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Yield Stability and Genotype × Environment Interaction of Advanced Bread Wheat (*Triticum aestivum* L.) Lines Across Environments in Southeastern Ethiopia.

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Abstract

Bread wheat is a crucial staple crop grown for food and cash across the world, including in Ethiopia. However, there are a number of environmental factors that restrict its production and productivity, which lead to yield reduction and poor adaptability. Moreover, genotype × environment interaction is a main constraint in identifying high and consistent bread wheat genotypes in terms of grain yield across production circumstances. Hence, during the 2024/25 and 2025/26 seasons, a field trial with multi-environment was conducted at three locations and two growing seasons, making up six environments in southeast Ethiopia. The experiment was conducted to test the stability and yield performance of 11 advanced bread wheat genotypes and two standard checks, Lemu and Dandea (a total of 13 genotypes). A randomized complete block design (RCBD) with three replications was used. Genotype performance and GXE interaction were characterized using combined analysis of variance, Additive Main Effects and Multiplicative Interaction (AMMI), AMMI Stability Value (ASV), Yield Stability Index (YSI), and GGE biplot. To analyze the agronomic and disease data recorded from 11 traits, R software version 4.5.2 was used. The results from the ANOVA revealed that for most of the traits, genotype, environment, and genotype-by-environment interaction (GEI) exhibited highly significant differences ($P<0.01$). AMMI1 biplot analysis revealed G4 and G11 as adaptive and high-yielding genotypes, whereas from the AMMI2 biplot and ASV analysis, G1, G12, and G7 were identified as the top three stable genotypes. The result of the yield stability index also revealed G1, G11, and G4 as the top-ranking genotypes. The two PCAs from the GGE biplot analysis explained 85.5% of the G+GE variation. G4 was a winner in four environments, and G11 was a winner in two environments, as revealed by the GGE biplot polygon. G4 was also identified as the most ideal genotype with favorable stability and high yield by both the ideal genotype view and the mean versus stability GGE biplot. Overall, G4 and G11 were identified as candidate genotypes due to their broad adaptation and yield advantage of 26.68% and 22.61% over the standard check, and they are proposed to the Ethiopian Agricultural Authority for further verification trials and potential release.

Key words: AMMI; Bread wheat; Grain yield; GGE biplot; Genotype × environment interaction; Yield stability

1. Introduction

Bread wheat (Triticum aestivum L.) belongs to the Triticeae tribe of the grass family (Poaceae) and is a hexaploid species with 2n = 6x = 42 chromosomes and an AABBDD genomic constitution. [1,2]. Due to

the large amount of land under cultivation, wheat holds the top spot among cereals and provides around 20% of the calories needed to feed the world's expanding population [3,4]. The fact that more than half of the world's population depends on wheat as a staple diet shows how important the crop is [5], and it is consumed in a multiplicity of ways, such as bread, chapatti, porridge, flour, suji, etc. For human nutrition, it also provides an essential proteins, minerals, vitamins, dietary fiber, and other phytochemicals [6–8].

In Most African countries, including Ethiopia the domestic yield of wheat is low; as a result, they have been importing a significant quantity of wheat to fulfill a required domestic wheat supply. This is the implication of finding high-yield and stable varieties [9]. Even though the productivity of bread wheat has significantly improved, meeting the needs of the world growing population, expected to reach approximately 9.8 billion by 2050, remains a significant challenge that requires further progress [10–12]. So, achieving high-yield products in existing agricultural land through improved bread wheat genotypes is crucial.

Globally, bread wheat occupies a crucial role in both production and distribution among the various wheat species [4,13]. Ethiopia produces a majority of wheat in Sub-Saharan Africa [14,15]. As a staple food in the country, the crop is primarily consumed as, injera, bread, local beer (Tella), boiled grain (Nifro), porridge (Genfo) and roasted grain (Kolo) [16]. Its straw is also widely utilized for animal feed and roofing material [17,18].

An important objective of plant breeding is to develop high-yielding, stable crop varieties [19]. According to [20] and [21], a genotype exhibiting consistent performance regardless of changes in the environment is known as a stable genotype. In addition to having a high yield potential, a newly developed variety should be stable and generally adaptable across different environments [19].

Genotype-by-environment interaction is one of the tools to determine the stability and broad adaptation of genotypes [22–24]. Plant breeders are highly interested in genotype-environment interaction (GEI) to address challenges in plant growth and development while achieving desirable yield and yield-related characteristics [25,26], which reflects the differential performance of genotypes across growing conditions, locations, and seasons [27]. Breeder can achieve rapid genetic advance before releasing the varieties by screening and selecting the genotypes that display higher stability under different environmental conditions . AMMI and GGE biplot analyses are widely used for addressing the challenges associated with data analysis from multi-environment trials [30,31].

Ethiopia harvested approximately 1.91 million hectares of wheat and produced about 6.20 million metric tons during the 2024/25 marketing year, with the average grain yield of 3.25 t/ha [32]. Despite the

substantial increase in wheat productivity in Ethiopia, the current average grain yield remains below its potential. This emphasizes the significance of evaluating genotypes over different environments to identify stable and high-yielding variety. Consequently, by using different environments in southeastern Ethiopia, evaluating the stability and yield performance of bread wheat genotypes is crucial. Therefore, assessing grain yield performance, genotype × environment interaction and yield stability of advanced bread wheat lines across contrasting environments in southeastern Ethiopia using AMMI, ASV, YSI, and GGE biplot analyses was the core objective of this study. Wheat breeding programs, agricultural extension services, and policymakers will benefit from this investigation. By utilizing the best genotypes, these stakeholders have the ability to register, release, and distribute the productive and resilient wheat genotypes in the tested region and similar agro-ecology.

