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Grain yield stability and genotype by environment interaction of quality protein maize hybrids in Ethiopia

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Abstract

Maize (*Zea mays* L.) production in Ethiopia spans across various agro-ecologies, encompassing humid highland, humid midland, dry lowland, and humid lowland areas. Identifying well-adapted and productive genotypes for target production environments could be achieved by evaluating new experimental hybrids across various representative test environments. This study aimed to examine the mean grain yield performance, grain yield stability, and genotype-by-environment interaction of quality protein maize (QPM) hybrids evaluated across environments in Ethiopia. Forty-eight QPM experimental hybrids, along with two commercial check hybrids, were evaluated across six environments. Analysis of variance for grain yield exhibited highly significant ($p \leq 0.001$) differences due to genotype, environment, and genotype by environment interaction (GEI). Additive main effect and multiplicative interaction (AMMI) analysis revealed that genotype, environment, and GEI effects contributed to 4.57%, 78.59%, and 16.84% of the total variation, respectively. The first two interaction principal component axes (IPCAs) explained 66.29% of the total variations attributed to GEI sum of squares, indicating that these IPCAs captured most of the interaction effects. The AMMI stability value identified G5, G19, G22, and G42 as stable and high-yielding QPM hybrids, while G5 was the most stable genotype identified by yield stability index analysis. Genotype main effects plus GEI (GGE) biplot analysis identified G13, G14, and G25 as the most desirable hybrids. Among the test environments, Holeta was identified as an ideal test environment, exhibiting the highest discriminating power among the tested hybrids and the most representative of the test environments. The polygon view of GGE biplot subdivided the testing environments into different groups, mainly represented by Holeta, and Haramayaand Kulumsa. Among the various analytical models, the GGE biplot proved to be the most effective and precise tool for identifying high-yielding and

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Abbreviations: AEC, average environment coordinate; AMMI, additive main effects and multiplicative interaction; ASV, AMMI stability value; BLUP, best linear unbiased prediction; DAP, diammonium phosphate; GEI, genotype by environment interaction; GGE, genotype main effects plus GEI; IPCA, interaction principal component axis; METs, multi-environment trials; PCA, principal component analysis; QPM, quality protein maize; YSI, yield stability index.

stable hybrids. Results of this study indicated the possibility of developing stable and high-yielding QPM hybrids suited to representative maize production environments.

Plain Language Summary

The performance of maize varieties can vary depending on where they grow, which makes it difficult to choose the best ones for wider use. In this study, we tested elite quality protein maize (QPM) hybrids in six different locations to find high-yielding and stable hybrids. QPM is a special type of maize that contains more of the essential amino acids, lysine and tryptophan, which help improve the nutritional value of maize, especially for people who rely on it as a major food source. Using different analysis methods, we found several QPM hybrids that performed well across multiple environments, showing strong potential to boost both food production and nutrition. Among the testing sites, Holeta was identified as the most useful location for evaluating these hybrids.

1 | INTRODUCTION

Maize (*Zea mays* L.) is one of the most important crops in the world (González-Barrios et al., 2019) that is used for fuel, feed, and food industries like oil, flour, and snacks (Kachapur et al., 2023). Maize plays a crucial role in global agriculture as it makes up a significant amount of the cultivated land worldwide, especially in tropical regions of lower and lower-middle-income countries (Prasanna et al., 2020). The global maize production was estimated to be about 1.2 billion metric ton harvested from nearly 204 million ha of area, with average productivity of 5.7 t ha^{-1} (Food and Agriculture Organization Corporate Statistical DataBase [FAOSTAT], 2024). In Ethiopia, maize is grown on about 2.6 million ha of land with estimated annual production of 10.7 million metric ton and national average yield of 4.0 t ha^{-1} (Food and Agriculture Organization Corporate Statistical DataBase [FAOSTAT], 2024), showing lower yield as compared to the global average. Maize production in Ethiopia spans across various agro-ecologies, encompassing humid highland, humid midland, dry lowland, and humid lowland areas (Mogesse & Zeleke, 2022). As one of the most widely grown crops by smallholder farmers in Ethiopia, it serves as a primary staple food for the country (Seyoum et al., 2019). In the Sub-Saharan Africa region, including Ethiopia, maize production is constrained by drought, low soil fertility, insect pests, diseases, low input accessibility (particularly improved seed and fertilizers), high cost, and limited usage of agricultural inputs (Engida, Tarekegne, et al., 2024).

Ethiopia has significant challenges related to food insecurity and poverty, exacerbated by insufficient human nutrition due to low productivity and slow adoption of nutritious crops such as quality protein maize (QPM) (Dosho et al., 2022). Currently, almost all maize varieties cultivated in Ethiopia are non-QPM genotypes, which are deficient in essential amino acids such as lysine and tryptophan and expose the people consuming maize as a staple food to malnutrition (Nedi et al., 2016). Worldwide, more than 167 QPM varieties were released out of which eight were released in Ethiopia (Tefera, 2020). However, the adoption rate of these QPM varieties is low despite observed nutritional and health benefits for both humans and animals (Yadesa & Diro, 2023). This indicates the need for an effective breeding program for the development and deployment of high-yield and farmer-preferred QPM varieties. In view of this, there are crossing programs and multi-environment trials (METs) conducted across different agro-ecologies in Ethiopia to identify high-yielding and stable QPM genotypes.

METs play a crucial role in plant breeding programs, allowing breeders to evaluate superior genotypes and understand their adaptability across various conditions (Alam et al., 2022). Yield stability and genotype by environment interaction (GEI) across environments can be assessed using several statistical methods or stability indices, which provide specific ranking patterns of genotypes in each environment. Thus, it is advisable to compute all possible statistics to select superior genotypes based on their yield performance and stability (Pour-Aboughadareh et al., 2022).

Stability indices, additive main effect and multiplicative interaction (AMMI) model, and genotype main effects plus GEI (GGE) biplot methods are among the commonly used methods to get a better understanding of genotypic stability. Stability indices like AMMI stability value (ASV), yield stability index (YSI), and joint linear regression analysis are univariate and can be parametric or non-parametric. ASV is based on the first and second interaction principal component axis (IPCA) scores for each genotype in the AMMI model (Mahmodi et al., 2011). Lower YSI values indicate varieties that possess high yield and stability (Engida, Yadesa, et al., 2024). The AMMI model and its associated traits, including ASV and YSI, have been widely used in METs, particularly for identifying elite varieties based on yield and yield-governing parameters (Dang et al., 2024).

A joint linear regression analysis was introduced by Eberhart & Russell (1966) to ascertain the average performance of a genotype in various locations with respect to the mean performance of all genotypes in the same locations. GGE biplot, which was introduced by Gabriel (1971) and Yan (2001), is a multivariate tool used to explore GEI. GGE biplot serves as a valuable tool for comparing genotypes across diverse environments. It facilitates the identification of genotype(s) that excel in a specific environment (specific adaptation) and helps to determine which environment(s) is/are most favorable for a given genotype (Yan & Tinker, 2006). González-Barrios et al. (2019) and Matongera et al. (2023) indicated the significance of GEI in identifying significant crossovers or changes in genotype rankings in various environments, for identification of unique winners under circumstances.

