-plot for grain yield across locations is indicated below in *Figure* . The GGE biplot analysis supports the classification of the studied genotypes and environments based on the performance of genotypes and the response of the growing environments [14, 16, 32].

In this study, a polygon with six sides is formed by connecting the markers of the genotypes that are further away from the biplot origin such that all other genotypes are encircled by the polygon. The genotypes placed at the polygon vertex in a section of the biplot where there is no environmental indicator are treated as poorly performed genotypes under all tested environments. However, genotypes attached with a vertex of the polygon in the sector where all environmental markers drop and the genotype gave greater yield such genotype considered as best performed genotype across the environments [33]. [34] Also stated that the equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex. In the current study, six environments fall into three sectors. G20 was the winner in environments Bako (BK), Pawe (PW), Assosa (AS) and Hawassa (HW). Whereas, G11 and G13 was the winner in Jimma (JM) and Arsi Negele (AN), respectively. The vertex genotype G1 was the poorest genotype in all of the test environments since it had the longest distance from the origin of the biplot on the opposite side of the environments (*Figure*).

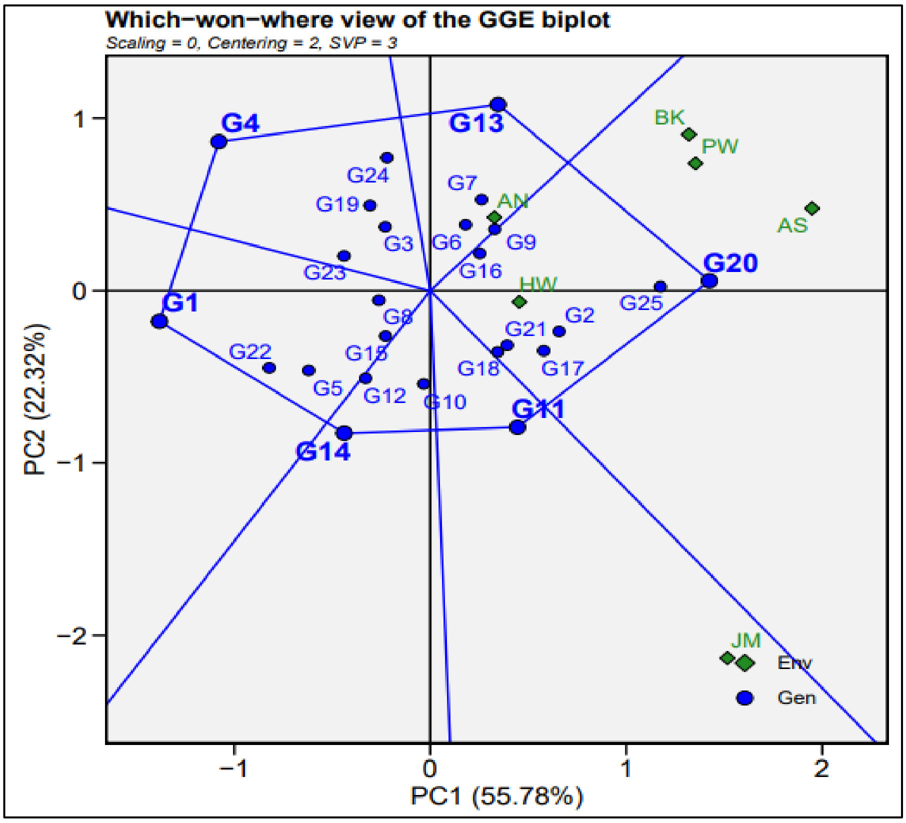

Figure 3. Which-won-where view of the GGE biplot for grain yield of maize genotypes across six environments.

