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Research article

Genotype by environment interaction and yield stability analysis of bread wheat (*Triticum aestivum* L.) varieties in East Gojjam Zone, Northwest Ethiopia

Alemnesh Eskezia *, Habtamu Kefale, Mekonen Asrat

Department of Plant Science, College of Agriculture and Natural Resources, Debre Markos University, P.O.Box 269, Ethiopia

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A B S T R A C T

Bread wheat (*Triticum aestivum* L.) is vital for over a third of the global population but faces significant production challenges due to limited adaptable varieties, poor management practices, and environmental factors. New wheat varieties often fail in unfamiliar environments, leading to crop loss. To address this issue, a study was conducted to evaluate the adaptability, performance, and yield stability of recently released high-performing wheat varieties over two years (2020/2021 and 2021/2022) in four districts of the East Gujjar Zone: Machakel, Debre Elias, Gozamin, and Baso-Liben. The trials were set up using a randomized complete block design (RCBD) with three replications, and data were collected on the main traits such as days to heading, maturity, plant height, tiller number, spike length, spikelet's per spike, biomass, and grain yield. AMMI and GEE biplot analysis were used to study genotype by environmental interaction. The combined analysis of variance for grain yield showed highly significant effects ($P < 0.001$) due to genotype (4.98 %), environment (66.83 %), and genotype × environment interaction (31.96 %). Grain yield varied across the environments, ranging from 3.72 t ha^{-1}in Baso-Liben to 3.11 t ha^{-1} in Machakel. Among the genotypes, Ogolcho had the highest mean yield (4.55 t ha^{-1}), whereas Wane had the lowest (2.70 t ha^{-1}). Genotype-by-environment interaction biplot analysis grouped the eight test environments and six genotypes into two mega-environments and three genotype groups. Wane, Lemu, and Ogolcho were the stable genotypes. This analysis identified the most favorable districts for wheat production and highlighted Ogolcho as the most productive wheat variety in the study area. The results suggest that farmers in these districts should adopt Ogolcho to enhance wheat yield and increase their income.

1. Introduction

Bread wheat *(Triticum aestivum* L.), a hexaploid species ($2n = 6x=42$*)*, is a crucial global crop that originated from natural hybrids of three diploid wild progenitors native to the Middle East [1,2]. It is a grain crop with approximately 25,000 cultivars worldwide [3]. In Ethiopia, wheat is a major cereal crop grown across diverse ecological zones at altitudes ranging from sea level to 3300 m a.s.l. [4]. It contributes 17.71 % of the country's cereal production, second only to teff [5,6].

Wheat is essential for Ethiopia's agricultural development and food security, serving as a critical source of protein and energy [7,8].

* Corresponding author.
E-mail address: alemnesh_eskezia@dmu.edu.et (A. Eskezia).

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Although wheat is a staple crop for about one-third of the world's population, Ethiopia needs to expand its wheat production to achieve food self-sufficiency [9]. Due to its nutritional value and versatility, wheat plays a crucial role in the country's agricultural plans and sustainable development initiatives [10]. In Ethiopia, wheat has covered approximately 1.87 million hectares, yielding approximately 5.8 million tons of grain in the 2021/22 cropping season [5]. The Amhara region had coverage and production of wheat of 689,614.06 ha and 1.92 million tons, with a productivity of 2.8 t ha^{-1} [11]. In the administrative zones of the Amhara region, the East Gojjam Zone ranked first in area coverage (166, 377.99 ha) and total production (0.53 million tons) of bread wheat, with an average productivity of 3.2 t ha^{-1} [11]. Overall, wheat is a staple crop in Ethiopia and is essential for food security and economic growth [12]. However, Wheat productivity is low in many regions, including the East Gojjam Zone. This is due to various yield-limiting factors such as diseases, pests, climate variability, the overuse of local varieties, lack of high-yielding and stable varieties, and poor communication between farmers and researchers [13,14].

Several bread wheat varieties have been released by Ethiopia's regional and national agricultural research institutes [15]. However, most of these varieties have not been evaluated nationwide, particularly in the northwestern regions of Ethiopia [16].

To address this gap, it is essential to generate evidence on genotypic performance and adaptation under varying environmental conditions that may be necessary to develop appropriate intervention strategies to improve crop yield and dietary self-sufficiency [17].

The stability analysis of bread wheat evaluates the consistency of cultivar performance across diverse environments, aiding breeders in selecting varieties with reliable yields under varying conditions [18,19]. By considering multiple locations and seasons, a stability analysis identifies cultivars with broad adaptability, ensuring stable bread wheat production [20]. Stability statistics are analytical tools used to assess the stability of crop cultivars in different environments, including the main effect and genotype-environment interaction (GGE) biplot analysis [21,22]. These statistics provide insights into genotype × environment interaction (GEI) and help breeders identify suitable environments and stable varieties with consistent performance [23,24].

Genotype × Environment Interaction (GEI) analysis of bread wheat in Ethiopia is an essential yet underexplored area of research. This analysis provides a new perspective on how various wheat genotypes respond to different environmental conditions, particularly in the East Gojjam Zone. The findings could bridge the existing knowledge gap and help identify optimal wheat varieties for specific regions, thereby enhancing yield stability and agricultural productivity in Ethiopia [25]. Increased genetic yield gains can be achieved through tighter varietal adaptations, maximizing yields by leveraging the interplay between genotype and environment [26,27].

The AMMI (Additive Main Effects and Multiplicative Interaction) model is a statistical method used to analyze genotype × environment interaction (GEI) in crop performance studies. It combines analysis of variance (ANOVA) with principal component analysis (PCA), to differentiate the effects of genotypes and environments from their interactions, helping to identify stable genotypes suited to specific environments. Similarly, the GGE (Genotype and Genotype × Environment) biplot serves as a powerful tool for analyzing multi-environment trials, focusing on genotype performance and genotype × environment interactions while excluding environmental main effects. This two-dimensional representation aids in identifying stable, high-yielding genotypes.

Additive Main Effects and Multiplicative Interaction (AMMI) and Genotype and Genotype by Environment (GGE-biplot) analyses are effective statistical methods for evaluating genotype by environmental interaction (GEI) [28,29]. These methods assist in identifying high-yielding and stable varieties suitable for different environmental conditions [30]. The main objectives of GGE biplots are

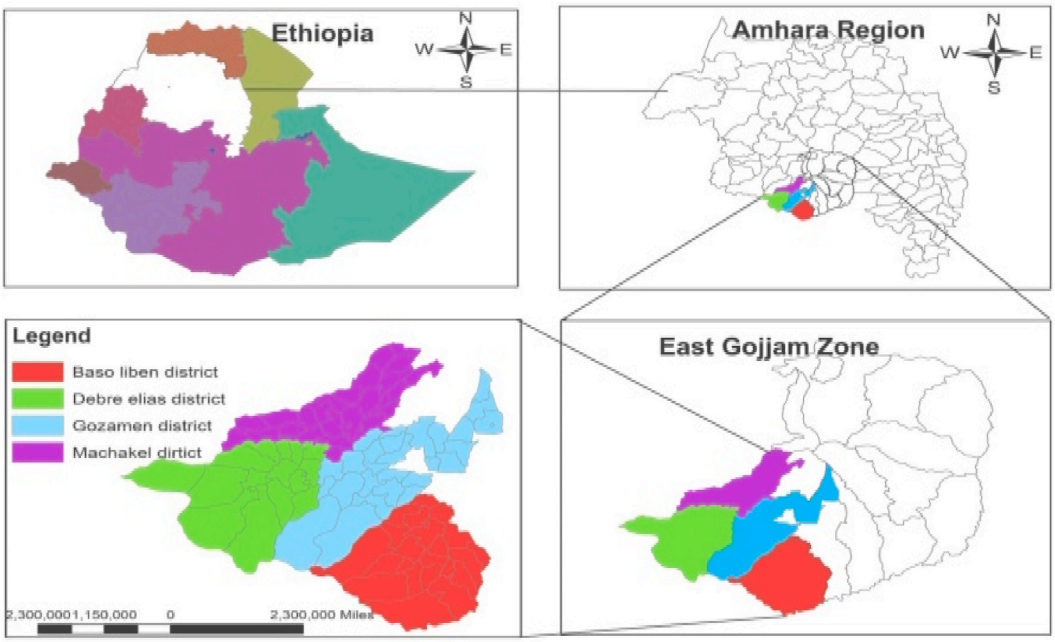

Fig. 1. Schematic map of the study area.