Studies on grain yield performance and stability of QPM have been reported by Mebratu et al. (2019), Ruswandi et al. (2022), Bankole et al. (2023), Pereira et al. (2023), and Engida, Tarekegne et al. (2024) in Sub-Saharan Africa regions. Each of these studies identified promising QPM hybrids for the target environments using various GEI analyses and stability models. The objective of this study was to examine the nature and extent of GEI and grain yield stability, and to identify high-yielding QPM hybrids suitable for commercial production in Ethiopia.

2 | MATERIALS AND METHODS

2.1 | Germplasm

The germplasm used in the study consisted of 50 hybrids that included 48 elite three-way cross QPM experimental hybrids and one QPM and another non-QPM commercial checks. The experimental hybrids were jointly developed by Ambo Agricultural Research Center and the International Maize and Wheat Improvement Center (CIMMYT) highland maize breeding program based in Ethiopia. The hybrids were previously evaluated in preliminary yield trials and selected for their high performances with respect to mean grain yield and other agronomic characteristics. The commercial checks, AMH852Q (QPM) and Jibat or AMH851 (non-QPM), are medium-maturing (about 170 days to maturity in highland environments such as Ambo) three-way cross hybrids and widely adopted to the highland and transitional highland maize-growing agro-ecologies of Ethiopia (Figure 1).

Core Ideas

- The test environment explained the largest portion (78.59%) of the total variation for grain yield, followed by genotype by environment interaction (GEI) (16.84%) and genotypes (4.57%).
- Quality protein maize (QPM) hybrids with high-yielding potential were identified across environments.
- Based on yield stability index (YSI) analysis, G5, G12, G20, and G26 with low YSI values were identified as more stable, while genotype main effects plus GEI (GGE) biplot analysis revealed G13, G14, and G25 as the most stable hybrids.
- GGE biplot was the most effective model for identifying high-yielding and highly stable hybrids.
- Holeta was the most discriminative and representative test environment.

2.2 | Environments and experimental design

The 50 hybrids were evaluated across six environments in Ethiopia (Table 1) during 2022 main cropping season. Fertilizer rates in each environment were used based on site-specific recommendations (Abakemal et al., 2016). Each entry was planted in a single row plot measuring 5.25 m in length, with plants spaced 25 cm and rows spaced 75 cm apart. Two seeds were planted per hill and thinned to one plant per hill after three to four leaf stages, with a final plant density of 53,333 plants ha^{-1}. Fertilizers were applied at the recommended rates of 150 kg ha^{-1} diammonium phosphate (DAP) and 200 kg ha^{-1} urea. Band application of phosphorus fertilizer in the form of DAP was applied at planting time. Urea fertilizer was applied in two splits, the first half was applied as a side dressing 35–40 days after planting, and the second half was applied prior to the flowering stage. The hybrids were established using a 5 × 10 alpha-lattice experimental design with two replications at each environment. Although data were recorded for various agronomic traits, only grain yield was used in this analysis. At each environment, the total grain weight from harvested ears of each plot was used to calculate grain yield per hectare after adjusting to 12.5% moisture content (Mebratu et al., 2019).

2.3 | Data analysis

Analysis of variance (ANOVA) was performed using a linear mixed model, treating both genotype and GEI as random effects in the best linear unbiased prediction (BLUP) model.

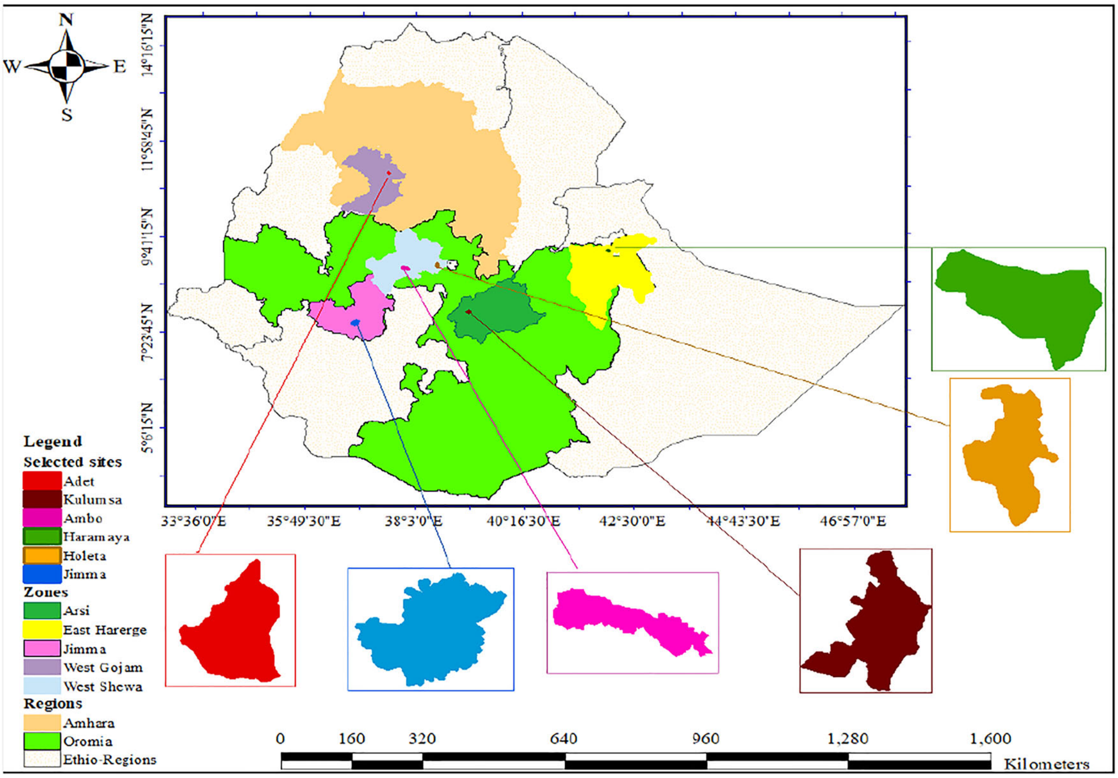

FIGURE 1 Map showing the geographic locations of the experimental sites used for the study sites across different highland maize production environments in Ethiopia.

TABLE 1 Description of the testing sites used to evaluate the quality protein maize hybrids.

No.	Environment	Altitude (masl)	Latitude	Longitude	Annual rainfall (mm)	Temperature	
						min (˚C)	max (˚C)
1	Ambo	2225	80˚57′ N	38˚ 7′ E	1115	11.7	25.4
2	Holeta	2400	9˚ 00′ N	38˚ 30′ E	1065	6.4	22.1
3	Kulumsa	2200	8˚ 5′ N	39˚ 10′ E	1078	10.0	23.0
4	Jimma	2300	7˚ 40′ N	36˚50′ E	1700	13.4	23.2
5	Adet	2240	11˚17′ N	37˚ 43′ E	1091	18.2	25.3
6	Haramaya	2020	9˚ 26′ N	2˚ 3′ E	728	8.99	25.15

Treating these effects as random allows for the estimation of variance components, which are essential for predicting genotypic values and assessing stability and adaptability across environments (Piepho, 1994). The mixed linear model utilized was as follows:

$$Y = X\beta + Zu + \varepsilon,$$

where Y is the vector of observations, u is the genotype + GEI effect, X and Z represent the matrix comprising β, u, and Y, and ε is the vector of random errors, β is the data vector of the fixed unknown effect, which is the average value of the block in each environment. Estimation was compared with the BLUP model (Piepho, 1994).