2. Material and Methods

2.1. Description of The Study Area

Using 11 bread wheat advanced lines and an improved variety, 'Lemu and Dandea,' a multi-environmental field trial was conducted. The genotype was evaluated across three districts (Robe, Agarfa, and Ginir-Harawa) in the Southeast Ethiopia region for yield and yield-related traits during the 2024/25 and 2025/26 seasons under rain-fed conditions. The list and descriptions of the testing environments are shown in Table 1.

Table 1. List of testing environments with descriptions

Environment	Geographic positions		Altitude (m a.s.l.)	Temperature (°C)		Annual rainfall (mm)	Growing season rainfall (mm)	Growing-season temperature (°C)		Soil type	Soil pH	Citation
	Latit	Longt		Min	Max			Min	Max			
Robe 2024/25	07°08′N	40°03′E	2480	9.0	24.0	820	377.7	8.57	21.31	Clay-textured soil	6.5	[33]
Robe 2025/26							392.5	8.61	22.05			
Agarfa 2024/25	07°16′N	39°49′E	2550	7.3	22.8	1000	330.7	8.24	21.33	Eutric Vertisol	5.97–6.37	[34]
Agarfa 2025/26							429.7	7.63	20.61			
Ginir 2024/25	07°08′N	40°42′E	1750	12.0	27.0	750	415.7	13.00	23.91	Clay to sandy loam	5.57–6.81	[35]
Ginir 2025/26							280.4	12.94	25.68			

2.2. Experimental Material and Design

The trial was started with the screening of 320 bread wheat landraces during 2021/22 by using grain yield and disease reaction as selection criteria. Kulumsa Agricultural Research Center was the initial source of the landraces. The researchers from the Department of Plant Science, Mada Walabu University, screened the line for yield performance and disease resistance prior to evaluation of the malti environmental trial. Based on gran yield performance and disease reaction, 100 promising genotypes were selected and subjected to a preliminary yield trial (PYT) at Robe and Agarfa during 2022/23. Following preliminary yield trial evaluation, only 70 lines were selected for further evaluation at Robe and Ginir during 2023/24. Subsequently, 11 advanced lines were selected based on resistance to yellow and stem rust diseases and their yield performance. The selected line was then subjected to a multi-environmental varietal trial (MEVT) along the standard check Lemu and Dandea. The genotype codes and pedigrees of the advanced lines, together with those of the standard checks, are presented in Table 2. A randomized complete block design (RCBD) with three replications were used across the location. Each plot consisted of six rows with a 3 m length and 1.2 m width and an inter-row spacing of 20 cm. Each experimental plot covered 3.6 m² (1.2 m × 3 m), and the distances between plots and blocks were 0.5 and 1 m, respectively.

Table 2. Description of the bread wheat advanced line used in the study.

S.N.	Genotype code	Initial Code/Pedgree	Original Germplasm Source	Source of Advanced Selection Seed
1	G1	EBW1920339	KARC	MWU
2	G2	EBW192762	KARC	MWU
3	G3	Lemu (Standard Check)	KARC	MWU
4	G4	EBW192681	KARC	MWU
5	G5	KU20BWElite-17-4-164	KARC	MWU
6	G6	EBW192671	KARC	MWU
7	G7	EBW192507	KARC	MWU
8	G8	EBW192336	KARC	MWU
9	G9	Dandea (Standard Check)	KARC	MWU
10	G10	KU20BWElite-2-6-15	KARC	MWU
11	G11	EBW192610	KARC	MWU
12	G12	KU20BWElite-6-1-60	KARC	MWU
13	G13	KU20BWElite-10-8-93	KARC	MWU

Abbreviations: MWU = Madda Walabu University, KARC = Kulumsa Agricultural Research Center.

2.3. D*ata Collection*

2.3.1. Data Collected on Plant Basis

Spike Length (SL): It was measured from the main tillers of ten randomly selected plants, excluding awns. Plant Height (PH): excluding awns the average value of 10 randomly selected plants from each entry was recorded from surface to the top of spike.

Grain per spike (GPS): Ten randomly selected plants of each entry were harvested and manually threshed; the main tiller kernel was counted and the average was taken.

2.3.2. Data Collected on Plot Basis

Days to heading (DH): The period from sowing to the stage when 75% of the spikes have completely emerged.

Days to maturity (DM): The period from planting until 90% of the plot plants reach physiological maturity, indicated by yellowing of the panicle straw.

Thousand Grain Weight (TGW): pure thousand kernels were randomly selected and weighed in grams using a sensitive balance to calculate the thousand-kernel weight

Biomass Yield (BY) (tone/ha): Before threshing, the total above-ground dry matter was harvested and weighed.

Grain yield (GY) (kg/ha): was measure from overall row after grain moisture is adjusted to 12.5%. Grain moisture content was determined using a GMM mini–Moisture Tester. After that, the formula was used to adjust grain yield.

$$GY_{adj} = \frac{100 - y}{100 - x}\, GY_{uadj}$$

Where, GY_{adj}= adjusted grain yield at 12.5% moisture content, y = the actual grain moisture content of the sample measured using GMM mini–Moisture Tester, x = the standard moisture content of wheat (12.5%), and GY_{uadj}= unadjusted grain yield.

