



## Research article

# Genotype-by-environment interaction and stability analysis of grain yield of bread wheat (*Triticum aestivum* L.) genotypes using AMMI and GGE biplot analyses

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## ABSTRACT

Bread wheat is a vital staple crop worldwide; including in Ethiopia, but its production is prone to various environmental constraints and yield reduction associated with adaptation. To identify adaptable genotypes, a total of 12 bread wheat genotypes (G1 to G12) were evaluated for their genotype-environment interaction (GEI) and stability across three different environments for two years using Additive Main Effect and Multiplicative Interaction (AMMI) and genotype main effect plus genotype-by-environment interaction (GGE) biplots analysis. GEI is a common phenomenon in crop improvement and is of significant importance in genotype assessment and recommendation. According to combined analysis of variance, grain yield was considerably impacted by environments, genotypes, and GEI. AMMI and GGE biplots analysis also provided insights into the performance and stability of the genotypes across diverse environmental conditions. Among the 12 genotypes, G6 was selected by AMMI biplot analysis as adaptive and high-yielding genotype; G5 and G7 demonstrated high stability and minimal interaction with the environment, as evidenced by their IPCA1 values. G7 was identified as the most stable and high-yielding genotype. The GGE biplot's polygon view revealed that the highest grain yield was obtained from G6 in environment three (E3). E3 was selected as the ideal environment by the GGE biplot. The top three stable genotypes identified by AMMI stability value (ASV) were G5, G7, and G10, while the most stable genotype determined by Genotype Selection Index (GSI) was G7. Even though G6 was a high yielder, it was found to be unstable according to ASV and ranked third in stability according to GSI. Based on the study's findings, the GGE biplot genotype view for grain yield identified Tay genotype (G6) to be the most ideal genotype due to its high grain yield and stability in diverse environments. G7 showed similar characteristics and was also stable. These findings provide valuable insights to breeders and researchers for selecting high-yielding and stable, as well as high-yielding specifically adapted genotypes.

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## 1. Introduction

Bread wheat (*Triticum aestivum* L.) is a hexaploid plant with the chromosome number  $2n = 6x = 42$ , AABBDD, which belongs to the Triticeae tribe of the grasses (Poaceae) [1,2]. It is the most commonly cultivated crop worldwide and accounts for around 20 % of the calories and the protein in human diet [3,4]. It is also a significant source of minerals, vitamins, dietary fiber, proteins, and other phytochemicals for human nutrition [5–7]. Achieving high yield output through improved bread wheat genotypes remains vital since the amount of agricultural land will not rise beyond the existing levels. Even though wheat productivity has increased significantly, more work needs to be done to keep up with the growth of world population, which is expected to reach about 9.8 billion people by 2050 [8–10].

Bread wheat holds a significant position among wheat species globally in terms of distribution and production [4,11]. Majority of sub-Saharan Africa's wheat production comes from Ethiopia [12,13]. Bread wheat is a staple food in Ethiopia, and it is mainly used for making bread, porridge (Genfo), local beer (Tella), roasted grain (Kolo), boiled grain (Nifro), and injera [14]. Wheat straw is frequently utilized as roofing material and as feed for animals [15,16]. Due to its importance for food security, substitution of imported food, and the provision of raw materials for the agro-processing sector, bread wheat is considered as one of Ethiopia's strategic crops [17,18].

Although wheat grown in Ethiopia is not enough to feed the growing population of Ethiopia, there are indications that wheat production is undergoing a paradigm shift of increased productivity [19,20]. However, closing the gap between supply and demand to improve bread wheat production level and self-sufficiency is a primary national goal [21]. Plant breeders are always trying to improve grain yield, quality, and adaptability to both abiotic and biotic stresses [22–24].

Trials involving multiple environments are crucial for identifying the best genotypes in different agroecological locations to ensure food security worldwide and plant breeding initiatives aim to generate new competitive, stable, and high yielding genotypes in a range of environmental conditions [25–28]. Stable and broadly adapted genotypes are largely determined by the interaction between genotype and environment [29–32]. To find sustainable solutions to problems related to the development and growth of plants with desirable yield, plant breeders are becoming more and more interested in genotype-environment interaction (GEI) [33–35], which literally describes how different genotypes function in different growing environments through different locations and cultivation years [36]. GEI often presents challenges when it comes to breeding, testing, and selecting the best genotypes [37,38]. By screening