The joint linear regression, AMMI, and GGE biplot models were performed using the statistical program GEA-R (Flores et al., 2014; Pacheco et al., 2015).

2.4 | AMMI analysis

In addition to partitioning the total variation into genotype, environment, and GEI effects, AMMI analysis was used to further partition GEI effects into IPCAs. In this analysis, the significance of genotype mean squares was tested using GEI mean square as the error term, while GEI mean squares were tested using pooled error to assess the significance of the variances. AMMI model analysis was performed as follows

(Mahmodi et al., 2011):

$$Y_{ij} = \mu + g_i + e_j = \sum_{k=1}^{n} \lambda_k \alpha_{ik\ Y_{jk}} + e_{ij},$$

where Y_{ij} is the yield of ith genotype in the jth environment, g is the mean of ith genotype minus the grand mean, λ_k is the square root of the eigenvalue of the principal component analysis (PCA) axis k, α_{ik} and Y_{jk} are the principal component values for PCA axis k of the ith genotype and the jth environment, respectively, and e is the residual. The environments and genotype PCA value are expressed as unit vectors by the square roots of the λ_k, that is, environments of PCA value, ${\lambda_k}^{0.5}\ Y_{ik}$; 0.5 genotype PCA value = ${\lambda_k}^{0.5}\alpha_{ik}$.

2.5 | AMMI stability value

The relative contribution of the principal component axes (IPCA1 and IPCA2) scores to the interaction of sum squares was used to observe the ASV for each genotype. The higher ASV, either positive or negative, indicates the genotype was more adapted to certain environments, whereas a low ASV score represents a genotype that was more stable across various environments (Mahmodi et al., 2011). ASV and YSI were performed as suggested by Mahmodi et al., 2011, using the following equation.

$$\mathrm{ASV} = \sqrt{\left[\left(\frac{\mathrm{IPCA1SS}}{\mathrm{IPCA2SS}}\right)(\mathrm{IPCA1\ score})\right]^2 + (\mathrm{IPCA2\ score\ })^2},$$

where ASV is AMMI stability value, SS is sum of squares, IPCA1 and IPCA2 are the first and second interaction principal component axes, respectively.

2.6 | YSI analysis

YSI was calculated as YSI = RASV + RGY, where RASV is the ranking of ASV and RGY is the ranking of genotypes across all test environments (Mahmodi et al., 2011).

2.7 | GGE biplot analysis

GGE biplot analysis was performed to assess the variation due to genotypes and GEI for grain yield (Yan, 2001). The GGE biplot was constructed using the first and second principal components (PC1 and PC2) derived from subjecting environment-centered yield data. The GGE model used was as follows:

$$Y_{ij} - \left(\mu + \beta_j\right) = \lambda_1\ \xi_{i1}\eta_{j1} + \lambda_2\xi_{i2}\eta_{j2} + \varepsilon_{ij},$$

where Y_{ij} is the measured mean of genotype i in environment j, μ is the grand mean, βj is the main effect of environment j, $\mu + \beta j$ is the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values for PC1 and PC2, respectively. ξ_{i1} and ξ_{i2} are eigenvectors of genotype i for PC1 and PC2, respectively. η_{1j} and η_{2j} are eigenvectors of environment j for PC1 and PC2, respectively. ε_{ij} is the residual associated with genotype i in environment j.

The METs data for GGE biplot analysis were environment-centered (“centering = 2”) and used to perform the which-won-where pattern and relationship among test environments. An average environment coordinate (AEC) was used to identify an ideal test environment as well as high-yielding and stable hybrids (Yan & Tinker, 2006). The GGE biplot analysis was performed using the adjusted hybrid means for the 48 experimental hybrids and the two commercial checks across all test environments.

2.8 | Joint linear regression analysis

A joint linear regression of the genotype means on the environmental mean as an independent variable was carried out following the Eberhart and Russell (1966) model. According to this model, stable genotypes were identified as those with high mean grain yields, regression coefficients (b_i) of 1.0 and deviation from regression (S^2d_i) = 0 (Eberhart & Russell, 1966). A joint linear regression model used was as follows:

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij,}$$

where Y_{ij} is the observed performance of the ith hybrid in jth environment, μ_i is the mean performance of the ith hybrid across all environments, bi is the regression coefficient of the ith hybrid observed on the environmental index (stability characters), and I_j is the environment index (the deviation of the mean of environment j from overall mean). δ_{ij} is the deviation from the regression ith hybrid in the jth environment.

3 | RESULTS

3.1 | Analysis of variances

The ANOVA for grain yield across the test environments showed highly significant variations ($p < 0.001$) among the

TABLE 2 Combined analysis of variance and means for grain yield of quality protein maize hybrids tested across six environments.

Source of variation	Degree of freedom	Sum of squares	Mean of squares
Replication	1	0.57	2.65^{ns}
Environment (E)	5	3022.37	604.47***
Genotype (G)	49	175.78	3.58***
G × E	245	647.6	2.64***
Pooled error	300	66.68	0.22
CV%			6.65
Mean			6.99
Minimum			5.93
Maximum			8.26

Abbreviations: CV, coefficient of variation; ns, non-significant.
***indicate significance at 0.001 probability level.

TABLE 3 Additive main effect and multiplicative interaction (AMMI) analysis for grain yield of quality protein maize (QPM) hybrids tested across environments.

Sources of variation	Degree of freedom	Sum of squares	Mean squares	%G × E contribution	%G × E cumulative
Environment (E)	5	3025.02	605.01***		
Genotype (G)	49	175.88	3.58***		
G × E	245	648.10	2.64***		
IPCA1	53	284.2	5.36***	43.68	43.68
IPCA2	51	147.1	2.88***	22.61	66.29
IPCA3	49	94.1	1.92***	14.46	80.75
IPCA4	47	85.8	1.82***	13.19	93.95
IPCA5	45	39.3	0.87***	6.04	100
Pooled error	300	66.68	0.22		

*** indicate significance at 0.001 level.

test environments, genotypes, and GEI (Table 2). Grain yield ranged from 5.93 to 8.26 t ha^{-1} with an overall mean of 6.99 t ha^{-1}. The highest yielding hybrids were G50, G13, and G5, with respective grain yields of 8.26, 7.90, and 7.77 t ha^{-1}. On the other hand, G40 (5.93 t ha^{-1}), G44 (5.93 t ha^{-1}), and G48 (6.10 t ha^{-1}) had lower grain yield. Among the test environments, Kulumsa (10.1 t ha^{-1}) and Holeta (9.3 t ha^{-1}) showed the highest mean grain yields, whereas Jimma had the lowest mean grain yield of 3.6 t ha^{-1}.