to rank the genotypes, examine the environment, and graphically represent GxE interaction [31]. Therefore, the present investigation evaluates and selects the best-adapted, high-yielding, and stable bread wheat varieties to enhance crop yield in the East Gojam Zone in Northwestern Ethiopia.

2. Materials and methods

2.1. Experimental location

The study was conducted across four key wheat-producing districts: Machakel, Debre Elias, Gozamin, and Baso-Liben, located within the East Gojjam Zone of Ethiopia (Fig. 1 and Table 1). Specifically, it was conducted at the Farmers Training Centers (FTC) in each district during the main rainy seasons between June and December 2020–2021 for two consecutive years. The soils in the East Gojam Zone are primarily Nitisols, Red, and Vertisols, with a pH of 5.5–7.0, moderate organic matter, and clayey texture. Key challenges include phosphorus deficiency, erosion, and waterlogging in lowlands. The locations for the study were chosen based on their wheat production potential.

2.2. Experimental plant materials

Five improved and high-yielding bread wheat varieties (Table 2) were selected and their seeds were obtained from the Kulumsa Agricultural Research Center (KARC), Ethiopian Institute of Agricultural Research. In addition, the Kakaba variety was selected as a standard check because of its wide adoption by farmers and the availability of seeds in the study area. The comprehensive descriptions and passport data for the varieties utilized in the experiments are summarized in Table 2.

2.3. Experimental design and trial management

The experiment was conducted in a randomized complete block design (RCBD) with three replications, in a plot size of 3.6 m^2 (2 × 1.8m). Each plot consisted of nine rows, 2 m long and 1.8 m wide, with 0.2 m between rows, 0.5 m between plots, and 1 m between blocks. Seeds of each wheat variety were sown manually (drilled in rows) at a rate of 150 kg ha^{-1} in well-prepared plots-fine soil. Uniform rates of urea (200 kg ha^{-1}) and NPSB blended fertilizers (100 kg ha^{-1}) were applied to all plots across all seasons and locations. The total multi-nutrient fertilizer supplying nitrogen, phosphorus, sulfur, and boron (NPSB blended fertilizer) (100 kg ha^{-1}) and ½ dose of urea (67 kg ha^{-1}) were applied during crop sowing, while 2/3 of urea (133 kg ha^{-1}) was used at the late tillering stage (35 days after sowing). Tillage, weed control, and pest management were carried out according to the recommendations outlined in the wheat production manual.

2.4. Data collected

Data for the nine traits were collected on both plant and plot basis. Measurements were taken from all plants in the central rows of each plot, with one border row left on each side. Agronomic traits such as crop phenology, growth, yield, and yield components were assessed during the study. Crop phenology included maturity day, whereas growth parameters, such as plant height, number of productive tillers, number of spikelets per spike, plant height, spike length, and yield-related traits, including biomass yield, grain yield, and harvest index, were recorded.

Days to heading (days): The number of days from sowing to when the tips of the spike first emerged from the main shoot in 50 % of the plant population within a plot was recorded.

Days to 90 % maturity (days): The number of days from sowing to physiological maturity was recorded. Physiological maturity was determined when 90 % of the crop stands in a plot showed a light yellow (straw) color in their stems, leaves, and floral bracts.

Number of productive tillers (no): The number of productive tillers was determined at maturity by counting all spike-producing tillers of 10 plants per plot.

Number of spikelets per spike (no): The number of spikelets per spike was counted from ten representative spikes per plant, and the average was calculated.

Plant height (cm) was measured from the base of the main stem to the tip of the spike from an average of ten randomly selected

Table 1
Geographical description of the study area.

Location	Code Year 2020/2021	Code Year 2021/2022	Alt. (masl)	Temp. min & max values (°C)	RF. Ave.(mm)	Soil type	Geographic location	
							Lat	Lon
Debre Elias	E1	E5	800–2220	18–27	1150	Red	10 °22′ N	37° 47′ E
Baso-Liben	E2	E6	2250	15–27	900–1200	Red	10 38′ N	10° 37′ E
Gozamin	E3	E7	2446	15–22	1380	Vertisol	10°21′ N	37° 43′E
Machakel	E4	E8	2145	19–30	1320	Red	10° 65′ N	37° 53′E

Where: Alt: Altitude, Temp.: temperature, and RF.: Rainfall, Lat: latitude, Lon: longitude.
Source: District administrative office.

Table 2
The descriptions of the varieties used in the experiment.

No	variety name	Code	Breeder center	year of release	grain yield (t ha^{-1})	Rainfall	Altitude (m.a.s.l.)
1	Ogolcho	G2	KARC	2012	3.3–5	400–500	1600–2100
2	Wane	G6	KARC	2016	5–6	700–1000	2100–2700
3	Lemu	G4	KARC	2016	5.5–6.5	800–1100	>2200
4	Kingbird	G5	KARC	2015	4.6–6.3	500–850	1500–2200
5	Kakaba	G3	KARC	2010	3.3–5.2	500–850	1500–2000
6	Danda'a	G1	KARC	2010	4.0–5.5	>600	2000–2600

Where: KARC is the Kulumsa Agricultural Research Center, t ha^{-1} (tons per hectare), masl (meters above sea level), and G: Genotype.
Source: ESA [5].

plants in the central four rows in each plot.

Spike length (cm): This was recorded at the physiological maturity stage by measuring the middle rows of 10 randomly tagged plants from the base of the spike to the tip of the spike (excluding the awns), and the average length of the plant was calculated.

Biomass yield (ton ha^{-1}): Aboveground total biomass was recorded after sun-drying, attained constant weight, and then converted to t ha^{-1}.

Grain yield (ton ha^{-1}): The weight of air-dried seeds harvested from each plot was recorded. Then, the yield from the net plot area was converted into t ha^{-1}

Harvest index (%): The ratio of grain yield per plot to biological yield per plot is expressed as a percentage.

$$\mathrm{HI}(\%) = \frac{Grain\ Yield}{Biomass} \times 100$$

2.5. Data analysis

Analysis of variance (ANOVA) was conducted to test for significant differences among wheat varieties for various traits in each year and location. All data were evaluated for normality, homogeneity of variance, and independence of observations using the Shapiro-Wilk test, Levene's [32] test, residual plots, and proper experimental design. Following this, a combined ANOVA was performed using the generalized linear model (GLM) procedure in SAS v 9.4 [33]. Variety and environment are fixed factors, whereas replication (within the environment is a random factor in this experiment). After testing the ANOVA, Fisher's least significant difference (LSD) test at a 5 % significance level was used for variety mean comparisons whenever significant differences among varieties were found.