Harvest Index (HI): the grain dry weight to above-ground biomass dry weight ratio was calculated and expressed as a percentage

Yellow rust (YR) and stem rust (SR): they were recorded weekly by visual assessments and their severity were changed to single value by the relative Area Under the Disease Progress Curve (AUDPC) calculation to get a single value on a 0–100% scale[36,37]

$$\text{rAUDPC}(\%) = \frac{\sum_{i=1}^{n-1} \left[\frac{(Y_i + Y_{i+1})}{2}\right] \times (X_{i+1} - X_i)}{(X_n - X_1) \times 100} \times 100$$

Where, Y_i is the rust severity percentage at the i^{th}scoring date, ($X_{i+1} - X_i$) is the time interval (days) between consecutive scores, and ($X_n - X_1$) is the total duration of the evaluation period.

2.4. Data Analysis

2.4.1. Analysis of variance (ANOVA)

All collected raw data were subjected to R software version 4.5.2 for RCBD to determine the effects of environment, genotype, and GEI. The *stats* package [38] and aov() function of R was used to analysis the combined ANOVA. Homogeneity of variances among environments, defined as location × season combinations, was assessed using Levene's test before data were combined. The combined ANOVA was performed according to [39] using the statistical model,

$$Y_{ijk} = \mu + G_i + E_j + (GE)_{ij} + R_{k(j)} + \varepsilon_{ijk}$$

Where, Y_{ijk} is the observed value of the trait for the ith genotype in the jth environment and kth replication; μ is the grand mean; $G_i$is the effect of the ith genotype; $E_j$is the effect of the jth environment; $(GE)_{ij}$ is the genotype × environment interaction effect $R_{k(j)}$is the effect of the kth replication nested within the jth environment; and $\varepsilon_{ijk}$is the random residual error.

2.4.2. AMMI analysis

The *agricolae* package [40] in R software with AMMI () function was used to analysis AMMI according to the formula proposed by [37].

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

Where Y_{ij} is the ith genotype grain yield in the jth environment; μ is the grand mean; E_j and G_i are the environment and genotype deviations from the grand mean, respectively; λ_k is the singular value associated with the kth principal component axis (IPCA); γ_{ik} and δ_{jk} are the genotype and environment principal component scores for the kth principal component axis, respectively; N is the number of principal components retained in the model; and ε_{ij} is the residual term.

The degrees of freedom (df) for each IPCA were calculated using the following simple method proposed by [41].

$$DF_{\mathrm{n}} = G + E - 1 - 2n$$

Where n is the order of the IPCA axis, G is the number of genotypes and E is the number of environments.

2.4.3. AMMI stability value (ASV) and Yield stability index (YSI) analysis

AMMI stability value (ASV) ranks and quantifies genotypes based on yield stability, but it is not a quantitative stability index[42]. Lower ASV genotypes are regarded to be more stable, while higher ASV genotypes are believed to be less stable [43]. AMMI stability value (ASV) and yield stability index (YSI) were calculated using the package agricolae in R Studio version 4.5.2 [40]. The ASV was calculated according to [44], while the YSI was calculated following the procedure described by [45] as follows:

$$ASV = \sqrt{\left\{\frac{SS_{IPCA1}}{(IPCA1_i)^2} + \frac{SS_{IPCA2}}{(IPCA2_i)^2} + \frac{SS_{IPCA3}}{(IPCA3_i)^2}\right\}}$$

Where: ASV = AMMI stability value; SS_{IPCA1} = sum of squares explained by the first interaction principal component axis, and SS_{IPCA2} = sum of squares explained by the second interaction principal component axis, SS_{IPCA3} = sum of squares explained by the second interaction principal component axis; $IPCA1_i$ = IPCA1 score of the ith genotype; $IPCA2_i$ = IPCA2 score of the ith genotype; $IPCA3_i$ = IPCA3 score of the ith genotype

By using the data obtained from 13 bread wheat genotypes, which were tested across six environments, the Yield Stability Index (YSI) was analyzed using the formula:

$$YSI = RASV + RY$$

Where: RY= mean grain yield rank of genotypes from different environments and RASV = AMMI stability value rank.

2.4.4. GGE biplot analysis

GGE biplot was analyzed using R software version 4.5.2, package *metan* [46] and function gge() on the basis of grain yield according to the model described by [47]

$$Y_{ij}^{*} = Y_{ij} - \bar{Y}_{.j} = \sum_{n=1}^{N} \lambda_n \alpha_{in} \gamma_{jn} + \varepsilon_{ij}$$

Where: = environment-cantered grain yield of genotype i in environment j, Y_{ij}= mean grain yield of genotype i in environment j, $\bar{Y}_{.j}$= mean grain yield of all genotypes in environment j, λ_n= singular value associated with the n^{th}principal component, α_{in}= genotype score for genotype i on PC n, γ_{jn}= environment score for environment j on PC n, N= number of principal components retained in the model, ε_{ij}= residual not explained by the retained principal components.

3. Results

3.1. Analysis for variance

Analysis of variance for the main effect of genotype and environments and combined data across the six environments (three locations over two seasons) is presented in Table 3. Accordingly, the ANOVA results for the main genotype effect indicated highly significant differences ($P < 0.01$) among genotypes across all traits evaluated, confirming the presence of genotypic variability for yield and its components.

The combined ANOVA from genotype by environment interaction was also highly significant ($P<0.01$) for all the traits considered, and significant ($p<0.05$) for days to heading and plant height. This indicates that the bread wheat genotypes considered performed differently across different environmental conditions and importance of environment-specific variety selection.