3.2 | AMMI analysis

AMMI analysis revealed that the environment accounted for the largest proportion of the total variation (78.59%), followed by GEI (16.84%) and genotype (4.57%) (Table 3). Partitioning of the GEI effects into IPCA using the AMMI model showed that the total pattern of GEI variation was explained by five IPCAs. Accordingly, IPCA1, IPCA2, IPCA3, IPCA4, and IPCA5 accounted for 43.68%, 22.61%, 14.46%, 13.19%, and 6.04%, respectively, of the GEI across environments. The analysis further indicated that mean squares for all the five IPCAs were highly significant ($p < 0.001$).

The list of four top-yielding hybrids and the values of IPCA1 and IPCA2 for each location are presented in Table 4. Low IPCA scores in AMMI analysis indicate a low contribution to GEI and a high contribution to genotype stability. Environments Adet, Ambo, and Jimma had low IPCA values, and hence, contributed to high stability of the hybrid grain yield (Table 4). Among these environments, Ambo was the ideal testing location, as it showed the lowest IPCA and highest mean grain yield.

3.3 | ASV and YSI analysis

In ASV analysis, a genotype with low ASV value is the one that adapts across environments, while genotype with high ASV adapts in a specific environment. Among the tested hybrids, G1, G8, G11, G19, and G35 had lower ASVs, whereas G40, G43, and G44 had higher ASV values. The YSI that combines ranking of grain yield with rankings of

TABLE 4 Additive main effect and multiplicative interaction (AMMI) analysis based on mean grain yield, the first two interaction principal component axes (IPCAs) values, and four top-yielding hybrids in each test environment.

Environment	Mean	IPCA1	IPCA2	1	2	3	4
Adet	5.9	−0.32	−0.29	G14	G19	G23	G6
Ambo	7.1	−0.26	0.009	G17	G42	G31	G7
Haramaya	5.6	−0.66	0.66	G43	G17	G31	G44
Holeta	9.3	1.0	0.61	G31	G25	G9	G13
Jimma	3.6	−0.32	−0.33	G30	G39	G34	G50
Kulumsa	10.1	0.56	−0.66	G50	G13	G29	G46

ASV identified hybrids with low YSI and high stability. Hybrids G5, G12, G19, G20, and G26 showed low YSI values (Table 5).

3.4 | Joint linear regression analysis

According to the Eberhart & Russell (1966) model, genotype adaptability can be measured by regression value (*bi*), whereas performance stability is measured by deviation from regression (S^2d_i). In this study, *bi* value among the tested hybrids ranged from 0.18 to 1.47, while deviation from regression (S^2d_i) ranged from 0.02 to 2.61 (Table 6). Hybrids with relatively good level of stability and high grain yield were G5 (grain yield = 7.77 ha^{-1}, *bi* = 1.11 and $S^2d_{i\,=}$ 0.33), G8 (grain yield = 7.03 ha^{-1}, *bi* = 1.11 and $S^2d_{i\,=}$ 0.17), and G12 (grain yield = 7.52 ha^{-1}, *bi* = 1.10 and $S^2d_{i\,=}$ 0.51). Higher yielding hybrids such as G13, G31, and G50 had *bi* values that were highly different from unity or S^2d_i different from zero or both, and hence not desirable in terms of stability.

3.5 | GGE biplot analysis

3.5.1 | Which-won-where pattern

The "which-won-where" polygon view of the GGE biplot for the tested hybrids is shown in Figure 2. The PC1 and PC2 contributed to 64.60% of the G + GEI variation in grain yield, with individual contributions of 43.32% and 21.28%, respectively. A polygon view was constructed by vertex hybrids G15, G17, G31, G40, G44, G49, and G50, which were found far away from the biplot origin such that all other hybrids were contained within the polygon. The test environments and genotypes were separated into different groups by the lines originating from the origin that are perpendicular to the line joining the farthest genotypes. The vertex hybrids were the highest yielding in the environments located within their respective sectors of the GGE biplot.

3.5.2 | Mean grain yield and stability of genotypes

The mean grain yield and stability performance of the tested hybrids are presented in Figure 3. The genotypes farthest from origin on the positive side of the AEC abscissa had higher mean grain yield, and those farthest from origin on the negative side of the AEC abscissa had lower mean grain yield. Accordingly, hybrids G13, G14, G25, G31, and G50 (AMH852Q) had higher grain yield, whereas G40, G44, and G48 were the lowest yielding hybrids (Figure 3). Among the high-yielding hybrids, G13, G14, and G25 were the most stable hybrids, while G31 and G50 were unstable, as shown by longer projections onto the AEC ordinate.

3.6 | Discriminating power and representativeness of the test environments

The discriminating power and representativeness of the test environments are indicated in Figure 4. The discriminating power of an environment refers to its ability to determine an ideal test environment, whereas representativeness refers to the ability of a test environment to represent the mega-environment. In GGE biplot, the length of the vector estimates the standard deviation within each test environment and measures the ability of the environment to discriminate among the hybrids. In this study, Holeta, Kulumsa, and Haramaya environments, with longer environmental vectors, were highly discriminative, whereas Jimma, Ambo, and Adet, with shorter environmental vectors, were less discriminative and highly representative (Figure 4).

3.7 | Relationships of test environments, ranking of the environments and genotypes

Environmental vectors connected to the biplot origin provide information on the interrelationships among the test environments. An acute angle between two vectors indicates a positive correlation, an obtuse angle indicates a negative cor-

TABLE 5 Mean grain yield (GY), AMMI stability value (ASV), and yield stability index (YSI) of 50 maize hybrids evaluated across six environments.