The AMMI (Additive Main Effects and Multiplicative Interaction) model is a statistical method used to analyze genotype × environment interaction (GEI) in crop performance studies. It integrates analysis of variance (ANOVA) and principal component analysis (PCA) to separate the effects of genotypes and environments from their interactions, allowing for the identification of stable genotypes suited to specific environments. The GGE-biplot is a powerful tool for analyzing multi-environment trials, focusing on genotype and genotype × environment interactions while excluding environmental main effects. It helps identify stable, high-yielding genotypes through a two-dimensional representation. AMMI analysis partitions the GEI sum of squares into interaction principal component axes (IPCAs) and generates scores for the first IPCA, which help estimate stability [25,34]. The AMMI analysis was performed using the R metan package. A biplot that provides a graphical view of GEI was constructed [35]. The interpretation in a bi-plot representation is that genotypes or environments that occur almost on perpendicular lines have similar interaction patterns. Genotypes and environments with large IPCA1 scores (positive or negative) had high interactions, whereas genotypes or environments with an IPCA1 score of zero (or nearly zero) had small interactions. The main goal of any wheat breeding program is to obtain new cultivars that will outperform existing cultivars in several traits. The ASV measures the stability of genotypes based on their interactions with the environment. Lower ASV values indicate more stable genotypes.

AMMI stability value was calculated as follows:

$$ASV = \sqrt{[(\mathrm{SSIPCA1}\ /\ \mathrm{SSIPCA2})\ (\mathrm{IPCA1\ score})]2 + (\mathrm{IPCA2\ score})2}$$

Where; SSIPCA1 and SSIPCA2 are the sums of the squares of the first and second principal component axes (IPCA), respectively. The IPCA 1 and IPCA2 scores are the interaction scores for the first and second IPCAs, respectively.

GGE biplot analysis is a graphical method that evaluates genotype performance and stability across environments by combining genotype and genotype-environment interaction effects, helping to identify the best and most adaptable genotypes.

The GGE-biplot is an effective tool for analyzing multi-environment trials by focusing on the combined effects of genotype and genotype × environment interactions while excluding environmental main effects. This two-dimensional representation allows for the identification of genotypes that are both stable and high-yielding.

3. Results and discussion

3.1. Combined analysis of variance (ANOVA)

The combined ANOVA for the two cropping years and four locations showed that most traits differed significantly ($P \leq 0.01$) among the tested bread wheat varieties (Table 3). The genotypes revealed highly significant (P < 0.01) variation in all nine evaluated traits. The year was significant for six of the traits, including grain yield, whereas a non-significant difference was observed for days to heading, tiller number, biomass yield, and harvest index. The main effect of location showed significant differences for most traits except tiller number. This indicates that while temporal factors influence certain agronomic traits, spatial factors (location) play a crucial role in determining the performance of bread wheat varieties across different environments. The interaction effect of location by year had a highly significant (*P* < 0.01) effect on several traits, including days to heading, maturity day, plant height, biomass yield/ ratio of biomass production to substrate consumption, and grain yield, whereas a significant effect (P < 0.05) was observed for tiller number. However, the number of spikelets per spike and spike length were not significantly affected. As shown in Table 3, the results indicate that the interaction effect of location and variety had a significant (P < 0.05) effect on plant height and biomass yield, but there was also a highly significant (P < 0.01) effect on the days to heading, maturity day, grain yield, and harvest index. There was no significant effect on the number of tillers, number of spikelets per spike, and spike length. The interaction effect of variety by year had a highly significant (P < 0.01) effect on days to heading, plant height, grain yield, and harvesting index, whereas a significant effect (*P* < 0.05) was observed on tiller number and number of spikelets per spike. A non-significant effect was observed on maturity day and biomass yield. These results are in agreement with previous studies [36], observing significant differences (P < 0.05) among bread wheat genotypes across all test locations and years in multi-environment trials.

Days to heading, maturity, plant height, biomass yield, grain yield, and harvest index were highly significant (P ≤ 0.01), whereas spike length was significantly influenced (P ≤ 0.05) by the interaction of year, variety, and location (Table 3). However, the tiller number and number of spikelets per spike were not influenced by the interaction effects of year, variety, and location. Overall, the combined analysis revealed significant variations among the six bread wheat varieties for most traits. In line with the present results, previous studies have reported highly significant differences (*P* ≤ 0.01) [37]. The significant genotype × environment interaction (GEI) effects indicated the inconsistent performance of genotypes across the tested environments, highlighting the differential discriminating ability of these environments. This indicates that it is possible to identify high-yielding and stable genotypes, meaning that the same crop variety might perform well in one environment but poorly in another because of differences in factors, such as climate, soil, or management practices. These findings are consistent with previous studies [38], reporting significant differences (P < 0.05) among bread wheat genotypes for grain yield across all individual test locations in multi-environment trials.

The coefficient of variation (CV) value for most traits indicated good experimental precision because the value was within an acceptable range for agricultural field experiments. The highly significant variation in wheat varieties agrees with the findings of [39]. The R^2 values for all traits were excellent, indicating a strong fit between the model and the experimental design. This demonstrates the effectiveness of the model in explaining the data variability.

3.2. Mean performance of grain yield in each test location and years

Among the testing locations, grain yield was the highest at Baso-Liben during the 2021 cropping season compared to the other three testing locations across two years and seven testing environments, with a mean grain yield of 5.56 t ha^{-1} followed by Gozamen in the 2021 cropping seasons (5.54 t ha^{-1}). The lowest grain yield was obtained in Machakel in 2021, with a mean yield of 2.3 t ha^{-1}. The superior performance of genotypes at Baso-Liben (5.56 t ha^{-1}) and Gozamen in 2021 (5.54 t ha^{-1}) could be attributed to the uniform distribution of rainfall and other environmental conditions throughout the cropping season as well as suitable ecological conditions for the genotypes. The tested genotypes showed inconsistent yield advantages in different environments. The mean grain yield of genotypes across all environments indicated that Ogolcho (4.55 t ha^{-1}), Danda'a (4.18 t ha^{-1}), and Kakaba (3.33 t ha^{-1}) were the top three highest-yielding varieties. In contrast, Kingbird (2.07 t ha^{-1}) and Lemu (2.90 t ha^{-1}) were low-yielding varieties (Table 4). The mean grain yield across environments ranged from 3.72 t ha^{-1} for Baso-Liben to 3.11 t ha^{-1} for Machakel. In contrast, the mean grain yields of the genotypes ranged from 4.55 to 2.66 t ha^{-1} for Ogolchoand Kingbird, respectively. Baso-liben and Debre-Elias were

Table 3
Mean squares of the two years (cropping season) combined ANOVA results of nine quantitative traits from four locations.