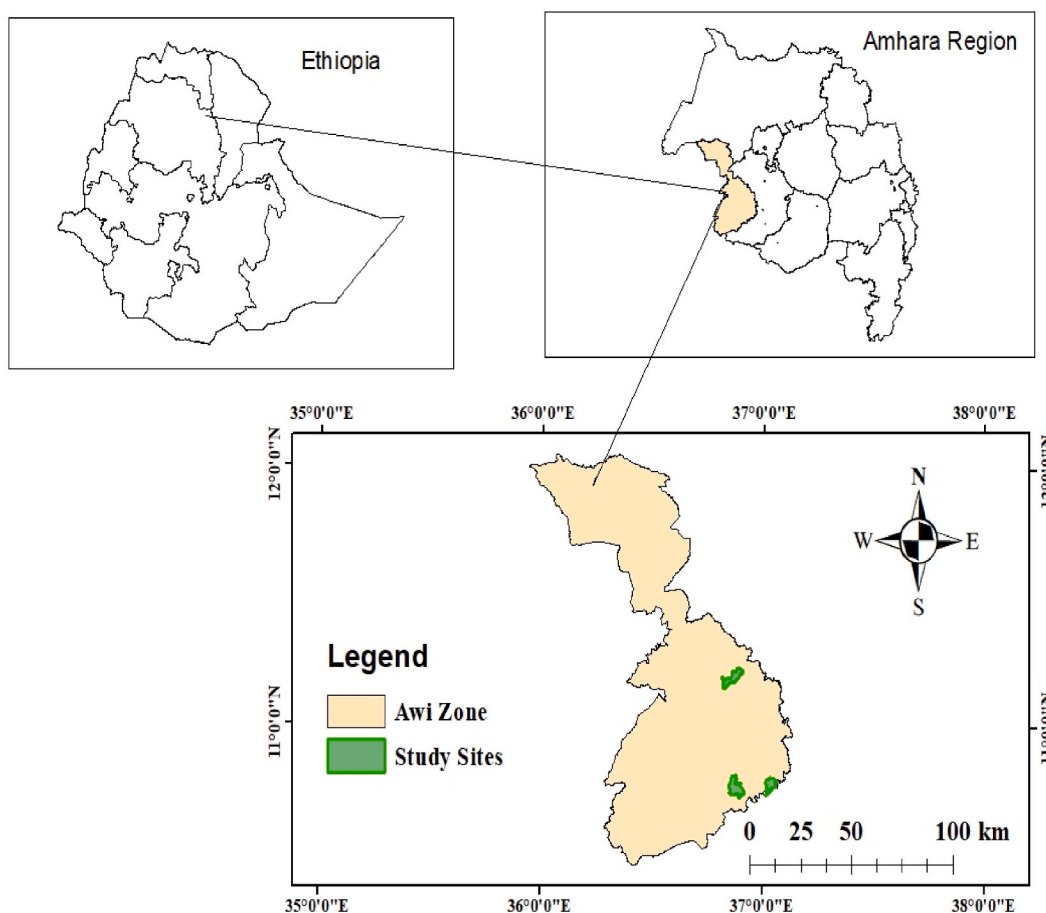


Fig. 1. Map of the study area.

and selecting genotypes that demonstrate high adaptability and stability under different environmental conditions, breeders can achieve rapid genetic progress before releasing them as cultivars [39,40].

Additive main effect and multiplicative interaction (AMMI) and genotype main effect plus genotype-by-environment interaction (GGE) biplot analyses are commonly employed techniques to address challenges in analyzing multi-environment trial data [41–43]. AMMI model emphasizes additive main effects and multiplicative interactions [44–46], and GGE biplots analysis considers genotype main effects and genotype-by-environment interaction effects [47–49]. These analytical methods are recognized as highly effective tools for interpreting and understanding the complex structures present in multi-environment data, specifically within breeding operations [50]. As a result, the use of AMMI and GGE biplot models allow visual assessment and differentiation of superior genotypes that exhibit wide adaptability across various environments, as well as those specifically suited for particular target sets of environmental zones [51].

Since farmers require stable cultivars that have great yield performance along with other critical agronomic features, identifying such high yielding and stable genotypes remains an ongoing problem for plant breeders all around the world. Lack of high yielding and stable genotypes in different environmental conditions remains to be a serious problem at the study area. Briefly, due to the scarcity of multi-agroecological, adaptive and stable bread wheat genotypes in Ethiopia as a whole, and at the study area, conducting this type of study is of paramount importance to benefit the agriculture sector. In the present study, the working hypothesis was that the performance of bread wheat genotypes vary with the environment, and the use of AMMI and GGE biplot analysis would provide insights into the genotype-by-environment interaction patterns. The study aimed to identify genotypes with high performance and stability across diverse environments, as well as genotypes with high performance in specific environments. To achieve these objectives, we conducted a two-year field trial experiment to evaluate the yield and stability of bread wheat genotypes in various environments.

## 2. Material and methods

### 2.1. Description of the study area

The study was conducted at three districts of Awi administrative zone (Dangila district, Ayehu guagussa district, and Guagussa shikudadad district) that have different environments (Fig. 1). Awi Zone is situated between 10°23'N and 10°85'N latitudes and 36°35'E and 36°57'E longitudes, with an altitude ranging from 1800 to 3100 m above sea level. The zone has a mean annual rainfall of 1,750 mm and a mean monthly temperature that ranges from 17 °C to 27 °C. The soil type in this region is nitosol, which is suitable for crop growing. Major staple crops grown in this district include potato, teff, maize, wheat, barley, millets, peas, and beans.

### 2.2. Experimental material and design

For this study, 12 varieties of bread wheat (Table 1), which were obtained from Kulmsa and Adet Agricultural Research Centers were evaluated under rain feed condition in 2021 and 2022. Eleven varieties collected from Kulmsa Agricultural Research Center, Oromia, Ethiopia, and one variety from Adet Agricultural Research Center, Amhara, Ethiopia, were sown on well-prepared plots. These 12 varieties are the 12 genotypes used at each of the three environments (locations). Each experimental unit (plot) consisted of 6 2-m rows with a spacing of 30 cm between rows, resulting in a plot area of 3.6 m<sup>2</sup> (1.8 m × 2 m). The field was ploughed three times before sowing, and rows for planting were created using a hand-pulled row marker. Seeds were manually planted using the hand drilling technique with a spacing of 10 cm between plants in each row. The spacing between plots was 0.50 m, and there was 1 m space between the three blocks. Since the two years (2021 and 2022) are also considered as blocks, the six combinations of the field blocks and the years are used as the blocks in the multilocation trial model. For each plot, a standard application of 100 kg/ha di-ammonium

**Table 1**

List of plant materials used in the study.

S. No.	Genotype Name	Code	Origin	Pedigree	Released by	Year of release
1	Shorima	G1	ICARDA	UTQUE96/3/PYN/BAU//MILAN 2011	KARC	2011
2	Biqa	G2	ICARDA	PASTOR//HXL7573/2*BAU/3/WBLL1	KARC	2014
3	Lemu	G3	CIMMYT	WAXWING*2/HELLO	KARC	2012
4	Kingbird	G4	–	TAM200/TUI/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1	KARC	
5	Ogolcho	G5	CIMMYT	WORRAKATTA/2*PASTOR	KARC	2012
6	Tay	G6	CIMMYT	ET-12 D4/HAR 604 or ET-12D4/4777 (2)//FKN/GB/3/PAVON F76 "S"	AARC	2005
7	Honqolo	G7	CIMMYT	NJORO SD-7	KARC	2016
8	Danda'a	G8	CIMMYT	KIRITATI//2*PBW65/2*SERI.1B	KARC	2010
9	Wane	G9	CIMMYT	SOKOLL/EXCALIBUR	KARC	2016
10	Balcha	G10	–	CROC_1/AE.SUARROSA (213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPTA	KARC	2019
11	Hulluka	G11	ICARDA	UTQUE96/3/PYN/BAU//MILAN 2012	KARC	2010
12	Pavon-76	G12	CIMMYT	VICAM-71//CIANO-67/SIETE-CERROS-66/3/KALYANSONA/BLUEBIRD	KARC	1982

KARC - Kulumsa Agricultural Research Center; CIMMYT - International Maize and Wheat Improvement Center; ICARDA - International Center for Agricultural Research in the Dry Areas; AARC - Adet Agricultural Research Center.

phosphate (DAP) and 150 kg/ha urea was done following recommendations for bread wheat. Half of the urea and the full amount of DAP were added during planting, while the remaining half of urea was applied during the mid-tillering stage. The seed rate used was 150 kg/ha. Weeding was carried out manually in all experimental fields across the three locations to manage weeds. No herbicides or fungicides were used to control weeds or diseases.