Genotype	GY (t ha^{-1})	GY rank	IPCA1	IPCA2	ASV	ASV rank	YSI
1	6.52	37	0.0269	0.170	0.18	4	41
2	6.42	40	−0.045	0.217	0.23	7	47
3	6.94	32	−0.336	0.232	0.68	41	73
4	6.95	31	−0.272	−0.077	0.58	32	63
5	7.77	3	0.127	−0.040	0.25	10	13
6	7.27	19	0.266	−0.150	0.53	27	46
7	7.29	17	−0.183	0.104	0.37	18	35
8	7.03	27	0.092	0.090	0.19	5	32
9	7.20	21	0.320	0.256	0.67	40	61
10	6.43	39	−0.009	−0.429	0.43	22	61
11	6.41	41	0.001	−0.124	0.12	1	42
12	7.52	10	0.148	0.158	0.33	14	24
13	7.90	2	0.353	0.068	0.68	42	44
14	7.67	5	0.215	0.139	0.44	23	28
15	6.25	46	0.241	−0.249	0.53	28	74
16	6.57	36	−0.271	−0.186	0.55	29	65
17	7.48	11	−0.351	0.343	0.76	44	55
18	7.05	26	0.236	0.075	0.46	25	51
19	7.10	23	−0.070	−0.004	0.14	2	25
20	7.53	9	0.172	0.122	0.35	15	24
21	7.07	24	−0.111	0.088	0.23	8	32
22	7.57	7	0.273	−0.187	0.56	31	38
23	7.27	18	0.308	0.128	0.61	36	54
24	7.18	22	−0.120	0.213	0.31	12	34
25	7.58	6	0.432	0.399	0.59	33	39
26	7.54	8	−0.117	0.065	0.23	9	17
27	6.20	47	−0.306	−0.016	0.59	34	81
28	7.03	28	−0.158	−0.049	0.31	13	41
29	7.05	25	0.153	−0.463	0.55	30	55
30	7.36	13	−0.322	0.041	0.62	38	51
31	7.70	4	0.337	0.995	1.27	48	52
32	6.41	43	0.255	−0.146	0.51	26	69
33	6.41	42	0.177	−0.075	0.35	16	58
34	7.34	14	0.202	0.024	0.39	20	34
35	6.30	45	0.068	−0.077	0.15	3	48
36	7.46	12	0.025	0.433	0.44	24	36
37	6.49	38	0.197	−0.087	0.39	21	59
38	6.63	35	−0.314	−0.018	0.61	37	72
39	7.31	16	−0.239	−0.382	0.59	35	51
40	5.93	50	−0.816	−0.237	1.6	49	99
41	6.65	34	0.113	−0.285	0.36	17	51
42	7.31	15	0.039	−0.239	0.25	11	26
43	6.33	44	−0.579	0.246	1.14	47	91
44	5.93	49	−1.00	0.001	1.93	50	99

(Continues)

TABLE 5 (Continued)

Genotype	GY (t ha^{-1})	GY rank	IPCA1	IPCA2	ASV	ASV rank	YSI
45	6.99	29	−0.309	0.168	0.62	39	68
46	6.71	33	0.327	−0.356	0.72	43	76
47	6.95	30	0.103	0.077	0.21	6	36
48	6.10	48	−0.088	−0.345	0.38	19	67
49	7.22	20	0.417	−0.248	0.84	45	65
50	8.26	1	0.393	−0.381	0.85	46	47

Note: IPCA1 and IPCA2, interaction principal component axes 1 and 2, respectively.

TABLE 6 Mean grain yield (GY), regression coefficients (*bi*), and deviation from regression (S^2d_i) analysis based on the Eberhart & Russell (1966) model.

Genotype	GY (t ha^{-1})	Rank	*bi*	S^2d_i	Genotype	GY (t ha^{-1})	Rank	*bi*	S^2d_i
1	6.52	37	0.98	0.17	26	7.54	8	0.84	0.02
2	6.42	40	1.13	1.12	27	6.20	47	0.70	1.09
3	6.94	32	0.65	0.39	28	7.03	28	0.86	0.28
4	6.95	31	0.78	0.78	29	7.05	25	1.19	1.24
5	7.77	3	1.11	0.33	30	7.36	13	0.72	0.71
6	7.27	19	1.14	1.68	31	7.70	4	1.15	1.11
7	7.29	17	0.88	0.30	32	6.41	43	1.11	1.74
8	7.03	27	1.11	0.17	33	6.41	42	0.95	1.13
9	7.20	21	1.20	0.86	34	7.34	14	1.03	0.71
10	6.43	39	0.97	1.29	35	6.30	45	0.89	0.99
11	6.41	41	0.98	0.39	36	7.46	12	1.07	1.09
12	7.52	10	1.10	0.51	37	6.49	38	1.06	0.92
13	7.90	2	1.47	0.35	38	6.63	35	0.76	0.25
14	7.67	5	1.25	0.57	39	7.31	16	0.87	1.44
15	6.25	46	1.03	1.72	40	5.93	50	0.22	1.32
16	6.57	36	0.78	0.88	41	6.65	34	1.17	0.65
17	7.48	11	0.71	0.88	42	7.31	15	1.13	0.34
18	7.05	26	1.29	0.35	43	6.33	44	0.65	2.51
19	7.10	23	0.94	0.35	44	5.93	49	0.18	2.61
20	7.53	9	1.28	0.43	45	6.99	29	0.80	0.62
21	7.07	24	0.85	0.03	46	6.71	33	1.25	1.38
22	7.57	7	1.20	0.49	47	6.95	30	1.12	1.04
23	7.27	18	1.30	0.13	48	6.10	48	1.02	0.79
24	7.18	22	0.87	0.16	49	7.22	20	1.41	0.95
25	7.58	6	1.42	1.21	50	8.26	1	1.43	1.99

relation, and an angle close to 90° shows no correlation among the environments. Jimma had negative association with most of the test locations (Figure 5). Similarly, negative correlation was observed between Kulumsa and Haramaya. On the other hand, Holeta, Ambo, and Adet had positive associations as depicted by <90° angle between environmental vectors.

In Figure 6, the small circle at the center of the concentric circle represents the "ideal environment." It is a virtual environment with the longest vector and most discriminative power of all environments. The nearer an environment is to the ideal environment, the more desirable that environment is for selecting superior genotypes. In this study, Holeta was an ideal environment. Figure 7 shows the ranking of the test hybrids relative to the "ideal hybrid." An ideal hybrid is defined by the greatest vector length represented by the center of the concentric circle with an arrow pointing to it. Hybrids with closer proximity to the ideal hybrid had highest mean grain yield and stability. In this study, the most desirable hybrids

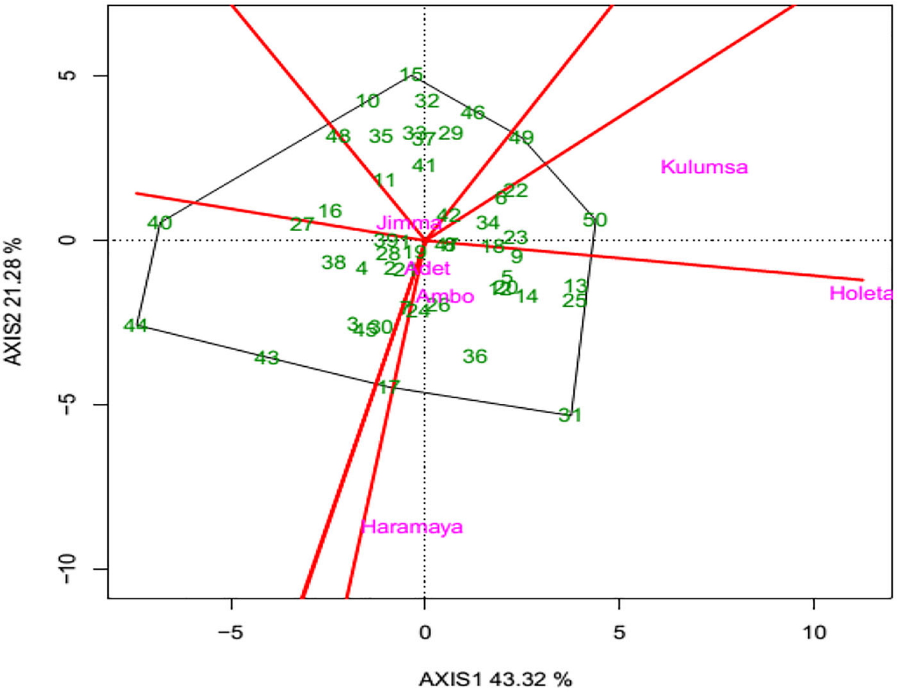

FIGURE 2 A "which-won-where" view of the genotypic main effects plus genotype × environment interaction (GGE) biplot for 48 quality protein maize hybrids and two commercial checks evaluated across environments.