Table 3. Mean squares from the combined analysis of variance for grain yield, yield components, and disease parameters of 13 bread wheat genotypes evaluated across six environments

Source	Df	DH	DM	PH	SL	NGPS	TSW	GY	BY	HI	SR	YR
Rep (E)	12	1.5 ns	10.7 ns	50.8**	1.8**	51.5**	11.6**	1.3**	2.6ns	19.2*	15.3ns	20.21ns
Env	5	100.7**	3895.5**	7452.7**	14.2**	1457.9**	753.6**	11.5**	43.9**	132.6**	316.1**	1638.1**
G	12	321.7**	607.9**	201.7**	10.4**	492.2**	146.6**	10.3**	35.9**	134.2**	10186.9**	10632.6**
G × E	60	4.2*	17.6**	23.7*	0.4**	42.9**	9.1**	1.2**	5.3**	24.9**	89.3**	62.4**
Error	144	2.72	6.37	14.81	0.20	18.06	4.82	0.33	1.67	9.14	24.46	27.44

Where: DH=days to 50% heading, DM=days to 75 % maturity, PH=plant height (cm), SL=spike length (cm), NGPS= numbers of grain per spike, TSW=thousand seed weight (gm), GY= grain yield, BY= biomass yield(tone), HI= harvest index**, d**isease assessment was recorded on 0-100 scale, where 0=resistant and 100= susceptible, SR = stem rust, YR = yellow rust

3.2. Ranges and Average Mean Performance of the Advanced Bread Wheat Selection

The estimated range and mean of the 11 traits studied are presented in Table 4. Considering the phenological characteristics considered, DH and DM, the genotypes can be categorized into three groups: early, late, and intermediate stages. Accordingly, days to heading ranged from 61 to 75 days with a mean value of 68. G13 completed 50% heading after 75 days from sowing, which was the longest among all genotypes studied, whereas G9 headed earlier after 61 days of sowing. Days to maturity ranged from 120 to 138, in which G5 had the longest days to maturity at 138 days, followed by G13, which get matured in 137 days. Some genotypes have different intervals of days of heading and days to maturity, and this difference implied the genotype grain-filling period variation which offers better options for selection.

The tested genotypes also showed broad range of variation with regard to plant height (86.03 cm for G1 to 95.97 cm for G5 with a mean value of 91.11). The top yielder genotypes, G4 and G11, exhibited an intermediate plant height of 86.52 cm and 94.79 cm respectively.

The genotypes likewise exhibited substantial variation in grain yield. Similar variation was also observed in its component traits, including TSW, BY, and HI. Accordingly, the yield varies from 4.63 to 7.18 t/ha, with a mean value of 5.71. The best grain yield (7.18 t/ha) was obtained from G4, followed by G11 (6.94 t/ha), G5 (6.12 t/ha), and G1 (5.98 t/ha), while the lowest yield was recorded in G13. The two standard checks, Lemu and Denda, yield 5.67 t/hac and 4.91 t/hac, respectively. G4 and G11 showed a yield advantage of 26.68% and 22.61% over the standard check genotype Lemu. These findings are crucial for breeding strategies aimed at increasing crop yield and adaptability.

Stem rust disease severity ranged from 7.28% to 76.67%, with a mean of 26.69%, whereas yellow rust severity ranged from 3.29% to 74.44%, with a mean of 27.36%. A moderately resistant reaction to both stem rust and yellow rust diseases was shown by more than half of the genotypes, indicating that a significant portion of the tested genotypes possesses valuable genetic resistance to both diseases. Among the top three high-yielding genotypes, G4 demonstrated highly resistant reactions, with severity levels of 7.28% for stem rust and 6.72% for yellow rust. G11 exhibited moderate resistance, with severity levels of 19.18% for stem rust and 17.06% for yellow rust. G5 exhibited a highly resistant response to yellow rust, with a severity of 3.29%, while it was moderately susceptible to stem rust, recording a severity of 46.11%. This implies that resistance to one type of rust disease does not automatically suggest resistance to another type.

Table 4. Mean of major agronomic and disease traits of wheat genotypes evaluated at Robe, Agarfa and Ginir during 2024/25 and 2025/26 cropping season.