### 2.3. Data collection

For each response variable, average of ten randomly selected plants from each experimental unit (plot) were used. The ten representative plants per plot were randomly selected from the central rows excluding the two border rows. The response variables measured were Tillers per plant (TPP), plant height (PH), kernels per spike (KPS), spikelet per spike (SkPS), spike length (SL), days to heading (DTH), days to maturity (DTM), grain filling period (GFP), grain yield (GY), 1000-kernel weight (TKW), above ground biomass (AGB), and harvest index (HI).

### 2.4. Statistical analysis

#### 2.4.1. Analysis of variance (ANOVA)

The ANOVA that shows the significance of the main effects of Environment and Genotype and their interaction effect on TPP, PH, KPS, SkPS, SL, DTH, DTM, GFP, GY, TKW, AGB, and HI was determined using a multilocation trials model [52]. The model consists of Block nested in Environment (random) effect, the two main effects of Environment (random) and Genotype (fixed), and the interaction effect of Environment and Genotype, which is a mixed effects model. The normal distribution and constant variance assumptions on the error terms were verified as described in Montgomery [53]. The analysis was conducted using Proc Mixed of SAS 9.4. AMMI analysis and GGE plot analysis was performed using GenStat version 18 [54] and PTools 1.4. PTools Software that is open-source and that was developed by the International Rice Research Institute IRRI biometrics team [55] was used for AMMI analysis of variance of the mixed effects model (genotype as fixed, and environment as random) [56].

#### 2.4.2. AMMI analysis

AMMI analysis is a statistical method used to assess genotype and environment effects in multi-environment trials [57]. It combines ANOVA and principal component analysis (PCA) to assess the multiplicative effects of the genotype by environment interaction [58]. AMMI model helps in understanding and visualizing the complex genotype by environment interaction, allowing for the identification of stable genotypes across different environments and the assessment of crop yield stability [59]. AMMI analysis was performed according to Ref. [60] using the following model.

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \varepsilon_{ij}$$

where  $Y_{ij}$  is the response variable obtained from the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment;  $\mu$  is the grand mean;  $G_i$  and  $E_j$  are the genotype and environment deviations from the grand mean, respectively;  $\lambda_k$  is the eigenvalue of the PCA analysis axis  $k$ ;  $\alpha_{ik}$  and  $\gamma_{jk}$  are the genotype and environment principal component scores for axis  $k$ ;  $n$  is the number of principal components retained in the model, and  $\varepsilon_{ij}$  is the error term.

#### 2.4.3. AMMI stability value (ASV) analysis

According to Ref. [61], AMMI stability value (ASV) is not a quantitative stability metric, but it quantifies and ranks genotypes based on their yield stability. Genotypes with lower ASV values are considered more stable, while those with higher ASV values are deemed less stable [62]. ASV is used to compare the stability of genotypes, with lower values indicating greater stability in different environments. It is calculated based on the AMMI model, which combines ANOVA to adjust the main effects and principal component analysis (PCA) to assess the multiplicative effects of the genotype by environment interaction. ASV helps in understanding and visualizing the complex genotype by environment interaction, allowing for the identification of stable genotypes across different environments and the assessment of crop yield stability. ASV can be estimated using the following formula [61].

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

ASV is the distance from zero in a two-dimensional scatterplot of IPCA1 (Interaction Principal Component Analysis axis 1) scores against IPCA2 scores. Since the IPCA1 score contributes more to  $G \times E$  sum of squares; it needs to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to total  $G \times E$  sum of squares. The Pythagorean Theorem is then used to calculate the distance from zero.

#### 2.4.4. Genotype selection index (GSI) analysis

GSI was calculated by the following formula [63]:

$$GSI = RASV + RY$$

where RASV is Rank of AMMI stability value, and RY is the rank of mean grain yield of genotypes. There are two types of stability indices used in plant breeding programs. The first index is GSI, where a low value of GSI indicates desirable genotypes with high genotype mean and stability. The second index is ASV, where a smaller ASV score indicates a more stable genotype across environments [25]. The IPCA score is another parameter used to determine the adaptability of a genotype to certain environments. A larger IPCA score (either negative or positive) indicates more specific adaptability of a genotype to certain environments [30]; whereas a smaller IPCA score (close to zero) indicates low specificity and a more stable genotype across environments [64].

### 3. Results

#### 3.1. Analysis for variance

The analysis of variance (ANOVA) results shown in Table 2 reveal that the environment by genotype interaction effect is either highly significant ( $p$ -value  $< 0.01$ ) or significant ( $0.01 < p$ -value  $< 0.05$ ) or marginally significant ( $0.05 < p$ -value  $< 0.1$ ) on all 12 traits, indicating environmental variations among the tested varieties for yield and yield-related traits. The presence of significant genotype by environment interaction reveals that varieties for high grain yield and other desirable traits should be identified for a specific environment.

#### 3.2. Additive main effect and multiplication interaction (AMMI) analysis

The AMMI model was used to assess genotype, location (environment), and genotype by location interaction [65]. This model is a powerful analytical tool for genotype  $\times$  environment studies that allows for the identification of adaptation targets, adaptive traits, and test sites. The AMMI model considers both the main effects and interaction effect of the factors, making it useful for identifying genotypes with desirable traits across different environments [65,66] (Table 3). The ANOVA for grain yield using the AMMI method showed that Bread wheat grain yield is significantly ( $p < 0.01$ ) affected by the main effects of environment (E) and genotype (G), and Genotype  $\times$  Environment (G  $\times$  E) interaction (Table 3). The first principal component is significant, while the second one is not (Table 3).

#### 3.3. AMMI biplot analysis

AMMI biplot with genotype and environment main effects for bread wheat yield on the X-axis and PC1 scores on the Y-axis for 12 bread wheat genotypes tested at three locations showing 95.9 % fitness in the model is shown in Fig. 2. The X-coordinate represents the main effects, which are the genotypes and environment mean, while the Y-coordinate represents the interaction effect, which is the IPCA1. The differences between genotypes in terms of direction and magnitude along the X-axis (yield) and Y-axis (IPCA 1 score) are significant in the AMMI 1 biplot. The displacement along the X-axis indicates differences in main (additive) effects, while the displacement along the Y-axis indicates differences in interaction effect. Environments characterized by low yielding performance (E1 and E2) were grouped in the quadrants of low yielding genotypes (G2, G9 and G11) in contrast to favorable environment (E3) being grouped in quadrants of high yielding genotypes (G1, G3, G4, G6, G7, G8, G10 and G12).