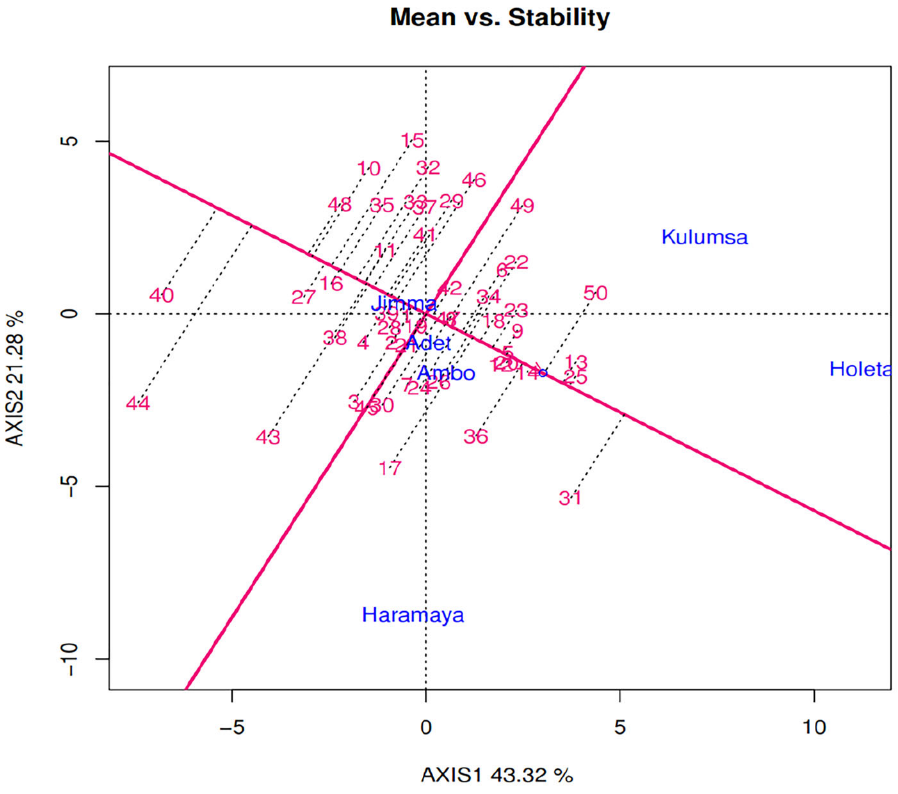

FIGURE 3 The mean and stability view of the genotypic main effects plus genotype × environment interaction (GGE) biplot for 48 quality protein maize hybrids and two commercial checks evaluated across environments.

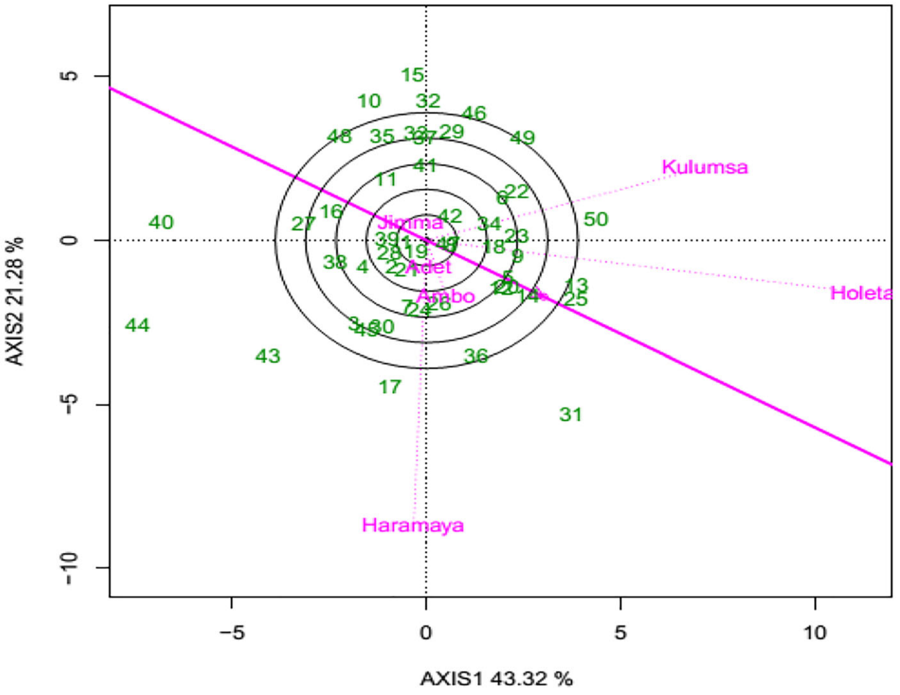

FIGURE 4 The genotypic main effects plus genotype × environment interaction (GGE) biplot showing the discriminativeness and representativeness of the test environments used to evaluate quality protein maize hybrids.

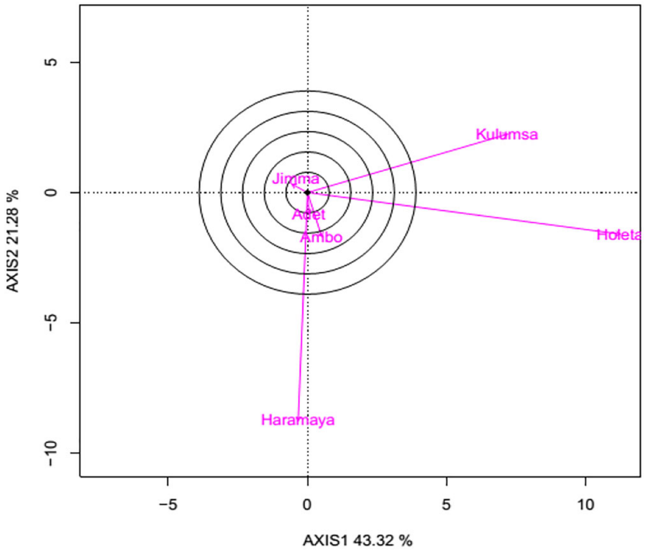

FIGURE 5 The genotypic main effects plus genotype × environment interaction (GGE) biplot showing the relationship among the test environments used to evaluate quality protein maize hybrids.