SOV	Mean squares									
	DF	DH	DM	PH	TN	SL	NSPS	BY	GY	HI
Replication	2	0.25ns	5.50ns	7.35ns	0.75ns	0.179ns	9.49ns	1.33ns	0.097ns	2.29ns
Variety(V)	5	250.8**	963.67**	1857.68**	23.65**	63.57**	732.54**	6.13**	14.36**	837.07**
Year (Y)	1	0.07ns	126.56**	176.02*	0.51ns	39.18**	421.34**	1.49ns	1.32**	29.49ns
Location(L)	3	7.50**	11.30*	1153.48**	0.59ns	3.57**	53.52*	12.17**	1.21**	148.43**
L*V	15	1.63**	21.13**	79.36*	0.28ns	0.59ns	8.74ns	2.28*	0.39**	36.54**
V* Y	5	3.04**	4.09ns	78.52**	1.04*	0.36**	44.04*	2.74ns	3.72**	182.86**
L*Y	3	7.75**	54.69**	292.56**	0.52*	0.97ns	16.12ns	19.60**	0.01**	132.33**
V*L*Y	15	1.50**	16.64**	92.54**	0.542ns	0.75*	7.16ns	3.97**	0.49**	21.42**
Error	22	3.17	1.72	32.62	0.31	0.40	11.67	0.95	0.08	9.13
R^2		0.92	0.97	0.84	0.82	0.91	O.81	0.72	0.93	0.89
CV%		2.88	1.24	6.48	11.87	4.57	9.67	8.86	8.31	9.55

Where: SOV: source of variation; **: highly significant at *P* < 0.01; *: significant at *P* < 0.05; ns: non-significant; DF: Degrees of freedom; DH: days to heading; DM: days to maturity; PH: plant height; TN: tiller number; SL: Spike length; NSPS: number of spikelets per spike; BY: biomass yield; GY: grain yield; and HI: harvest index.

relatively high-yielding environments compared with Gozamen and Machakel. Additionally, the bread wheat varieties with higher grain yield at specific locations included Ogolchoand Danda'a, Baso-liben and Debre Elias, and Kakaba at Machakele and Gozamen. The variety Ogolcho exhibited the highest performance across most environments, with Danda'a following closely behind. The high variation in grain yield among the six bread wheat varieties at the eight locations may be attributed to the extensive variability in climatic and soil conditions. Similarly, inconsistent grain yield performances of bread wheat varieties have been reported across locations [40–42]**.** This indicates that it is possible to identify high-yield genotypes for potential use in these areas. The results of this study are in agreement with previous studies [43], and the high variation in grain yield among the six bread wheat varieties across the eight location-year environments might be due to extensive variability in climatic and soil conditions.

3.3. *Additive main Effect and Multiplicative Interaction (AMMI) analysis*

The Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for grain yield among six bread wheat genotypes evaluated across eight environments is shown in Table 5. The AMMI analysis revealed significant genetic variation and potential for the selection of stable genotypes. The results indicated that the variation among E, G, and GxE was highly significant ($P <$ 0.01). The partitioning sum squares (SS) showed that the environmental impact was the most critical contributor to yield fluctuation, followed by the genotype × environment interaction and the genotype main effect. Notably, changes in G and G × E were typically smaller, suggesting that environmental factors predominantly explain the differences in genotype variation [44]. Furthermore, the AMMI model's first two principal component axes (IPCAs) were found to be highly significant ($P < 0.01$) when used for partitioning genotype-environment interaction (GEI). The AMMI, which includes IPCA1 and IPCA2, is the best prediction model for cross-validating yield variation explained by the genotype-environment interaction [1,45]. Variations in the grain yield components from the AMMI analysis indicated that genotype, environment, and genotype by environment interaction (GEI) all had significant effects ($P < 0.01$), explaining variability across both environments and genotypes. This suggests opportunities for selecting genotypes high-yielding, stable, and well-performing genotypes.

The total sum of squares analysis revealed that 66.83 % of the variation in grain production was attributed to environmental factors, 4.98 % to genotype differences, and 31.96 % to genotype by environment interactions. The analysis of the sum of squares for environments (Table 5) confirmed significant diversity among the test environments, indicating that environmental differences predominantly influence variations in grain yield. This underscores the rationale for conducting multi-environment experiments. Variations in temperature, precipitation, soil type, fertility, and moisture availability are likely the primary contributors to these environmental differences [46,47].

According to the AMMI analysis, the first and second interaction principal components (IPCA1 and IPCA2) explained 73.61 % and 22.08 % of the interaction sum squares, respectively (Fig. 2b). This indicates that IPCA1 and IPCA2 collectively accounted for 95.69 % of the total genotype-environment interaction (GEI). The model effectively explained the GEI component, allowing for the ranking of genotypes based on their AMMI Stability Value (ASV) scores, with lower scores indicating more stable genotypes.

The model effectively explained the genotype × environment interaction (GEI) component, allowing for the ranking of genotypes based on their AMMI Stability Value (ASV) scores, with lower scores indicating more stable genotypes. Based on ASV, the most stable genotypes for grain yield were G6, G4, G4, and G2, which had the lowest ASV scores. Genotypes G1, G5, G6, and G3 exhibited the highest stability, characterized by the lowest AMMI Stability Value (ASV) ranks. In contrast, genotypes G6, G1, G2, and G4 were less stable but demonstrated higher dry matter content (Table 5 and Fig. 2a) This information was derived from the analysis of genotype × environment interactions and stability in selected cassava cultivars in South Africa [48].

Table 4
Mean performance of grain yield (t ha^{-1}) in each test location and across years.

Genotypes tested	Locations and Years										Overall	
	2021					2022					Mean	Rank
	E1	E2	E3	E4	Mean	E5	E6	E7	E8	Mean		
Danda'a	3.71 cb	3.62b	3.72b	3.69b	3.62b	3.42b	2.97b	3.17c	**2.56c**	3.93b	4.18b	**2**
Ogolcho	4.68a	5.56a	5.54a	4.91a	5.17a	4.54a	4.35a	4.02b	**2.82bc**	4.75a	4.55a	**1**
Kakaba	3.74b	3.46b	3.86b	3.40bc	3.61b	4.52a	4.76a	4.88a	**4.82a**	3.03b	3.33d	**3**
Lemu	3.34 cb	3.48b	3.38b	2.70cd	3.22c	4.52c	2.48c	3.19c	**3.05b**	2.886c	2.90de	**4**
Kingbird	3.43 cb	**2.41c**	2.51c	2.30d	2.66d	2.78c	2.76bc	2.68d	**2.72bc**	2.74cd	2.07e	**6**
Wane	3.71 cb	3.16b	2.51c	2.60d	2.99c	3.01bc	3.05b	2.50d	**2.70bc**	2.81cd	3.33c	**5**
Mean	3.62	**3.72**	3.58	3.27		3.51	**3.31**	3.41	**3.11**			
CV%	5.86	8.78	8.73	12.30		7.70	**7.15**	5.60	**8.42**			
LSD (0.05)	0.39	0.57	0.57	**0.73**		0.49	**0.44**	0.34	**0.44**			
±SD	0.499	1.015	0.954	**0.942**		0.578	1.023	0.999	0.967			

Where: E1 = D/Elias, E2 = B/Liben, E3 = Gozamin, E4 = Machakel 2021/22 cropping season and **E5 =** D/Elias, E6 = B/Liben, E7 = Gozamin, E8 = Machakel 2022/23 cropping season, CV = Coefficient of variation, LSD = least significant difference, and SD = standard deviation.

Table 5
Additive main effects and multiplicative interaction (AMMI) analysis of variance for seed weight of bread wheat varieties across environments.