#### 3.4. GGE biplot analysis

##### 3.4.1. Which-won-where

The GGE biplot analysis, which is used to summarize genotype and genotype by environment interaction, was employed to identify the best-performing genotypes in each environment and assess their stability [67]. One of the most notable features of the GGE biplot is its polygon view, which illustrates the “which-won-where” pattern of multi-environment data, showing crossover genotype by environment interaction, mega-environment differentiation, and specific genotype adaptation. The polygon is formed by connecting the genotypes located farthest from the origin, known as vertex genotypes, with all other genotypes enclosed within the polygon. Vertex genotypes, being the most responsive, are the genotypes located at the edge of the polygon [68,69].

In this study, partitioning genotype and genotype by environment interaction through GGE bi-plot analysis showed that IPCA1 and IPCA2 explained 98.2 % (PC1 contributing 82.4 % and PCA2 contributing 15.8 %) of the total variation for grain yield (Fig. 3). IPCA1

**Table 2**

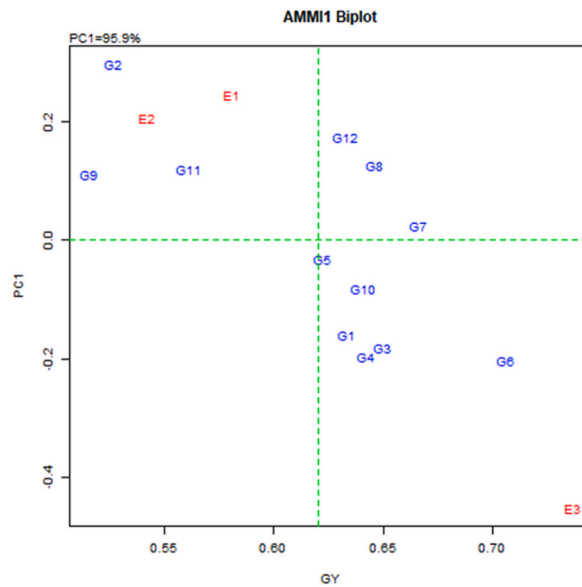
ANOVA p-values that show the significance of the main effects Environment (E), Genotype (G), and Block nested in E (Block(E)), and the interaction effect of E and G on Tillers Per Plant (TPP), Plant Height (PH), Kernels Per Spike (KPS), Spikelet Per Spike (SkPS), Spike Length (SL), Days To Heading (DTH), Days To Maturity (DTM), Grain Filling Period (GFP), Grain Yield (GY), 1000-Kernel Weight (TKW), Above Ground Biomass (AGB), and Harvest Index (HI).

Source of variation	TPP	PH	KPS	SkPS	SL	DTH	DTM	GFP	GY	TKW	AGB	HI
E	0.214	0.004	0.001	0.152	0.007	0.024	0.008	0.004	0.185	0.158	0.191	0.477
G	0.182	0.001	0.010	0.002	0.001	0.001	0.001	0.070	0.019	0.007	0.071	0.296
Block(E)	0.001	0.007	0.001	0.001	0.003	0.001	0.001	0.001	0.001	0.001	0.001	0.004
E $\times$ G	0.001	0.013	0.001	0.001	0.059	0.002	0.065	0.001	0.001	0.022	0.001	0.001

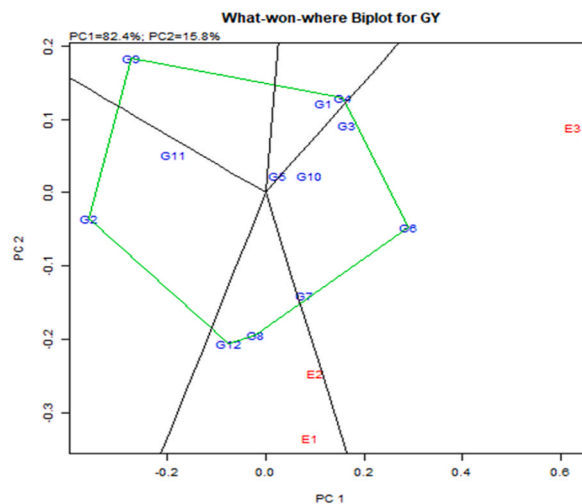
**Table 3**  
 AMMI analysis of variance for grain yield of 12 bread wheat varieties tested at three environments.

Source of variation	DF	SS	MS
Genotype (G)	11	0.4	0.036 <sup>a</sup>
Environment (E)	2	0.09	0.045 <sup>a</sup>
Interaction (G × E)	22	0.3	0.014 <sup>a</sup>
IPCA1	12	0.19	0.016 <sup>a</sup>
IPCA2	10	0.008	0.001

<sup>a</sup> Significant at the 1 % level of significance. DF = Degree of freedom, SS = Sum of squares, MS = Mean squares, IPCA1 and IPCA2 = Interaction principal component axis one and two, respectively.



**Fig. 2.** AMMI-1 model biplot for grain yield of 12 Bread wheat genotypes evaluated at three locations. E1 - Ayehu Guagussa district; E2 - Dangila district; E3 - Guagussa Shikudada district; and 12 genotypes G1 – Shorima; G2 – Biqa; G3 – Lemu; G4 – Kingbird; G5 – Ogolcho; G6 – Tay; G7 – Honqolo; G8 – Danada; G9 – Wane; G10 – Balcha; G11 – Hulluka; G12 - Pavon-76.



**Fig. 3.** Polygon view of GGE biplot (which-won-where) for 12 bread wheat genotypes evaluated at three locations: E1 - Ayehu Guagussa district; E2 - Dangila district; and E3 - Guagussa Shikudada district; and 12 genotypes: G1 – Shorima; G2 – Biqa; G3 – Lemu; G4 – Kingbird; G5 – Ogolcho; G6 – Tay; G7 – Honqolo; G8 – Danada; G9 – Wane; G10 – Balcha; G11 – Hulluka; and G12 - Pavon-76.

and IPCA2, the primary and the secondary principal components, derived from subjecting environment-centered yield data to singular value decomposition summarize the genotype and genotype-environment interaction. This method is commonly used in agricultural research, particularly in the analysis of multi-environment trial data. The primary and the secondary principal components play a crucial role in understanding the genotypic response across different environments [70,71].