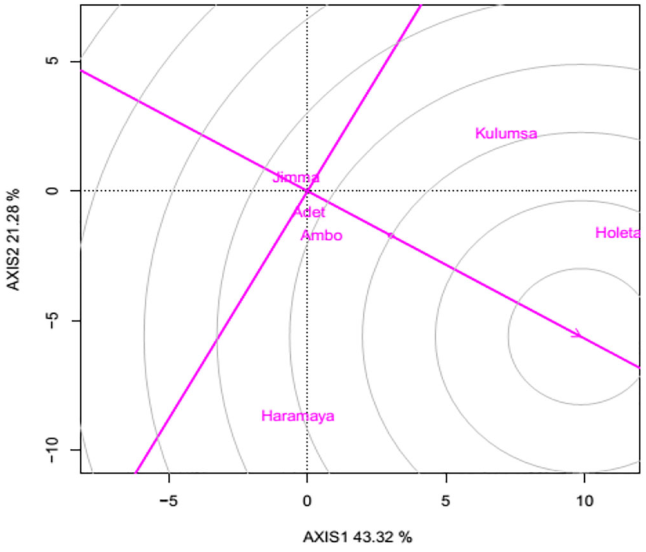

FIGURE 6 The genotypic main effects plus genotype × environment interaction (GGE) biplot showing ranking of environments relative to the "ideal environment."

with the highest mean grain yield and stability as well as with closer proximity to the ideal genotype were G13, G14, G25, and G31. G40 and G44 had undesirable performances across test environments as the hybrids were located far away from the center of the concentric circles (Figure 7).

4 | DISCUSSION

The significant variations observed among the test environments indicated that each environment has its own unique characteristics. Similarly, the variations observed

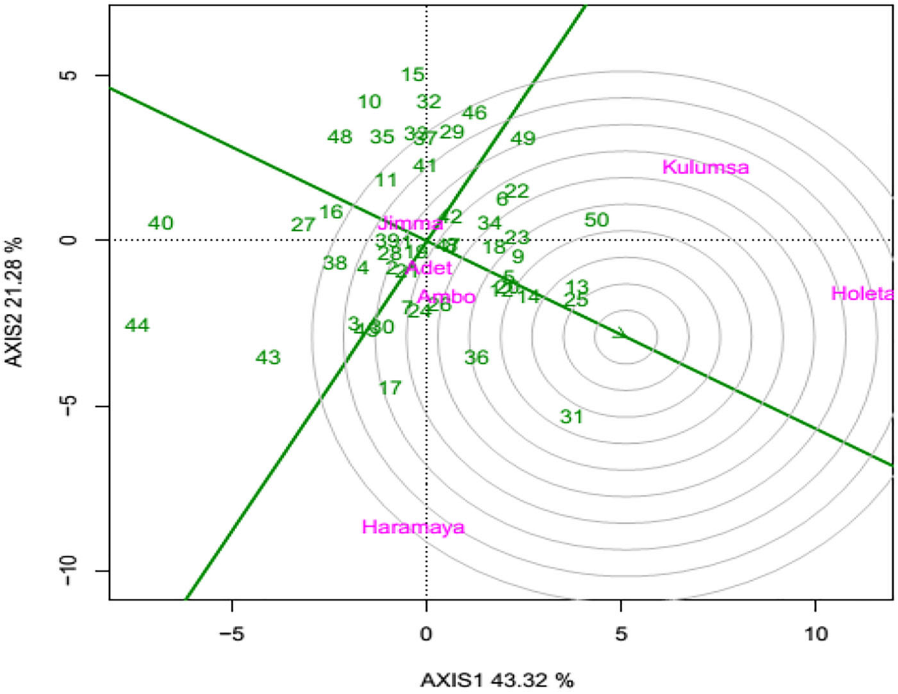

FIGURE 7 The genotypic main effects plus genotype × environment interaction (GGE) biplot showing ranking of quality protein maize hybrids relative to an ideal genotype.

among the experimental hybrids for grain yield indicated the possibility of selecting desirable hybrids. Similar to the current findings, previous studies reported significant variations among QPM experimental hybrids for grain yield (Abakemal et al., 2016; Mebratu et al., 2019). Significant GEI effects indicated that the hybrids exhibited differential performance and changes in ranking across environments, justifying the need for GEI and stability analysis to identify stable and high-performing hybrids. Engida, Tarekegne et al. (2024) and Mebratu et al. (2019) also reported the presence of significant GEI effects in QPM hybrids evaluated across diverse environments in eastern and southern Africa.

The existence of significant GEI effect indicates the need for extensive testing of genotypes across locations to avoid discarding hybrids that perform well in some but not in all locations (Uberti et al., 2023). Several findings suggested the use of complementary methods to assess the grain yield performance and stability of maize genotypes across METs to improve the reliability in the selection of superior maize genotypes adapted to and stable in target environments (Abakemal et al., 2016; Alam et al., 2022; Engida, Yadesa, et al., 2024; Uberti et al., 2023).

AMMI analysis demonstrated that the environmental effects explained a larger proportion of the total variation (78.59%) as compared to genotype (4.57%) and GEI effects (16.84%) (Table 3). This suggests that the overall variation in the grain yield performances of the QPM hybrids was largely influenced by environmental variables. Similarly, Mushayi et al. (2020) used the AMMI model and reported highly significant variations, with environment accounting for 63.33%, genotype for 5.83%, and GEI for 15.83% of the total variation. Contrary to the current findings, Bocianwski et al. (2024) reported that a larger proportion of the total variation in grain yield was explained by genotype (35.20%), followed by environment (25.12%) and GEI (21.18%) in AMMI model analysis.

High genotype stability is associated with low ASV, which captures the main effects of genotype and environment, as well as the significant GEI effects displayed on the genotype × environment biplot (Hailemariam, 2022). In this study, G1, G8, G11, G19, and G35 showed lower ASV values and were the most stable genotypes across the test environments suggesting grain yield performance of these hybrids was less influenced by GEI effects. However, hybrids with higher ASV values, G40, G43, and G44, were unstable in their performance across environments, indicating effects of GEI impacted grain yield performances of these hybrids.

According to YSI analysis, hybrids with low YSI values and high yield potential are considered stable and desirable, whereas those with high YSI value are considered unstable (Mahmodi et al., 2011). In this study, hybrids G5, G12, G19, G20, and G26 were identified as more stable hybrids based on their low YSI values (Table 5). While ASV focuses solely on genotype stability across the test environments, YSI provides the added advantage of identifying hybrids that are both high-yielding and stable, indicating its strength in identifying suitable hybrids in METs. These findings are in strong agreement with the reports of Dosho et al. (2022), Engida, Yadesa et al. (2024), and Mwendo et al. (2024).

According to Eberhart & Russell (1966), regression coefficients >1 indicates genotypes with higher sensitivity to environmental change (below-average stability), with specific adaptation to high-yielding environments. A Regression coefficient value ˂1 explains higher resistance to environmental change (above-average stability), with a tendency to specific adaptation at low-yielding environments. In this study, 27 out of 50 QPM hybrids showed a regression coefficient >1, indicating that these hybrids responded to favorable environments and produced higher grain yield in such environments, while the remaining 23 QPM hybrids had a regression coefficient ˂1, responding to broader environments and having more stability (Table 6). Based on this analysis, G5, G8, and G12 were identified as the most promising hybrids in terms of yield and stability. These results are in conformity with the report of Shojaei et al. (2022).