Source	DF	Sum Sq	Mean sq	F values	Pr(>f)	Proportion	Accumulated
ENV	7	66.83	0.7123**	7.65	3.94e-04	NA	NA
REP(ENV)	6	1.490	0.0931**	1.15	3.25e-01	NA	NA
GEN	5	4.986	13.3665**	165.26	1.18e-40	NA	NA
GEN:ENV	35	31.967	0.9133**	11.29	4.44e-19	NA	NA
PC1	11	23.923	2.1748	26.89	0.00e+00	17.8	74.8
PC2	9	4.639	0.5155	6.37	0.00e+00	14.5	89.3
PC3	7	2.424	0.3463	4.28	5.00e-04	7.6	96.9
PC4	5	0.685	0.1369	1.69	1.46e-01	2.1	99.1
PC5	3	0.297	0.0989	1.22	3.08e-01	0.9	100.0
Residual	80	6.470	0.0809	NA		NA	NA
Total	178	43.713	0.874	NA		NA	NA

Genotype rank based on AMMI stability value

Number	Genotype	Mean yield	Rank	IPCA 1	IPCA 2	ASV	Rank
1	Danda	4.18	2	0.41639	0.2011	1.584	6
2	Ogolcho	4.56	1	1.15208	0.31064	0.948	3
3	Kekeba	3.33	3	−1.07965	0.63702	1.484	5
4	Lemu	3.06	4	0.00375	0.00217	0.756	2
5	Kingbird	2.91	5	−0.38088	−0.43675	0.953	4
6	Wane	2.70	6	−0.1117	−0.71418	0.009	1

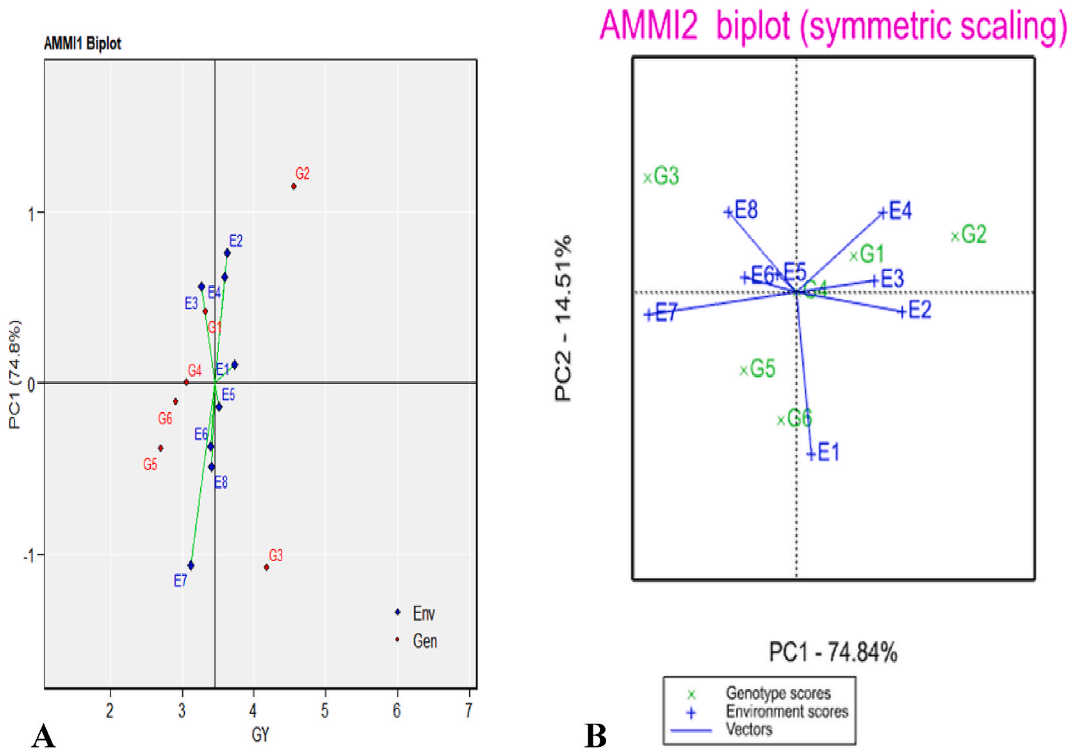

Fig. 2. AMMI-1 and AMMI-2 Analysis model biplot for grain yield of bread wheat genotype evaluated at eight environments. **A)** AMMI1 biplot showing the interaction of genotypes (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane) with environments (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Elias in 2021 cropping season and E5: Gozamen, E6: Baso-Liben, E7: Machakel, E8: Debre Elias in 2022 cropping season). The red numbers connected to the polygon represent the genotypes, whereas the blue numbers represent the locations/test environments. **B)** AMMI2 biplot (symmetric scaling) showing the relationship between genotypes and environments based on two principal components (PC1 and PC2). Genotype scores are represented by green marks (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane), and environment scores are represented by blue marks (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Elias in 2021 cropping season, E5: Gozamen, E6: Baso-Liben, E7: Machakel, E8: Debre Elias in 2022 cropping season).

3.4. Stability analysis and mega-environment classification using GGE biplot

3.4.1. GEI analysis for which-won-where patterns using GGE biplot

The results GGE analysis were similar to those obtained through AMMI and combined ANOVA. A "which-won-where" biplot serves as a graphical tool for analyzing genotype × environment interactions, aiding in the identification of mega-environments, specific regions where certain genotypes consistently excel. By plotting genotype performance across various environments, this biplot effectively highlights the "winning" genotypes for each mega-environment, facilitating the selection of the most suitable genotypes for specific conditions (Fig. 3). A polygon view of the GGE biplot was constructed to show which genotypes performed best in the environment (Fig. 3). PC1 and PC2 accounted for 95.69 % of the G + G × E variation in grain yield, with contributions of 73.61 % and 22.08 %, respectively (Fig. 3). In the analysis, the genotype markers that were furthest from the biplot origin in each direction were designated as the vertices of the polygon ensuring that all genotype marker were contained within the final polygon. This analysis identified four genotypes as the markers located furthest from the biplot origin, with one genotype falling inside this polygon and another outside it. Previous studies indicate that the vertex genotype in each vector represents the genotype that produced the highest yield in the corresponding environment [49–51]. The vertex genotypes identified were G1 (Danda'a), G2 (Oglocho), G3 (Kakaba), and G5 (Kingbird) (Fig. 3). This identification aids in understanding which genotypes are best suited for specific environmental conditions, enhancing selection strategies in breeding programs. Scavo et al. have reported similar findings [52], suggesting that an ideal genotype should exhibit high mean performance and stability. The genotypes that performed best or worst in specific environments were located furthest from the biplot's origin, indicating their sensitivity to environmental changes and categorizing them as specifically adapted genotypes [53]. Then, it can be advised select the best environments within their respective sectors in the GGE-biplot's polygon view [54]. Therefore, G2 (Oglocho) had the highest yield in Baso-Liben, Debre Elias, and Machakele. The most effective method for identifying superior genotypes and visualizing the patterns of interaction between genotypes and environments in data analysis is the polygon view of the GGE biplot, which helps estimate the potential existence of various mega-environments [55,56]. Vertex genotype G1 falls in the first and second quadrants, whereas G5 is located in the first and fourth quadrants. This positioning explains their performance in the environments represented by these two quadrants. Genotype G1 (Danda'a) was the best-performing genotype at Gozamin. Previous studies suggest that the polygon view of a GGE biplot suggests the existence or absence of distinct mega-environments among the test environments and indicates the presence or absence of crossover or non-crossover genotype-environment interactions (GEI) involving the most responsive genotypes [57]. The vertex genotype G3 performed the poorest in almost all test environments, as it was located farthest from the origin of the biplot on the opposite side of the environment. According to Kebede et al. vertex genotypes with the highest yield in a given sector are those located farthest from the origin in the polygon view [58]. The vertex genotypes in the current study included G1, G3, G5, and G2. Several lines that emerge from the origin and are perpendicular to the line connecting the vertex genotypes provide valuable insights for analyzing the relationships between the genotypes [59,60]. Therefore, the eight testing environments were categorized into two mega environments, while the six genotypes were divided into three genotypic groups (Fig. 3). The two mega environments consisted of Group I (E1, E2, E3, and E4) and Group II (E5, E6, E7, and E8).