In the polygon biplot analysis, the genotypes located on the vertices of the polygon were G2, G4, G6, G8, G9, and G12 (Fig. 3). According to Refs. [72,73] certain genotypes are highly responsive to environmental changes and are considered specifically adapted genotypes. These genotypes are either the best or the worst performers in some or all environments. The identification of such genotypes is crucial for improving crop productivity and breeding programs. Specifically, adapted genotypes can be targeted to respond well under the environmental conditions prevailing in a given area, provided that these conditions are within the range of the target population environment. Environments within the same sector share the same winning genotype. G6 was the highest yielding genotype at E3. The vertex genotype G2 and G9 were the poorest genotypes in almost all test environments.

The most responsive genotypes, also known as corner genotypes, can be visually identified from the GGE biplot. These genotypes are the ones that are located farthest from the midpoint and exhibit the highest degree of response to environmental changes.

These corner genotypes were G2, G4, G6, G9, and G12. As can be seen in Fig. 3, locations were divided into two sectors. The first sector represents Guagussa Shinkurta (E3), with genotypes G3, G6, G7, and G10. So, the vertex genotypes, G6 and G7 that connects the two vertex genotypes; G6 and G12 were the most favorable. The second sector represents Dangila (E1) and Ayehu guagusa (E2), with genotype G8 and G12 being the most favorable. The three other corner genotypes, G2, G4 and G9 were the poorest-yielding varieties (Fig. 3).

### 3.4.2. Comparison of environments

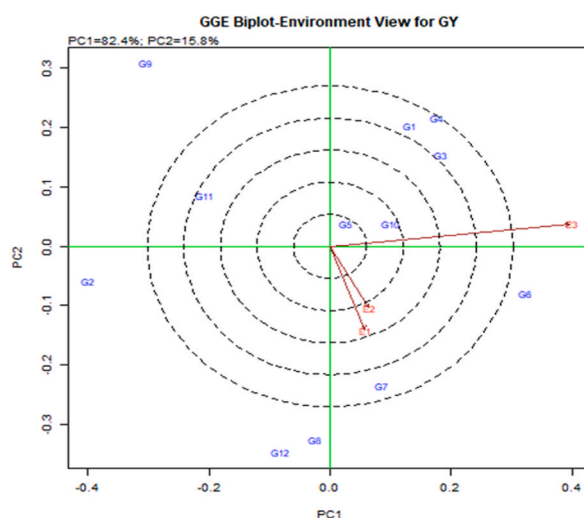
An environment that has a small angle with the average environment axis (AEA) is considered more representative compared to other test environments [73]. Representativeness refers to the ability of an environment to allow genotypes to perform similar to how they would in any other environment [74]. In the GGE biplot's environmental vector view, the lines connecting the test environment to the biplot origin are referred to as environment vectors. The cosine of the angle between two environment vectors provides an approximation of the correlation between those environments [75]. The GGE biplot's vector view (Fig. 4) provides a brief overview of the correlation between the environments in this study. The findings indicate that E1 and E2 environments had a positive correlation with each other, and both of these environments were also positively correlated with E3.

### 3.4.3. Discriminating ability and representativeness of test environments

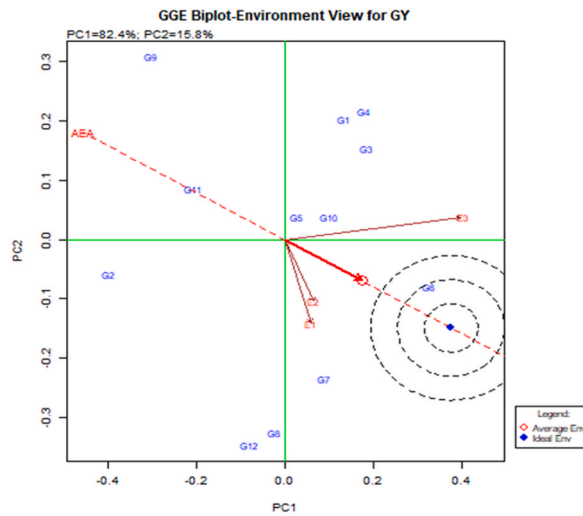
The analysis of the GGE bi-plot for grain yield showed that each environment is linked to the bi-plot origin with a vector to evaluate how well the test environments could distinguish between genotypes (Fig. 5). Environments with longer vectors are recognized to have a stronger ability to differentiate between genotypes compared to those with shorter vectors [75,76]. In this study, environment E3 has the longest environmental vector. In contrast, E1 and E2 exhibited the smallest environmental vectors compared to E3.

### 3.4.4. Varieties relative to an ideal variety

The method of average environment coordination (AEC) is used to graphically display the mean grain yield and stability performance of varieties [47]. This approach provides a visual representation of the performance and stability of genotypes across different



**Fig. 4.** Average genotype axis (AGA) in view of GGE bi-plot environment view graph for grain yield. The three locations are: E1 - Ayehu Guagussa district; E2 - Dangila district; and E3 - Guagussa Shikudada district; and the 12 genotypes are: G1 - Shorima; G2 - Biqa; G3 - Lemu; G4 - Kingbird; G5 - Ogolcho; G6 - Tay; G7 - Honqolo; G8 - Danada; G9 - Wane; G10 - Balcha; G11 - Hulluka; and G12 - Pavon-76.

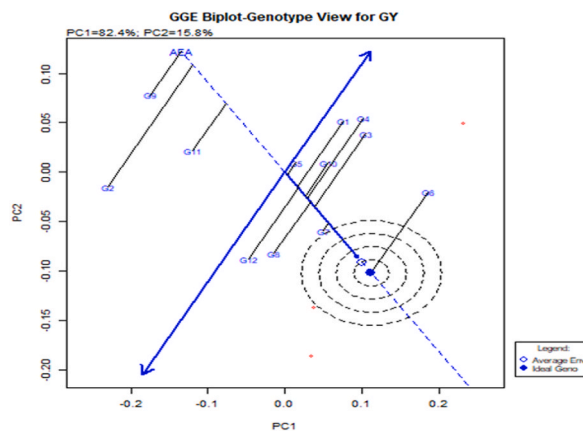


**Fig. 5.** Average environment axis (AEA) in view of GGE bi-plot graph for grain yield. The three locations are: E1 - Ayehu Guagussa district; E2 - Dangila district; and E3 - Guagussa Shikudada district; and the 12 genotypes are: G1 – Shorima; G2 – Biqa; G3 – Lemu; G4 – Kingbird; G5 – Ogolcho; G6 – Tay; G7 – Honqolo; G8 – Danada; G9 – Wane; G10 – Balcha; G11 – Hulluka; and G12 - Pavon-76.