Genotype	DH	DM	PH	SL	NGPS	TSW	BY	GY	HI	Disease (0-100)	
										SR	YR
G1	64.39^{b}	123.83^{b}	86.03^{a}	8.18^{a}	47.28^{c}	46.40^{a}	15.17^{bc}	5.98^{bc}	39.26^{bc}	20.89^{g}	34^{e}
G2	66.78^{f}	125.22^{gh}	89.84^{bc}	8.89^{g}	43.78^{f}	46.71^{a}	15.50^{ab}	5.79^{bc}	37.34^{cde}	20.33^{fg}	19.11^{c}
G3	69.17^{cd}	132.61^{c}	94.17^{a}	9.97^{c}	54.96^{ab}	42.88^{c}	14.42^{cd}	5.67^{cd}	39.30^{bc}	16.31^{de}	3.93^{a}
G4	70^{e}	132.33^{c}	86.52^{d}	8.91^{fg}	55.26^{a}	43.65^{bc}	16.32^{a}	7.18^{a}	43.99^{a}	7.28^{a}	6.72^{ab}
G5	73.39^{b}	138.39^{a}	95.97^{a}	9.53^{d}	48.55^{de}	46.85^{a}	15.73^{ab}	6.12^{b}	38.95^{bcd}	46.11^{h}	3.29^{a}
G6	73.67^{b}	134.44^{b}	93.97^{a}	9.22^{e}	52.19^{bc}	45.96^{a}	15.55^{ab}	5.78^{bc}	37.20^{de}	75.00^{i}	4.36^{ab}
G7	67.83^{ef}	128.39^{de}	89.35^{bc}	10.27^{b}	55.52^{a}	40.96^{d}	15.58^{ab}	5.80^{bc}	37.23^{de}	10.83^{b}	44.22^{f}
G8	67^{f}	126.17^{fg}	95.02^{a}	8.53^{h}	44.16^{f}	39.22^{f}	14.42^{cd}	5.32^{de}	37.06^{de}	76.67^{i}	29.67^{d}
G9	61.22^{h}	121.00^{i}	89.95^{bc}	9.53^{d}	42.62^{fg}	40.71^{de}	13.73^{d}	4.91^{fg}	35.70^{e}	12.56^{bc}	74.44^{h}
G10	62^{h}	120.39^{i}	90.87^{b}	8.28^{hi}	39.95^{g}	39.92^{def}	11.97^{e}	4.87^{fg}	40.59^{b}	10^{ab}	67.78^{g}
G11	70.17^{c}	129.78^{d}	94.79^{a}	10.60^{a}	53.45^{ab}	44.48^{b}	15.56^{ab}	6.94^{a}	44.64^{a}	19.18^{efg}	17.06^{c}
G12	68.33^{de}	127.28^{ef}	90.20^{bc}	9.20^{ef}	50.48^{cd}	42.63^{c}	14.29^{d}	5.21^{ef}	36.52^{e}	14.42^{cd}	43.44^{f}
G13	74.89^{a}	137.50^{a}	87.85^{cd}	10.01^{bc}	50.61^{cd}	39.40^{ef}	11.79^{e}	4.63^{g}	39.28^{bc}	17.36^{def}	7.67^{b}
Range	61.22–74.89	120.39–138.39	86.03–95.97	8.18–10.60	39.95–55.52	39.22–46.85	11.79–16.32	4.63–7.18	35.70–44.64	7.28–76.67	3.29–74.44
Mean	68.38	128.92	91.11	9.32	49.15	43.05	14.62	5.71	39.01	26.69	27.36
LSD	1.08	1.66	2.54	0.29	2.80	1.4	0.38	0.85	1.99	3.26	3.45
CV	2.41	1.96	4.22	4.82	8.65	5.10	10.07	8.85	7.75	18.53	19.15

Means with the same letters are not statistically significant. Where: DH=days to 50% heading, DM=days to 75 % maturity, PH=plant height (cm), SL=Spike length (cm), NGPS= numbers of grain per spike, TSW=thousand seed weight (gm), GY= grain yield, BY= Biomass Yield(tone), HI= Harvest Index**,** Disease assessment was recorded on 0-100 scale, where 0=resistant and 100= susceptible, SR = Stem Rust, YR = Yellow Rust

Table 5. Grain yield (t/ha) of wheat genotype at Robe, Agarfa and Ginir in 2024/25 and 2025/26 cropping seasons

Genotypes	Robe		Agarfa		Ginir		Mean Grain	Yield
	2024/25	2025/26	2024/25	2025/26	2024/25	2025/26	yield (t/ha)	Adv. (%)
G1	6.63	6.39	5.01	5.60	6.97	5.26	5.98	
G2	5.57	6.55	5.87	5.31	6.44	4.98	5.79	
G3	6.13	6.94	5.32	5.02	5.73	4.86	5.66	
G4	7.25	7.59	7.99	7.06	7.35	5.78	7.17	26.68
G5	7.53	6.86	5.95	5.17	6.91	4.32	6.12	
G6	6.79	6.63	6.07	5.03	6.13	4.06	5.79	
G7	7.03	6.06	5.45	5.22	5.97	5.05	5.80	
G8	6.14	5.22	4.63	5.61	5.25	5.06	5.32	
G9	6.30	3.54	3.96	5.10	5.71	4.85	4.91	
G10	5.33	4.58	3.89	5.93	4.59	4.89	4.87	
G11	7.24	7.14	6.68	7.36	6.77	6.47	6.94	22.53
G12	5.54	6.01	4.54	5.43	5.44	4.31	5.21	
G13	4.79	6.48	3.80	4.10	4.62	3.97	4.63	
Mean	6.33	6.15	5.33	5.53	5.99	4.91	5.87	
LSD	1.27	0.86	0.89	1.15	0.69	0.81	0.98	
CV	11.88	8.33	9.95	12.35	6.86	9.77	13.44	
F-Value	**	**	**	**	**	**	**	

3.3. Additive Main Effect and Multiplicative Interaction (AMMI) Analysis

Highly significant differences were shown by the AMMI analysis of variance for grain yield among the main effects of genotypes, environment, and GEI with variance sum of squares of 48.79, 22.66, and 28.55 in that order (Table 5). The result indicated that there is considerable genetic variation among the 13 genotypes, that performed differently across the six environments. Interaction principal component analysis (IPCA) was utilized to further decompose the genotype × environment interaction (GEI). The result showed that the first three IPCA explained 52.31%, 24.35%, and 14.71% of the total variation, respectively, with a total variation of 91.38. The ordination approach identified highly significant ($p < 0.001$) effects for the first three IPCA axes, suggesting that the GEI contained a lot of statistically significant interaction patterns.