3.3.2. Average Yield and Stability Performance

Average environment coordination (AEC) views for GGE bi-plot based on environment-focused scaling for the means performance and stability of 25 maize genotypes shown below in *Figure* . The mean yield performance and stability of genotypes were evaluated by an average environment coordination (AEC) method[14, 15]. In the AEC system, the AEC X axis (PC1) passes through the origin of GGE biplot with an arrow indicating the positive end of the axis and indicates the mean performance of genotypes. The AEC ordinate (vertical) separates genotypes which had grain yield below-average means located at the left side from those with above-average means located at the right side. Thus, in this study, some genotypes with above-average means were G20>G25>G2>G17>G21>G13>G9>G16 whereas some genotypes with below-average means were G1<G4<G22<G5 < G14 *Figure* .

The vector projections for the genotypes, which are parallel to the AEC ordinate or perpendicular to the AEC abscissa (horizontal axis) in either direction, indicate the extent of genotypic stability across testing environments [14, 15, 35]. In other ways, genotype stability is explored by the length of their projection from AEC abscissa (horizontal axis). The genotypes that fall on the AEC abscissa (horizontal axis) and had almost zero projection onto the AEC ordinate (vertical axis) are considered to be the most stable while genotypes with the longest contact in either direction with the AEC abscissa are considered to be less stable across the environments or vice versa. The best genotype is the one with the highest yield and stability across environments. In other ways, the best genotypes have large PC1 scores (high mean yield) and small PC2 scores (high stability). A greater projection onto the AEC ordinate, regardless of the direction, means greater instability[17]. Among high yielding genotypes, G20, G25, G2, G17, G16 and G21 were considered as stable genotypes. G4, G14 and G24 from the low yielding genotypes and G13 and G11 from the high grain-yielding genotypes had longer projections from AEC abscissa indicating that these genotypes have inconsistent performance across environments.

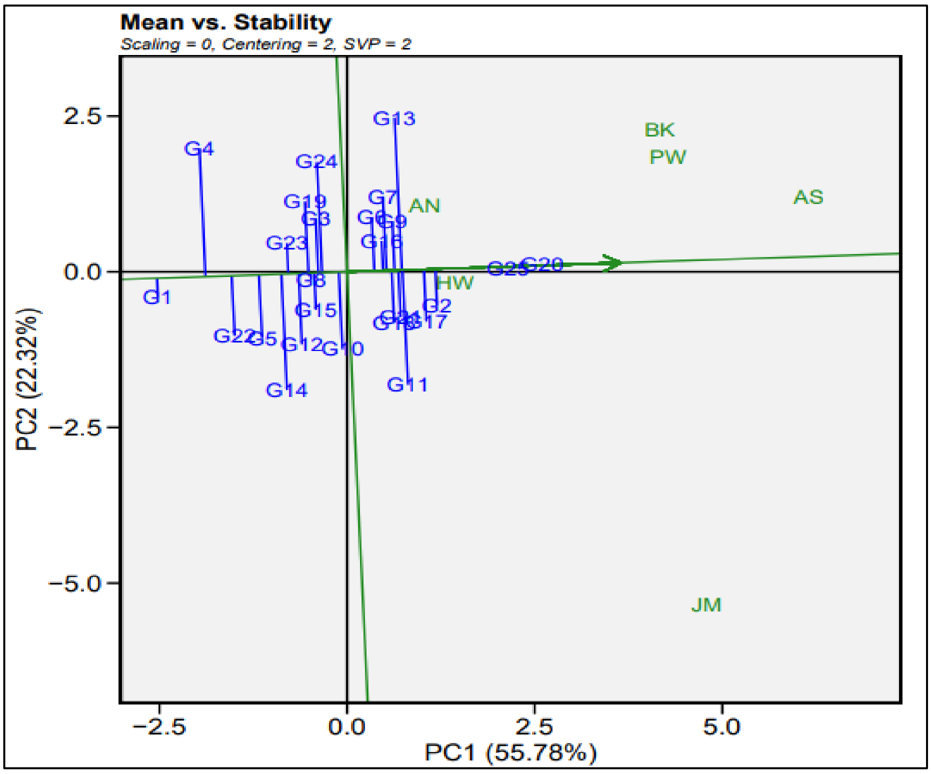

Figure 4. Average environment coordination (AEC) views for GGE bi-plot based on environment-focused scaling for the means performance and stability of genotypes.