environments. The AEC method is particularly useful for assessing the stability of genotypes in terms of their performance across multiple environments, making it a valuable tool in plant breeding and variety selection [45]. In the present study, there is a single arrowhead line that originates from the biplot’s origin and passes through the marker representing the average environment (Fig. 6). This line points towards higher mean values and is known as the AEC abscissa. Perpendicular to the AEC abscissa, there is another line passing through the biplot’s origin, referred to as the AEC ordinate. Varieties located furthest from the origin on the positive side of the AEC abscissa are associated with higher mean grain yield, while those located furthest from the origin on the negative side of the AEC abscissa are associated with lower mean grain yield. This is supported by the study of [47]. The arrow’s direction indicates the order of varieties in ascending rank based on their performance for higher trait values, as indicated on the AEA abscissa. The order of the genotype is as follows: G6 > G7 > G3 > G8 > G4 > G10 > G12 > G1 > G5 > G11 > G2 > G9 (Fig. 6).

### 3.5. Stability performance - AMMI stability value (ASV)

The AMMI stability value and mean yield are combined in the Genotype Selection Index (GSI), providing a single criterion that incorporates both mean yield and stability [77]. A low GSI value indicates desirable genotypes with high mean yield and stability. This index is useful for identifying genotypes that perform well across different environments and have consistently high yields [78,79]. The AMMI stability values (ASV) of the 12 bread wheat genotypes (G1 to G12) are shown in Table 4. Based on the mean grain yield, the ranking of the 12 genotypes is G6 > G7 > G8 > G12 > G3 > G10 > G4 > G5 > G1 > G11 > G2 > G9. Based on ASV G5, G7, G10 and G9 are the four most stable genotypes and based on GSI G7, G8, G10, G6, G12 and G3 were the most stable compared to the others. The



**Fig. 6.** Ranking varieties based on both mean and stability relative to an ideal variety for grain yield. The 12 varieties are: G1 – Shorima; G2 – Biqa; G3 – Lemu; G4 – Kingbird; G5 – Ogolcho; G6 – Tay; G7 – Honqolo; G8 – Danada; G9 – Wane; G10 – Balcha; G11 – Hulluka; and G12 - Pavon-76.



maximum grain yield of bread wheat in this study (0.67 kg/plot) was obtained from genotype G6 and the minimum (0.5 kg/plot) from G9 (Table 4).

## 4. Discussion

### 4.1. Analysis of variance for grain yield and related traits of 12 bread wheat genotypes

The presence of genetic variation is crucial in crop breeding programs aimed at producing new varieties with improved yield potential and consistency of yield under diverse climatic conditions [80–82]. According to the ANOVA results, the interaction between environment and genotype was significant on all traits. This finding shows that both genetic and environmental factors play an important role for determining the performance of crops in different environmental conditions, and variety selection should be done specific to a given environment. Understanding this interaction can help breeders to develop more adaptable and high-yielding varieties. Similarly, previous studies showed differences among genotypes in terms of the number of days to maturity, number of days to heading, plant height, spike length, number of seeds per spike, thousand seed weight, and grain yield per plots [22,23]. Other studies on bread wheat [14,83] also showed highly significant differences among genotypes, which aligns with the findings of our study.

Although ANOVA can effectively determine the significance of the main and interaction effects of genotype and environment, it does not provide insights into the specific reasons what these effects are significant [84,85]. Understanding the specific genotypes and environments that contribute to  $G \times E$  interactions is important for crop breeding programs aimed at improving yield potential and consistency under diverse climatic conditions [86].

The GGE, which stands for genotypic main effect (G) and Genotype by Environment interaction ( $G \times E$ ), plays a crucial role in cultivar evaluation in multi-locational trials [37]. This means that understanding the interaction between genotype and environment is essential for crop breeding programs aimed at improving yield potential and consistency under diverse climatic conditions. The highly significant ( $G \times E$ ) interaction effect on yield (Table 3) suggests that genotypes may be selected for adaptation to specific environments, which is in agreement with the findings of [87,88]. By analyzing  $G \times E$  interaction, breeders can identify stable genotypes across environments and develop more adaptable and high-yielding varieties.

The ANOVA results of stability, as proposed by Ref. [89], and the AMMI model (Table 4) demonstrated that the variance due to genotypes and environments was significant for grain yield per plot. This implies that, the performances of genotypes and the environments were different, indicating that genotypes had differential responses to changes in environmental conditions, which is in accordance with what was reported by Refs. [56,90]. The significant interaction between genotype and environment suggests that the grain yield of genotypes varied across different environmental conditions as reported previously [91,92]. By understanding the impact of genotypes and environments on grain yield, breeders can develop strategies to enhance the stability and performance of crops in various conditions, ultimately leading to the identification of stable genotypes across environments and the development of more adaptable and high-yielding varieties, which in turn helps for having sustainable agriculture and food security.

### 4.2. AMMI biplot analysis

The Additive main effects and multiplicative interaction (AMMI) model integrates a univariate approach to assess the additive effects of genotypes and environments with a multivariate method to evaluate the multiplicative effect of genotype by environment interaction ( $G \times E$ ) [93]. The AMMI model is extensively employed to evaluate genotype by environment data and is especially useful in assessing the  $G \times E$  interaction on grain yield. The model's combination of additive and multiplicative components provides a comprehensive approach for evaluating genotype performance across diverse environmental conditions, facilitating the selection of stable and high-performing varieties in multi-environment trials [94,95].

Based on the result of the AMMI biplot analysis (Fig. 2), the genotypes and environments, indicated by their corresponding codes on the right side of the Y-axis, demonstrated higher yields in comparison to those positioned on the left side of the Y-axis. This implies that

**Table 4**  
Stability parameters from AMMI model with mean grain yield ranks of 12 bread wheat varieties evaluated at three environments.