Table 6. AMMI analysis of variance for grain yield among 13 bread wheat genotypes evaluated across three environments

Source of variation	df	SS	MS	% Total variation (SS) explained	% G×E explained	% G×E cumulative
Genotype	12	123.813	10.318**	48.79		
Environment	5	57.509	11.502**	22.66		
G × E	60	72.441	1.207**	28.55		
IPCA1	16	37.893	2.368**		52.31	52.31
IPCA2	14	17.643	1.260**		24.35	76.66
IPCA3	12	10.659	0.888**		14.71	91.38
IPCA4	10	4.398	0.440 ns		6.07	97.45
IPCA5	8	1.848	0.231 ns		2.55	100.00

3.4. Additive Main Effects and Multiplicative Interaction (AMMI) Biplot Analysis

3.4.1. AMMI Biplot Analysis

The AMMI1 and AMMI2 biplots, which illustrate the relationships between environments and genotypes were shown in Figures 1 and 2, respectively. The AMMI1 biplot revealed significant genotypic differences in both direction and magnitude along the X-axis (yield) and Y-axis (IPCA1 score). In this biplot, the IPCA1 explains 52.3% of the total GEI pattern. Accordingly, the genotype with a large absolute value of the IPCA1 score contributes more to the GEI pattern and vice versa. Robe-2024, Robe-2025, and Ginir-2024 have relatively high environmental means associated with high-yielding genotypes such as G4, G11, G5, G1, and G7, whereas Agarfa-2024, Agarfa-2025, and Ginir-2025 were associated with lower-yielding genotypes such as G13, G10, G9, G8, and G12 (Fig. 1). The superior performance of certain genotypes under particular environmental conditions demonstrates the role of genotype × environment interaction in grain yield determination.

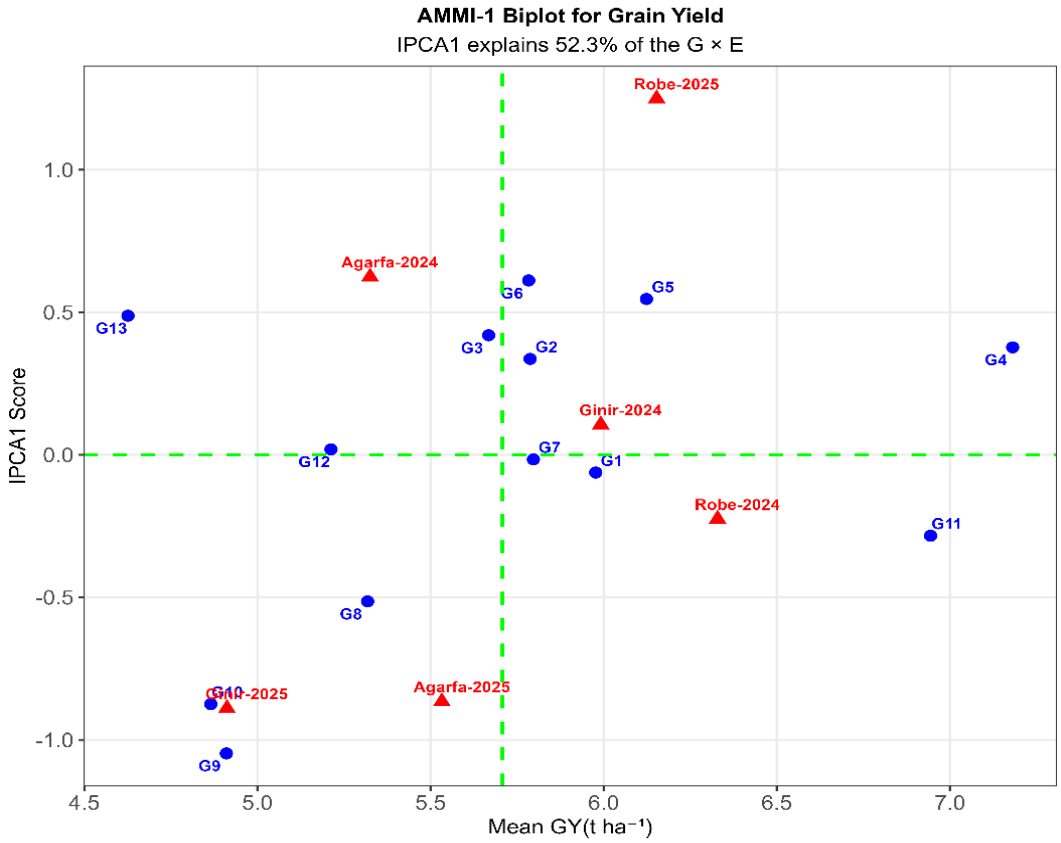

Figure 1. AMMI$_1$ biplot for grain yield of the 13 bread wheat genotypes evaluated at six Environments

3.4.2. AMMI$_2$ Biplot Analysis

In AMMI2, the first two IPCAs were explained by 76.7% of the total interaction pattern (Fig. 2). The genotypes close to the origin have small magnitudes of GEI patterns, meaning they are relatively stable in that particular environment. Similarly, an environment close to the origin has a relatively small interaction pattern with the genotype. Accordingly, G1, G12, G7, and G4 are the genotypes closest to the origin; partly suggesting their being having relative stability. With regard to test environments, Ginir-2024 is relatively closer to the origin than the other environments, which could signpost its relatively smaller interaction pattern with the genotype. On the other hand, the genotype and environment in the opposite direction have negative interaction patterns, while positive interaction pattern was exhibited between genotype and environment in the same direction. Accordingly, G5 and G6 exhibited the same interaction direction with Agarfa-2024 and Ginir-2024, while G9 showed a similar interaction direction with Robe-2024. Likewise, G10 showed a similar interaction pattern with the Ginir-2025 and Agarfa-2025 (Fig. 2).