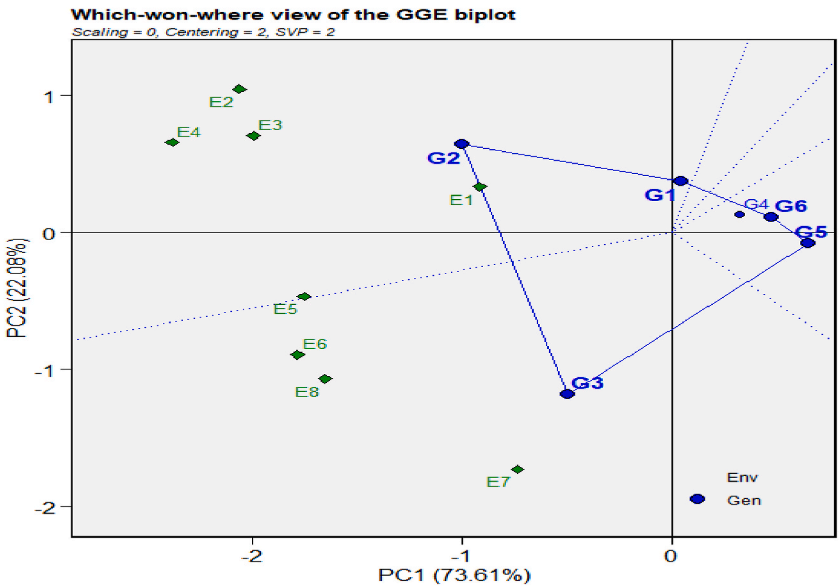

Fig. 3. Which-win-where view of GGE biplot for grain yield of bread wheat genotypes. Where: Genotype scores are represented by blue marks (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane) with environment scores are represented by green marks (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Eliasin 2021 cropping season and E5: Gozamen, E6: Baso-Liben; E7: Machakel and E8: Debre Elias) in 2022 cropping season.

3.4.2. Evaluation of environments relative to the ideal environment

As shown in Fig. 4, the discriminating ability and representativeness of the environments for the bread wheat variety declined in the following order: E5 (Gozamen year-2), E4 (Debre Elias year-1), E1 (Gozamen year-1), E6 (Baso-liben year-2), E3 (Machakel year-1), E8 (Debre Elias year-2), E2 (Baso-liben year-1), and E7 (Machakel year-2). A test environment with a small angle to the average environmental axis is considered to be more representative of other test environments. In this study, Gozamen (E5) and Debre Elias (E4), were identified as the most representative environments, as they are located at the center of the concentric circle and exhibit the longest vector lengths along the smallest angles to the average environmental axis (Fig. 4). This positioning indicates that these environments provide reliable insights into genotype performance across different conditions, making them ideal for selecting broadly adapted genotypes. Therefore, Gozamen and Debre Elias are relatively ideal locations for bread wheat cultivation among the test environments. The discriminating ability of a location is related to the composition of genotypes; however, the presence of genotype-environment interaction (GEI) complicates the selection of the best test site [61,62]. The test environments should have small absolute values for PC2 scores to be more representative of the overall locations, while large PC1 scores are necessary to effectively discriminate genotypes based on the genotypic main effect [63]. The ideal location should be both highly discriminating for the genotypes under test and representative of the intended areas. Similar to the perfect genotype, the ideal environment is located in the first concentric circle of the environment-focused biplot, with favorable environments situated near the ideal environment. Similarly, Ayed et al. reported that GGE analysis effectively supported local potato breeding by selecting high-yielding, stable cultivars across the Mediterranean climate and grouping the genotypes into three mega-environments [64].

3.4.3. Evaluation of genotypes relative to ideal genotype

An ideal genotype has the highest mean grain yield and is stable across the environments [62]. The discriminating ability of a location is related to the composition of the genotypes, with those closer to the ideal being more desirable. To help visualize the difference between genotypes and the ideal genotype, concentric circles were drawn starting from the center and pointed with an arrow [56,65]. Selection can be based on the ideal genotype as a reference. In early breeding cycles, genotypes that are far from the ideal genotype may be rejected, while those close to the ideal genotype may be considered for subsequent testing [58,66]. If a genotype is more similar to the "ideal" genotype, it is considered more desirable [67]. The ideal genotype is located in the first concentric circle of the biplot (Fig. 5). Therefore, Wane (G6) was closer to the ideal genotype and can be regarded as an ideal genotype for wheat grain production because of its stable characteristics. Similarly, Wane (G6), Lemu (G4), and Ogolcho(G1) were close to the ideal genotype and were considered good genotypes based on their yield performance and stability (Fig. 5). On the other hand, the lowest-yielding genotypes, G5 (Kingbird) and G3 (Kekeba), were considered undesirable because they were placed far from the ideal genotype. This study confirms the findings of Assefa et al. identifying outstanding genotypes near the ideal genotype in sorghum over two consecutive

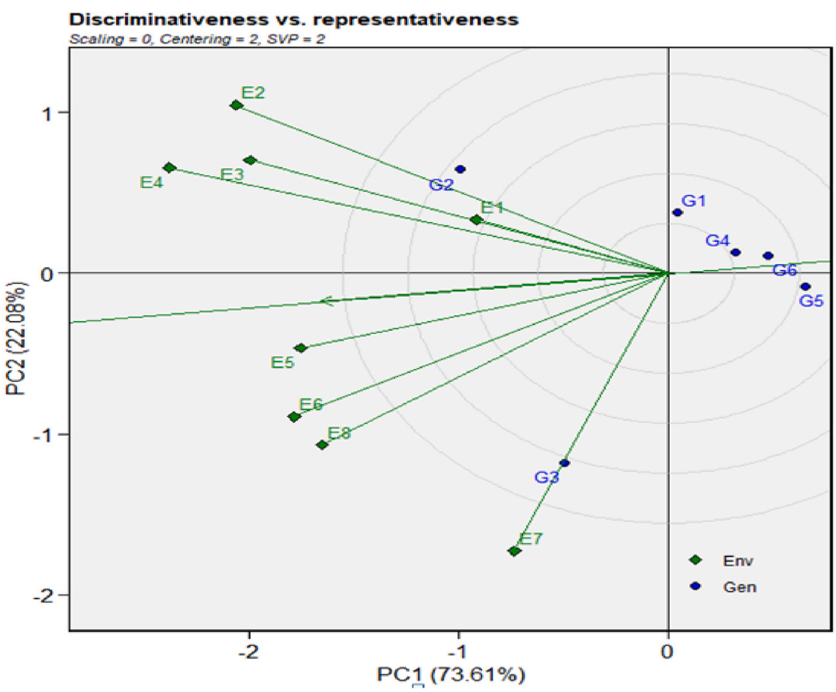

Fig. 4. GGE biplot based on environment-focused scaling to rank environments relative to the ideal environment. Where: Genotype scores are represented by blue marks (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane) with environment scores are represented by green marks (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Eliasin 2021 cropping season and E5: Gozamen, E6: Baso-Liben; E7: Machakel and E8: Debre Elias) in 2022 cropping season.