Genotype	GYM	Rank(A)	IPCA1	IPCA2	ASV	RASV(B)	GSI(A + B)	RGSI
G1	0.59	9	-0.16	-0.07	0.78	7	16	6
G10	0.62	6	-0.08	-0.01	0.39	3	9	2
G11	0.55	10	0.12	-0.07	0.59	5	15	5
G12	0.63	4	0.17	0.08	0.83	8	12	3
G2	0.53	11	0.3	0.07	1.47	12	23	12
G3	0.62	5	-0.18	0.01	0.88	9	14	4
G4	0.61	7	-0.2	0.01	0.97	10	17	7
G5	0.59	8	-0.03	0.02	0.14	1	9	2
G6	0.67	1	-0.2	0.13	0.98	11	12	3
G7	0.65	2	0.02	-0.14	0.17	2	4	1
G8	0.64	3	0.13	0.03	0.63	6	9	2
G9	0.5	12	0.11	-0.06	0.55	4	16	6

GYM - Grain mean yield; RASV - Rank of AMMI stability value; RGSI - Rank of genotype selection index; The 12 genotypes are: G1 – Shorima; G2 – Biqua; G3 – Lemu; G4 – Kingbird; G5 – Ogocho; G6 – Tay; G7 – Honqolo; G8 – Danada; G9 – Wane; G10 – Balcha; G11 – Hulluka; and G12 - Pavon-76.

certain genotypes showed superior performance under specific environmental conditions, underscoring the importance of genotype by environment interaction in shaping grain yield. This is also supported by the findings of [96,97].

When interpreting a biplot assay, if the main effects have an IPCA (Interaction Principal Component Analysis) score close to zero, it indicates minimal interaction effect or stability. However, a higher IPCA score (in absolute magnitude) suggests instability and adaptation to specific environments [98]. Among the genotypes, G6 and G8 exhibited higher yields and had higher IPCA1 scores, with G6 being the best-performing genotype overall. This indicates that G6 was specially adapted and the highest-yielding genotype in the corresponding environments. In contrast, genotypes G5 and G7 showed IPCA1 values close to zero, suggesting greater stability and relatively less interaction with the environment. The findings of this study are supported by the findings of [44,99,100]. This finding is valuable for identifying genotypes that demonstrate stability and high performance across different environments, which is essential for crop breeding programs aimed at improving yield potential and consistency under diverse climatic conditions [35]. Genotypes closer to the mean axis and on the positive axis are considered more stable. Based on this criterion, G7 is identified as the most stable and high-yielding genotype. This information is of utmost importance for crop breeding programs focused on enhancing yield potential and consistency in various climatic conditions. It helps for identifying genotypes that exhibit both stability and high performance across diverse environments, thus assisting in the improvement of crop yields. These findings are supported by other related studies [101,102] who reported the usefulness of genotypes having higher stability for breeding programs. A stable genotype refers to one that maintains consistent performance regardless of variations in the surrounding environment [103].

The AMMI biplot uses grain yield of wheat as the main effect on the abscissa and PC1 on the ordinate [104]. In the present study, genotypes or environments situated on the same vertical line indicate similar yields, while those on the same horizontal line demonstrate similar interaction patterns. Additionally, genotypes with vectors having a PC1 score close to zero indicate general adaptability, while those with larger PC1 scores are more specifically adapted to a particular environment. In general, genotype G7 demonstrated general adaptability across all environments, with an IPCA score close to zero, making it a leading candidate for the current study. The studies by Refs. [41,105] support the idea that genotypes with high yields have the least interaction with the environment, indicating that they are broadly adapted with high yields in all environments. Unstable genotypes with high yields are adapted to specific environments. The AMMI Biplot analysis is conducted and visualized to determine differences among environments, to evaluate stable and wide-adaptable genotypes, and to assess the environments that differentiate the genotypes [31]. In this biplot, a genotype or an environment with an IPCA score of nearly zero is considered stable. The results of the present study are in line with this interpretation.

#### 4.3. GGE biplot analysis

The GGE biplot is a graphical tool that displays the genotype by environment two-way data [106,107]. It is used to identify the ideal environments, and the best genotypes that have good adaptability to the ideal environments. The vertex varieties in each sector are the best variety at environments whose markers fall into the respective sector [108,109]. These varieties also have the largest distance from the origin indicating the varieties are more responsive to varying environments. If all environment markers fall into a single sector, it indicates that a single cultivar had the highest yield in all environments. If environment markers fall into different sectors, it indicates that different cultivars win in different sectors [110,111].

The GGE biplot, through the IPCA1 and IPCA2, accounted for a high percentage of the variability 98.2 %, which indicates a strong and complex genotype by environment interaction (GEI) in the multi-environment yield trial data. The highest grain yield values were observed in environment E3 from genotype G6, which was positioned at the vertex of the biplot. Conversely, genotypes G9 and G2, located farthest from the origin on the opposite side of the environments, performed poorly in most test environments, suggesting a high contribution to the existing GEI, which aligns with previous reports [112–114].

The GGE biplot, a widely used tool in plant breeding and agricultural research, is valuable for evaluating genotype by GEI and identifying ideal test environments [48]. When all environment markers fall into a single sector, it suggests that a single cultivar had the highest yield in all environments, indicating a non-crossover type of GEI [110]. On the other hand, if environment markers fall into different sectors, it indicates that different cultivars performed better in different sectors [115,116]. The purpose of test-environment evaluation is to identify environments that effectively distinguish superior genotypes and are representative of the mega-environment [117]. In this study, the test genotypes G1, G2, G4, G5, G9, and G11 did not outperform G6 in any of the test locations, revealing a non-crossover type of GEI. This is in agreement with previous reports [118,119] and emphasizes the importance of identifying ideal test environments for successful breeding and cultivar evaluation.

The GGE biplot analysis showed that E1 and E2 environments are positively correlated as the angle between them was less than 90°. This suggests that these two environments share similar characteristics and have comparable effects on genotype performance. Additionally, E1 and E2 were positively correlated with E3; and the length of the vectors representing test environments indicates their ability to discriminate between genotypes. Longer vectors indicate higher discriminative power, while shorter vectors provide limited information about genotype differences [120,121]. The correlation between environments is determined by the angle between their vectors: angles smaller than 90° indicate a positive correlation, an angle of 90° indicates independent environments, and angles larger than 90° indicate a negative correlation [76,122]. The present findings have implications for selecting appropriate test environments in crop breeding programs, emphasizing the importance of choosing discriminating environments to effectively differentiate between genotypes. This result is also supported by the findings of [123,124].