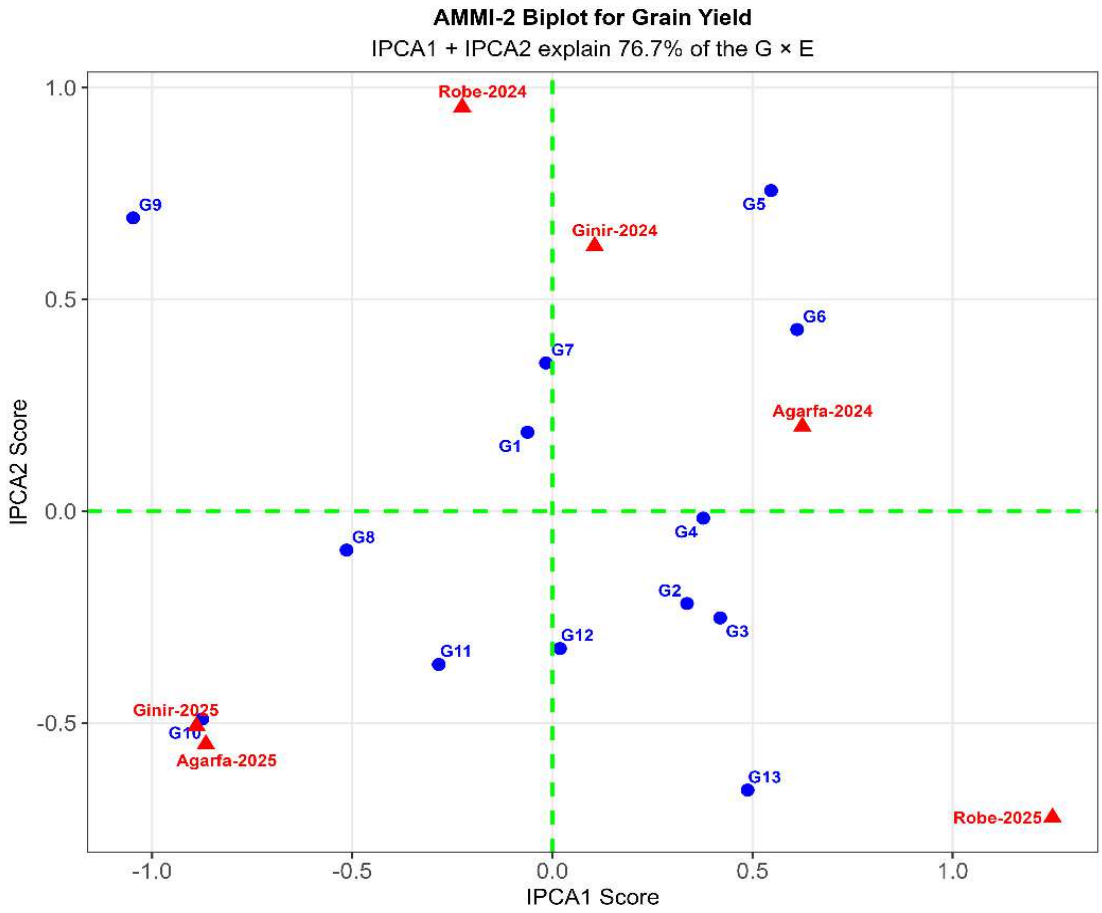

Figure 2. AMMI$_2$ biplot for grain yield of 13 bread wheat genotypes evaluated across six environments

3.5. AMMI Stability Value (ASV) and Yield Stability Index (YSI)

Table 7 presents the ASV and YSI results for the 13 genotypes evaluated across six environments. The results reveal that G4 (7.18 t ha^{-1}) is ranked first for its high grain yield performance, followed by G11, G5, and G1, while G13, G9, and G10 are the least ranked genotypes, respectively. On the other hand, the minimum AMMI Stability Value (ASV) score for grain yield was exhibited by G1 (0.23), followed by G12, G7, and G11, whereas genotype G9 exhibits the highest instability, with an ASV value of 2.35, followed by G10, G5, and G6. This suggests that while genotypes with low ASV may exhibit high stability across different environments, stable genotypes do not necessarily have high mean yield performance.

From yield stability index results shown in table 7, G1, G11, G4, G7, and G2 were the five top-ranking genotypes, exhibiting both stability and strong grain yield performance. According to [41] and [49], the ideal genotype should exhibit both a high stability and high average grain yield. On the other hand, G9 and G10 demonstrated the lowest grain yield performance and the highest instability and ranked the least (Table 7).

Table 7. Mean grain yield, AMMI stability value (ASV), and yield stability index (YSI) with their respective ranks and IPCA for 13 bread wheat genotypes evaluated across six environments

Genotype	Mean (t ha^{-1})	GYR	ASV	RASV	YSI	RYSI	IPCA1	IPCA2	IPCA3
G1	5.98	4	0.23	1	5	1	-0.06	-0.19	-0.47
G2	5.79	6	0.76	5	11	5	0.34	0.22	0.24
G3	5.67	8	0.93	7	15	8	0.42	0.25	-0.25
G4	7.18	1	0.81	6	7	3	0.38	0.02	0.97
G5	6.12	3	1.39	11	14	7	0.55	-0.76	-0.20
G6	5.78	7	1.38	10	17	9	0.61	-0.43	0.20
G7	5.80	5	0.35	3	8	4	-0.02	-0.35	-0.14
G8	5.32	9	1.11	8	17	9	-0.51	0.09	-0.01
G9	4.91	11	2.35	13	24	12	-1.05	-0.69	-0.08
G10	4.87	12	1.94	12	24	12	-0.88	0.49	0.10
G11	6.94	2	0.71	4	6	2	-0.28	0.36	0.34
G12	5.21	10	0.33	2	12	6	0.02	0.32	-0.09
G13	4.63	13	1.22	9	22	11	0.49	0.66	-0.61

Where: GYR= Grain yield rank; ASV=AMMI stability value; RASV= AMMI stability valuer rank = YSI=Yield stability index; RYSI - Yield stability index rank.