3.3.3. Ranking Genotypes Relative to the Ideal Genotypes

GGE-biplot based on genotype-focused scaling for comparison of the genotypes with the ideal genotype depicted below in *Figure* . [36, 37] stated that the ideal genotype is one with the highest mean performance and absolutely stable. This is assumed to be in the center of the concentric circles the arrow pointing to it. The ideal genotype which is found at the center of the concentric circles can be used as a benchmark for selection. Genotypes located closer to the ideal genotype are more desirable than the others located farther away. Hence, in the current study genotypes G20 and G25 were identified as the best and ideal genotypes in terms of higher-yielding ability and stability. G2 and G17 were also the 3rd and 4th desirable genotypes, respectively (*Figure*). However, G4 is the farthest away from the concentric circle, which was the least desirable genotype in terms of both yield performance and stability. In agreement with the current result, different authors reported the best and least desirable genotypes in maize [38, 39]; in Coffee [22].; in Wheat [40]. [19]pointed out desirable genotypes that were in proximity to ideal quality protein maize genotypes under optimum, drought, and low N management in their studies.

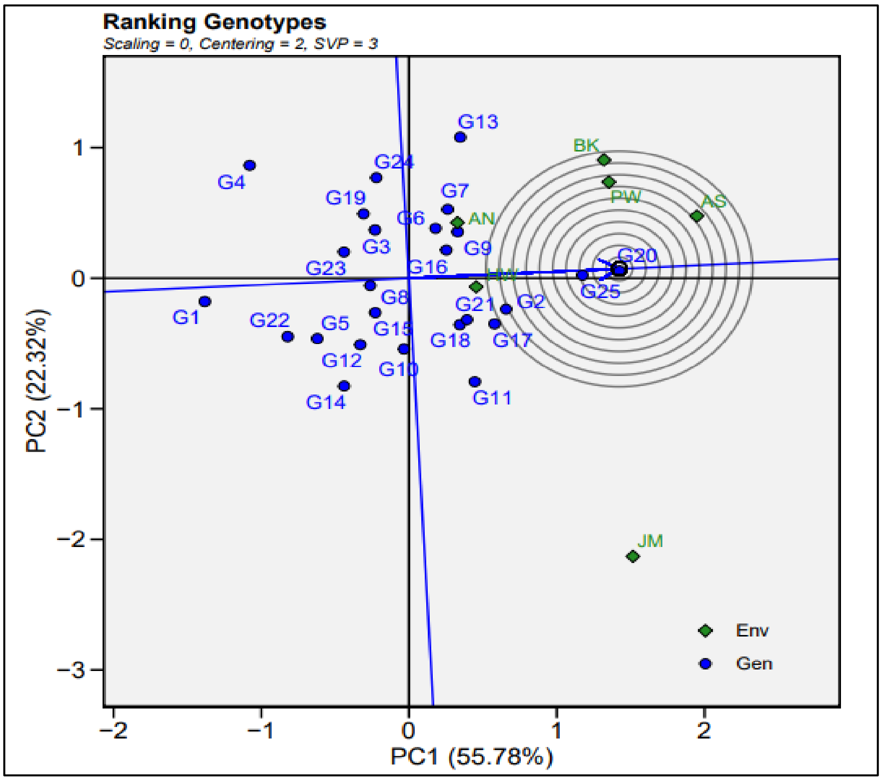

Figure 5. Ranking genotypes relative to ideal genotypes view of the GGE biplot based on grain yield data of 25 maize genotypes evaluated in six environments.