Based on the results shown in Fig. 5, environment E3 has the longest environmental vectors, while environments E1 and E2 have the shortest. This suggests that E3 was the least discriminating environment. In the context of GGE biplots, an environment is more desirable when located closer to the center of a circle or to an ideal environment [125–127]. The GGE biplot uses the environment

vector to measure discriminative ability, with longer vectors indicating higher standard deviation within the environment and, consequently, greater discriminating power [110,128,129]. Therefore, in the present study environment E3 had the longest vector with large IPCA, which is near to the concentric circles and is considered an ideal environment in terms of being the most representative of the environments with the longest environmental vectors. This implies their ability to discriminate varieties based on their genotypic performance, which is also supported by the findings of previous studies [78,130–132].

The representativeness of a test environment is crucial in obtaining accurate information about genotypes. A test environment that is not representative of the target environments can be misleading and biased [133]. An acute angle between the testing environment and the average environment coordinate axis indicates a positive correlation and is considered representative, while an obtuse angle indicates a negative correlation and is least representative [134,135]. Although obtaining an ideal test environment is difficult, environments near a small circle located in the center of concentric circles and an arrow pointing to it are identified as the best desirable testing environments [74,135,136]. In the present study, Guagussa shikudad district (E3) was identified as an ideal environment that is most representative of overall environments and powerful in discriminating genotypes. This finding is valuable for plant breeders and researchers when choosing suitable test environments for crop breeding programs and for accurately distinguishing between different genotypes in the study area. This suggestion is consistent with that suggested by Refs. [137,138].

The results obtained from the present study showed that Tay (G6) is the most ideal genotype based on its high mean grain yield and stability across variable environments. Other genotypes, such as G7, which are close to the ideal genotype are also stable. Such an ideal genotype is defined by having the greatest vector length of the high-yielding genotypes and with zero  $G \times E$  interaction. Previous studies [28,64,139] have reported similar findings, suggesting that an ideal genotype should have high mean performance and stability. Although identifying an ideal genotype may be difficult, it can serve as a reference point for genotype evaluation, and genotypes that are close to the ideal genotype are desirable. The implication of this study is that identifying an ideal genotype can help in selecting genotypes that perform well across different environments, leading to improved crop yields and more stable agricultural production.

The study suggests that genotypes located in the inner circle are more desirable than those in the outer circle. To visualize the distance between each genotype and the ideal genotype, concentric circles were drawn around the central circle that contains the ideal genotype. This approach helps to understand the relationship between genotypes and their proximity to the ideal genotype [30,59,140].

#### 4.4. Stability performance

Adaptability and yield stability are crucial for successful crop cultivation in agro-climatic regions. Plant breeders are particularly interested in genotypes that exhibit stable yields across various environments. Yield stability is a highly desirable trait for a genotype to be considered as a cultivar, and the ultimate goal of plant breeders is to develop high-yielding varieties with consistent performance across different environments [78,141,142].

To assess the stability of genotypes, the AMMI biplot method utilizes the Interaction Principal Component Axes 1 and 2 (IPCA1 and IPCA2) scores. These scores represent the stability of the genotypes across different environments. Genotypes with lower IPCA scores indicate higher stability, while higher IPCA scores suggest lower stability. In other words, genotypes with IPCA scores closer to zero are considered more stable across all locations. This approach, as mentioned by Refs. [143–145], allows plant breeders to evaluate and identify genotypes that exhibit stability in yield performance across diverse environmental conditions.

Genotypes that have higher IPCA scores, whether positive or negative, indicate a more specific adaptation to certain environments. In AMMI analysis, a low ASV (Additive Main Effects and Multiplicative Interaction Variance) suggests high stability of genotypes across different environments. However, it is important to note that stable genotypes may not necessarily have high mean yield performance, as pointed out by Refs. [24,88,146], which is supported our findings.

In agriculture, grain yield is considered as the most important characteristic for breeders in field crops because it combines all essential traits and genes into a valuable biological and economic benchmark. That is why stable and high yielder genotypes are important [147]. Based on the results shown in Table 4, G5, G7, and G10 are identified as the three most stable genotypes. Genotypes that consistently rank similarly across different environments are classified as stable, as mentioned by Ref. [148]. An ideal genotype would possess both high average grain yield and high stability, as highlighted by Refs. [149,150]. In this study, G7 is identified as the most stable genotype, being the second highest-yielding genotype after G6 (Table 3). The results from ASV further confirm that although G6 is the best high-yielding genotype, it is considered unstable and ranks third in terms of stability based on GSI (Genotypic Stability Index). Having unstable genotypes even if they have high yield and high average rank is not uncommon as reported by Refs. [27,151].

## 5. Conclusions and recommendations

The result obtained in this study indicated that there is significant variability in bread wheat genotypes in terms of agronomic traits related to yield. Based on the analysis of genotype by environment interaction and stability for grain yield of bread wheat genotypes using AMMI and GGE biplot, it can be concluded that there is a significant interaction between genotype and environment. The AMMI and GGE biplot analysis revealed that genotype G7 was the most stable and high yielding across different environments. On the other hand, genotypes G6 showed high yield potential but less stable across environments according to ASV. However, G6 (0.67 kg/plot), G7 (0.65 kg/plot) and G8 (0.64 kg/plot) were the three most stable genotypes and high yielding genotypes according to the rank of genotype selection index. Environment three (E3) is selected as the most suitable environment for screening the genotypes. The use of AMMI and GGE biplot analysis can provide valuable insights into the performance of genotypes across different environments and help

in identifying stable and high yielding genotypes. Based on the findings of the study, it is recommended that breeders and researchers should consider the genotype by environment interaction and stability analysis for selecting high yielding and stable genotypes for different environments. Thus, it is advisable to use Tay (G6) and Honqolo (G7) genotypes for future production of bread wheat in the study area.

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## Data availability statement

Data will be made available on request.

## CRediT authorship contribution statement

**Destaw Mullualem:** Writing – review & editing, Writing – original draft, Visualization, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Alemu Tsega:** Writing – review & editing, Supervision, Formal analysis. **Tesfaye Mengie:** Writing – review & editing, Supervision, Formal analysis. **Desalew Fentie:** Writing – review & editing, Supervision, Methodology, Investigation, Formal analysis. **Zelalem Kassa:** Writing – review & editing, Supervision, Methodology, Formal analysis. **Amare Fassil:** Writing – review & editing, Writing – original draft, Formal analysis, Data curation, Conceptualization. **Demekech Wondafere:** Writing – review & editing, Writing – original draft, Supervision, Data curation. **Temesgen Assefa Gelaw:** Writing – review & editing, Writing – original draft, Supervision. **Tessema Astatkie:** Writing – review & editing, Methodology, Formal analysis.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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