In the GGE biplot, the first two PCs explained 64.60% (PC1 = 43.32% and PC2 = 21.28%) of the total grain yield variation attributed to genotype and GEI (Figures 2–6). The "which-won-where" polygon view of GGE biplot (Figure 2) describes how genotypes and environments interact, exhibiting the existence of crossover GEI, mega-environment identification, and specific adaptation pattern (Yan & Tinker, 2006). In addition, GGE biplot was used to determine the best genotypes in each mega-environment and assess the stability of tested genotypes. The polygon vertices were represented by hybrids, G15, G17, G31, G40, G44, G49, and G50. These hybrids were extremely far from the biplot origin in various directions, indicating that these hybrids were more responsive than those within the polygon.

The GGE biplot subdivided the testing environments into different sectors. Environments grouped in different sectors had high-yielding hybrids specifically adapted to those sectors. This study identified two main sectors, one represented by Kulumsa, with G50 as the vertex hybrid, and the other represented by Holeta and Haramaya, with G31 as the vertex hybrid (Figure 2). The other test environments, Adet, Jimma, and Ambo, were located near the biplot origin, indicating the absence of a dominant hybrid in these environments. Furthermore, no environment fell within the sectors containing the other vertex hybrids, suggesting that these hybrids were not specifically adapted to any of the test environments. These results are in conformity with the findings of Bankole et al. (2023), Kunwar et al. (2024), and Omar et al. (2022). Similarly, several other investigators reported that genotypes located on the vertices of polygon show either the best or the poorest performance in one or more test environments (Amelework et al., 2023; Birhanu et al., 2024; Yan & Tinker, 2006; Bocianowski et al 2024).

The mean versus stability view of the GGE biplot (Figure 3) identifies ideal genotypes with high mean performance and stability, serving as a benchmark against which the tested hybrids were ranked (Yan et al., 2007). Similarly, genotypes with above-average means and those below-average means were separated by the AEC ordinate. In the current study, G13, G25, and G14, which had closer proximity to the ideal genotype, were identified as the most desirable hybrids. On the other hand, G40 and G44, located at a farther distance from the ideal genotype, were highly undesirable. However, high stability is only desirable when it is clearly correlated with the best mean yield performance (Singamsetti et al., 2021; Yan & Tinker, 2006). The findings of this study agree with the results previously reported by Dang et al. (2024) and Mullualem et al. (2024).

The ability of an environment to distinguish among genotypes is referred to as discriminating power, whereas its capacity to represent the overall mega-environment is known as representativeness (Yan et al., 2011). In this study, Holeta, Kulumsa, and Haramaya were highly discriminative (Figure 4), indicating the effectiveness of these environments to distinguish among genotypes in terms of grain yield performances. The discriminating and nonrepresentative environment can be used for culling unstable hybrids if the target location is a single mega-environment (Agyeman & Ewool, 2022). In contrast, Jimma, Ambo, and Adet were less discriminative but more representative of the overall testing environments. The representative test environments can be used to select the best yielding genotypes that will perform consistently across different environments (Engida, Yadesa, et al., 2024). The findings of this study agree with the results previously reported by Bankole et al. (2023) and Ma et al. (2024).

The significant association between test environments indicated similarity in genotype performance between these environments. Positive associations among Holeta, Ambo, and Adet (acute angle between the vectors) indicated that higher-yielding hybrids in one of these environments are likely to perform similarly in the others. In contrast, the angles between Haramaya and Kulumsa as well as between Jimma and Holeta were >90°, indicating negative associations. This implies that hybrids with high grain yield in one of these environments may exhibit reduced performance in the other environments (Figure 5). Obviously, the strong negative association between environments suggests high crossover interaction (Yan & Tinker, 2006). The presence of significant association between environments demonstrated that there is a possibility of reducing test environments without significantly influencing the validity of the data. These findings are in harmony with the findings of Daemo and Ashango (2024) and Li et al. (2023). Generally, similarity (covariance) between two locations is measured by both the length of their vectors and cosine of the angle between them (Fekadu et al., 2023; Yan et al., 2011).

Environments with long vectors and closer to the ideal environment are useful for evaluating cultivars (Akinyosoye, 2022; Yan et al., 2007). In this study, Holeta was identified as a highly discriminating environment for the hybrids tested (Figure 6), indicating the suitability of this environment for the identification of desirable hybrids. As illustrated in Figure 7, the most desirable hybrids identified in this study were G13 and G25 due to their closest proximity to ideal genotypes, which are the highest yielding and the most stable. In line with the current study, Mushayi et al. (2020) identified ideal hybrids using GGE analysis in METs.

Among the different models applied in this study, GGE biplot was the most effective for identifying high-yielding and stable hybrids, as it simultaneously integrates mean grain yield performance and GEI into a single framework. As noted by Yan et al. (2007), the mean versus stability view of GGE biplots enables breeders to identify superior genotypes that combine both high yield and stability, which traditional stability parameters cannot achieve. In line with this, the hybrids G13, G25, and G14, identified as superior by the GGE biplot, also recorded the highest mean yields across the six test locations, providing strong empirical support for the effectiveness of the GGE biplot model.

5 | CONCLUSION

The current study revealed a high level of genetic variation among the tested QPM hybrids for grain yield, indicating the potential for genetic improvement through effective selection. The most promising QPM hybrids identified in this study include G5, G13, G14, and G31. The commercial check G50 (AMH852Q) was also among the top-yielding hybrids. The significant GEI effect further justifies the need for genotype by environment and stability analysis to identify high-performing and stable hybrids across diverse environments. The various stability models used in this study showed inconsistencies in identifying stable hybrids. However, the GGE biplot approach proved to be the most effective in selecting outstanding hybrids based on both grain yield and stability. The hybrids identified as most desirable through different views of the GGE biplot had superior grain yield performance across the test environments. Among the test environments, Holeta was the most ideal environment for its discriminating power and representativeness. The present study identified promising QPM hybrids that could be extensively tested under farmers' production conditions for eventual commercialization to enhance food and nutritional security and improve the livelihood of maize producers and consumers in Ethiopia and across East Africa.

AUTHOR CONTRIBUTIONS

Diriba Beyene: Conceptualization; data curation; formal analysis; investigation; methodology; writing—original draft; writing—review and editing. **Dagne Wegary**: Conceptualization; data curation; formal analysis; investigation; methodology; resources; supervision; validation; visualization; writing—original draft; writing—review and editing. **Bulti Tesso**: Conceptualization; data curation; investigation; methodology; supervision; writing—original draft; writing—review and editing. **Zerihun Jalata**: Conceptualization; data curation; formal analysis; investigation; methodology; supervision; writing—original draft; writing—review and editing. **Negash Geleta**: Conceptualization; data curation; methodology; supervision; writing—original draft; writing—review and editing. **Kasahun Sadessa**: Conceptualization; data curation; formal analysis; investigation; methodology; software; writing—original draft; writing—review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data will be made available on request

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