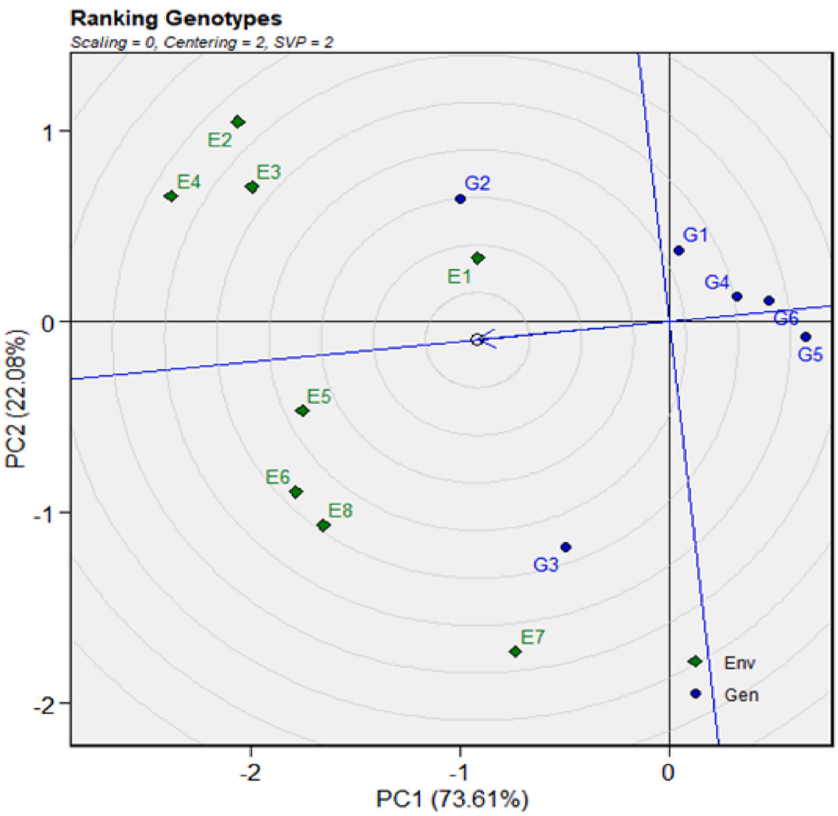

Fig. 5. Ranking of genotypes based on yield performance and stability. GGE biplot based on genotypes-focused scaling to rank genotypes relative to the ideal genotypes. Where: Genotype scores are represented by blue marks (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane) with environment scores are represented by green marks (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Eliasin 2021 cropping season and E5: Gozamen, E6: Baso-Liben; E7: Machakel and E8: Debre Elias) in 2022 cropping season.

years [68]. The relative contributions of stability and grain yield in identifying desirable genotypes, as determined by the ideal genotype procedure of the GGE biplot, were also similar to those observed in maize hybrid stability studies [69]. Both environmental and genetic factors play critical roles in determining wheat yield [70]. Environmental factors, such as temperature, rainfall, soil quality, and sunlight, directly affect plant growth, water uptake, and nutrient availability. For instance, extreme temperatures or drought can significantly reduce wheat yield by inhibiting photosynthesis and limiting grain formation [71,72].

3.4.4. Interrelationship among environments

The environment-vector view of the GGE-biplot provides detailed information regarding the discriminating ability of the environments and illustrates their relationships with one another. In this instance, an environmental vector demonstrated a high degree of genotype discrimination ability [73]. Previous studies state that the cosine of the angle between two environments is used to approximate the correlation between them: a wide obtuse angle indicates a strong negative correlation, an acute angle indicates a positive correlation and an angle close to 90° indicates no correlation [74]. Thus, if two environments are strongly correlated, the highest-yielding genotypes in one environment are likely to perform well in other environments as well. Conversely, in contrasting situations, the best-yielding genotypes in one environment may perform poorly in another, and vice versa. In the present study, as shown in Fig. 6, Gozamen and Debre Elias which have angles less than 90°, are positively correlated with each other. In contrast, the Machakel and Baso-liben environments were greater than 90°, indicating a negative correlation between them. Breeders can reduce testing costs and increase efficiency by using fewer test environments, provided they have reliable information on the similarity of environments and how they can be grouped into similar categories [62].

3.4.5. Mean grain yield and stability performance of genotypes

The genotype mean grain yield and stability performance were graphically represented using the average environmental coordination (AEC) approach (Fig. 7). Combining grain yield with genotype stability performance can help identify the genotypes that yield the highest and most stable results [73]. The genotype with the highest mean performance and greatest stability across all test environments is considered ideal [75,76]. According to the AEC view comparison biplot, a desirable genotype is located close to the ideal genotype, which is usually at the center of the concentric circles or arrows. The mean performance axis of the genotypes is represented

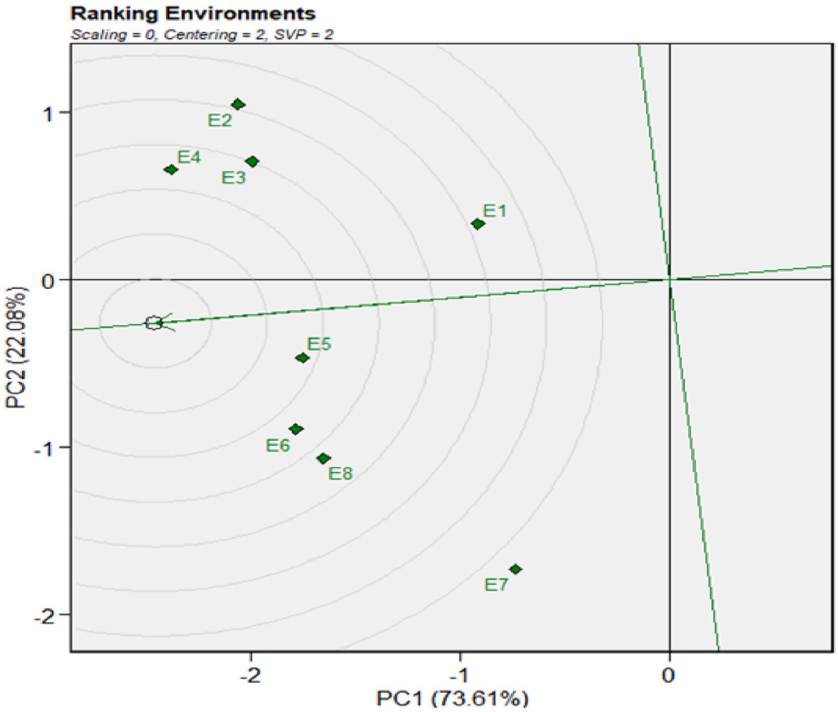

Fig. 6. The environments were ranked to identify which environment was suitable for the tested genotypes. Where: Enviroment (E1: Gozamen, E2: Baso-Liben, E3: Machakel, and E4: Debre Elias in 2021 cropping season, while E5: Gozamen, E6: Baso-Liben; E7: Machakel and E8: Debre Elias) in 2022 cropping season.