3.4. Environment Evaluation Based on GGE biplot

3.4.1. Discriminativeness vs. Representativeness Pattern of GGE biplot

GGE bi-plot view of ranking the test environments based on discriminating ability and representativeness shown in *Figure* . Environments with both longer vectors and larger PC2 scores have high discriminating power, whereas those with longer/shorter vector lengths coupled with smaller angle between the AEC abscissa and vectors indicate the representativeness of the environments [15, 16, 34] . In the current study, among testing environments, Jimma (JM) followed by Asossa (AS), Bako (BK) and Pawe (PW) had longer environmental vector which indicates these sites represents a high capacity to discriminate the genotypes and Hawassa (HW) followed by Arsi Negele (AN) had a shorter vector indicates least discriminating and provided little information about genotype differences in *Figure* .

Regarding to representativeness, a test environment that has a smaller angle with the AEA is more representative of other test environments [34]. In this study, among the test environments, AS followed by HW, PW and BK has smaller angle with AEA. Thus AS was the most representative site where as JM is least representative.

The test environment AS followed by BK and PW were the both representative and discriminating sites for selecting generally adapted genotypes. JM was the most discriminating but non-representative sites which is useful for selecting unstable genotypes since categorized as a single mega environment. [34] stated a discriminating but non-representative test environment are useful for selecting unstable genotypes if the target environment is a single mega-environment or useful for selecting specifically adapted genotypes *if* the target environments can be divided into mega-environments. In line with the current result, different authors in their study reported representative and discriminating environments in maize [19, 25].

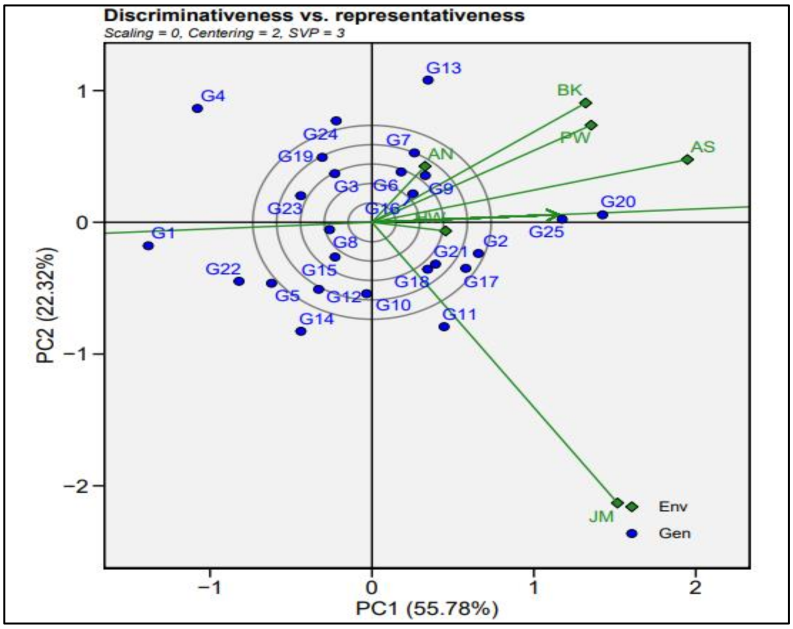

Figure 6. The discriminating ability and representativeness view of the GGE biplot based on grain yield data of 25 maize genotypes evaluated in six environments.

3.4.2. Ranking Testing Environments Relative to the Ideal Environment

Ranking environments relative to ideal environments view of the GGE bi-plot based on grain yield data of 25 maize genotypes indicated below in Figure .An ideal environment is representative and has the highest discriminating power [34]. The ideal environment is located in the first concentric circle in the environment-focused GGE bi-plot and the environments that are close to the ideal environment are defined as the desired environments for selecting superior genotypes. Consequently, the GGE bi-plot identified AS followed PW and BK as best environments which were close to ideal environments. The most acceptable is the one closest to the sketch of the ideal environment[14].