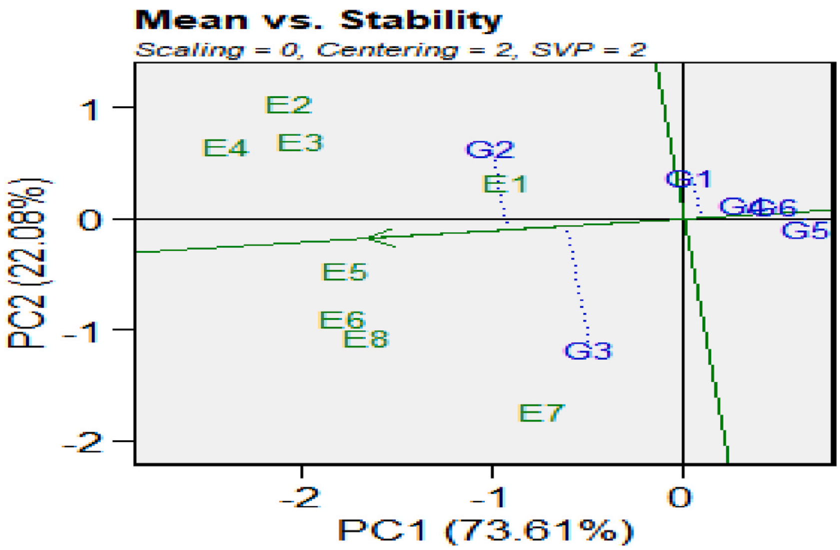

Fig. 7. Ranking varieties based on both mean and stability relative to an ideal variety for grain yield. Where: Genotype scores are represented by blue marks (G1: Danda'a, G2: Oglocho, G3: Kakaba, G4: Lemu, G5: Kingbird, G6: Wane) with environment scores are represented by green marks (E1: Gozamen, E2: Baso-Liben, E3: Machakel, E4: Debre Eliasin 2021 cropping season and E5: Gozamen, E6: Baso-Liben; E7: Machakel and E8: Debre Elias) in 2022 cropping season.

by an arrow on the AEC X-axis (PC1), which intersects the biplot origin in the Average Environmental Coordinate (AEC) system.

On the positive side of the AEC abscissa, genotypes located closer to the origin had a higher mean grain yield. In contrast, genotypes farther away from the origin on the negative side had a lower mean grain yield. Additionally, a genotype's projection becomes less stable the farther it is from the origin, in absolute terms. This trend indicates a higher mean yield across environments. In the present study, G2 yielded the highest mean yield, followed by G1, G4, and G6. The performances of the remaining genotype groups (G3 and

G5) were below the grand mean yield (Fig. 7). An ideal genotype is completely stable across a wide range of environments and has the highest average performance of any genotype [53].

Higher genotype × environment interactions and lower stability are indicated by points that lie further from the origin along this axis, in either direction [77]. Based on this, G6, G4, and G1, which had the shortest vector from the AEC axis, were identified as the most stable genotypes. In contrast, G2 and G3, with the longest vector from AEC, were classified as unstable genotypes. In contrast, G2, followed by G1, scored higher in grain yield, whereas G5 and G3 attained inferior grain yields across all environments (Fig. 7). An ideal genotype for a specific environment has the highest mean yield and responds best in that particular environment while being less stable in other environments. This necessitates recommendations for the specific environment [78]. Stability is reported to have a lower heritability than mean performance. It is important to note that stability pertains to the genotype's relative performance and is significant only when linked to the mean [79]. Environmental factors such as temperature, rainfall, and soil quality along with genetic factors like drought resistance and nutrient efficiency jointly influence yield-related parameters, including biomass, spike length, and the number of tillers. Wheat varieties with favorable genetic factors tend to perform better under various environmental conditions, resulting in improved overall yield [80,81].

3.4.6. Stability parameter

3.4.6.1. The regression coefficient. The performance of a genotype in an environment is determined by its mean performance, environment-responsiveness as a linear function, and departure from regression. A linear regression coefficient and the variance of the regression deviations to evaluate crop responses to environmental changes [82]. The average stability is indicated by a regression coefficient (bi) that approaches one and a deviation from regression (S2di) of zero. In this model, regression scores above one indicate varieties that are more sensitive to changes in the environment (below-average stability) and are specifically adaptable to high-yielding environments [83]. Conversely, regression coefficients below one enhance the specificity of adaptability to low-yielding environments by demonstrating greater resistance to environmental change (above-average stability). The present results indicated that linear regression for the average grain yield of a single genotype on the average yield of all varieties in each environment resulted in regression coefficients (bi values) ranging from 0.67 to 3.21. This variation in the regression coefficients indicates different responses of the varieties to environmental changes (Table 6). A mean regression coefficient (bi) that is close to one, minimum values for deviation from regression, and grain yields higher than the grand mean indicate that the aforementioned varieties Kingbird, Wane, Lemu, and Danda'a are well adapted to all environments, indicating broader adaptation across different environments. In contrast, Kekeba and Ogolcho, are poorly adapted to all environments. It is recommended that these varieties be cultivated under unfavorable conditions, as they demonstrate resilience to environmental variations. Several researchers reported similar findings [84].

3.4.6.2. Limitations of the study. This study has several limitations. First, while the transportation analysis assumed efficient access to the Districts, the actual distance from the zone administration presented logistical challenges not fully addressed. Additionally, environmental factors, particularly the variability in harvesting times across different crop varieties, were not controlled, which may have influenced transportation timing and efficiency.

4. Conclusions and recommendation

Analysis of genotype × environment interaction (GEI) is necessary to determine the stability and performance of varieties across different environments. The combined analysis of variance over the years showed that the varieties differed significantly for all traits, including grain yield. Variety Ogolcho, followed by Danda'a, consistently revealed higher phenotypic performance of all traits under study. A combined analysis of variance showed highly significant variation for genotypes, environments, and G × E interactions, suggesting a need for further analysis of the sources of variation in GxE × interaction. Ogolcho and Danda'a were the first and second highest-yielding genotypes, with a yield of 4.55 and 3.66-tons ha^{-1}, respectively. The results also demonstrated that the variety Danda'a could be potentially productive for specific adaptations to boost grain production in Baso liben, Kakaba at Machakele, and Gozamen. The first principal component (PC1) contributed significantly to the interaction, accounting for 73.61 %, whereas the second principal component (PC2) explained an additional 22.08 %, together accounting for 95.69 % of the genotype-by-environment interaction.

The genotype-by-environment interaction biplot analysis grouped the eight test environments and six genotypes into two mega-environments and three genotype groups. The Gozamen and Debre Elias test environments revealed good discriminating ability and representativeness, making them ideal environments that provide more information on genotype performance. The GEI analysis revealed significant differences in the stability and performance of wheat varieties across diverse environments. The GGE biplot analysis identified G6 (Wane), G4 (Lemu), and G2 (Ogolcho) as the most stable and high-yielding genotypes. Cultivating Ogolcho and Danda'a in the East Gojjam zone and other similar wheat-growing areas is recommended due to their high and moderate stability. Further exploration of genotype-by-environmental interactions can help refine the varietal selection for optimal performance in specific environments.

CRediT authorship contribution statement

Alemnesh Eskezia: Writing – review & editing, Writing – original draft, Supervision, Methodology, Formal analysis,

Table 6
The various models of stability were used to partition the G x E for grain yield in the test bread wheat varieties.

Genotypes	Mean	Bi	s2di	R2
G1	4.18	1.31	0.08	0.42
G2	4.56	3.21	0.41	0.52
G3	3.33	1.44	0.34	0.21
G4	3.06	0.97	0.08	0.3
G5	2.7	0.67	0.08	0.2
G6	2.91	1.27	0.09	0.37

$\mathbf{R^2}$ = Coefficient of determination, **bi** = Eberhart and Russell (1966) stability value of regression coefficient, and $\mathbf{S^2di}$ = Eberhart and Russell (1966) stability deviation value from regression.

Conceptualization. **Habtamu Kefale:** Writing – review & editing, Visualization, Validation, Supervision, Methodology, Investigation, Conceptualization. **Mekonen Asrat:** Writing – review & editing, Visualization, Validation, Supervision, Software, Methodology, Investigation, Data curation, Conceptualization.

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Data availability statement

The data are available upon request from the authors.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Alemnesh Eskezia reports administrative support was provided by Debre Markos University. Alemnesh Eskezia reports a relationship with Debre Markos University that includes: employment. Alemnesh Eskezia has patent pending to Pending. There is no confilict of interest If there are other authors, they 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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