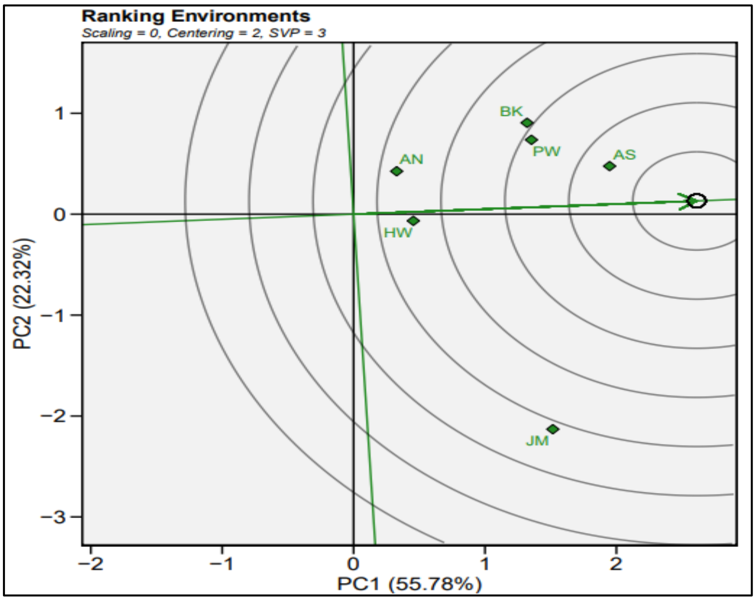

Figure 7. Ranking environments relative to ideal environments view of the GGE bi-plot based on grain yield data of 25 maize genotypes evaluated in six environments.

Summary and Conclusion

The grain yield performance of maize genotypes is usually inconsistent across environments due to variations in genotype and environment main effects and their interaction effects. Twenty-five maize genotypes on six test locations for grain yield were evaluated for stability analysis and selection using AMMI and GGE biplot. Genotypes, environments, and genotype × environment interaction in combined ANOVA were significant; the interaction items in AMMI ANOVA were significant, too which indicates hybrids performed differently with respect to yield in each of the six test environments and their relative performance varied from one environment to another. The AMMI biplot showed the largest variability among the environments (60.3%) followed by GEI (21.4%) and among the tested hybrids (18.3%) for grain yields. Both AMMI1 and GGE biplot discriminated the study area into three mega-environments which seemed to be linked to the yielding potential. Among genotypes, some genotypes that had mean grain yield above the grand mean in this study were G20, G25,G2, G17, G21, G13, G9 and G16.

Based on which-won-where view of GGE bi plot, the winning genotype at the first mega environments Bako (BK), Pawe (PW), Assosa (AS) and Hawassa (HW) was G20. Genotypes G11 and G13 was the winner in Jimma (JM) and Arsi Negele (AN), respectively. Among environments, AS, PW and BK discriminating and representative of the other environments. The most discriminating and representative environment was AS followed PW and BK which were close to ideal environments and identified as best environments. JM as single mega environment and most discriminating but non-representative test environment which will be useful for selecting unstable genotypes.

Among top yielder genotypes, G20, G25, G2, G17 and G16 had relatively consistent yield performances across environments. Among these high-yielder and stable genotypes, G20 was considered the ideal genotype while the remaining genotypes were desirable genotypes.

Generally, based on AMMI1 and GGE biplot analysis, among environments AS, PW and BK were the high yielder, discriminative and representative environments useful for selecting generally adapted genotypes. Genotypes G25 (BH520) and G17 (BH549) were released varieties whereas genotypes, G20 (3XM2110426), G2 (3XM2110423) and G16 (CZH15523) were have not been yet released. Therefore, these genotypes recommended for the next breeding stage or verification and release after confirming through further evaluation in similar agro ecologies of Ethiopia.

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Conflict of Interest

The authors declare that there is no conflict of interest.

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