3.6. Genotype Plus Genotype by Environment Interaction (GGE) Biplot Analysis

3.6.1. Which-Won-Where

To GGE biplot analysis was used to identify the most promising genotypes and determine their stability across different environments. This method provides a useful way to visualize genotype performance and genotype × environment interaction [50]. The genotypes farthest from the origin, known as vertex genotypes, are connected to form a polygon in the GGE biplot, while the remaining genotypes are enclosed within it. A vertex genotype is the potential winning genotype for different mega environments, which are pointed at the end edge of the polygon [51,52]. In the present study, the first two principal components (PC1 and PC2) accounted for 68.6% and 16.9% of the G + GE variation, respectively, explaining 85.5% of the total variation captured by the GGE biplot (Fig. 3). In the polygon biplot analysis, seven genotypes (G4, G5, G6, G9, G10, G11, and G13) are located on the vertices and forming the polygon indicating different response patterns among the genotypes. However, only G4 and G11 have a winning environmental sector, and the rest of the genotypes have no tested environmental sector. G4 is

a winner in four environments (Robe-2025, Agarfa-2024, Ginir-2024, and Robe-2024), and G11 is a winner in two environments (Ginir-2025 and Agarfa-2025). This finding implies the six tested environments were differentiated into two major genotype-response sectors, with G4 and G11 being the respective winning genotypes (Fig. 3).

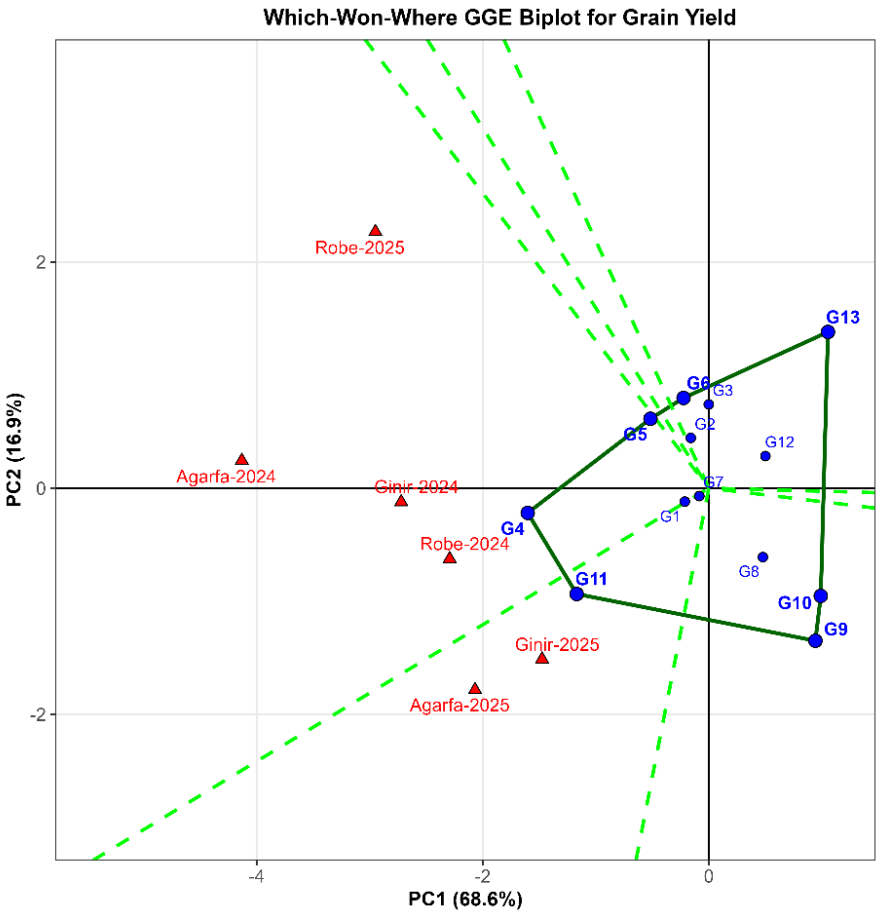

Figure 3. Polygon view of GGE biplot (which–won–where) for the 13 bread wheat genotypes evaluated across three locations and two seasons, representing six environments

3.6.2. Association among the Environments

In the GGE biplot under the environment vectors model, the lines joining the test environment to the origin of the biplot are called environment vectors. The similarity between two environment vectors can be assessed from the cosine of the angle separating them [48,53–55]. The vector view of the GGE biplot (Fig. 4) gives a quick summary of how the environments in this study are correlated. All the six environments are positively correlated with different strengths of the association among environment pairs. From the enter-vector angle of the biplot (Fig. 4), there are strong positive associations between Ginir-2025 and Agarfa-2025, Agarfa-2024 and Ginir-2024, and Ginir-2024 and Robe-2024, due to the

small vector angles between the environments. This indicates that genotypes exhibited similar responses among correlated environments and tended to preserve a similar relative performance across them.

3.6.3. Discriminating Power and Representativeness of the Tested Environments

To evaluate the discriminating ability and representativeness of environments, each environment is linked to the biplot origin (Fig. 4). Accordingly, Agarfa-2024 and Robe-2025 have the longest environmental vector, implying their high discriminating ability. On the other hand, Ginir-2025, which has the shortest environmental vector, has the lowest discriminating ability. This suggests that the environment's genotype discriminating power is based on their genotypic performance[48,56]. In terms of representativeness, Ginir-2024 and Robe-2024, followed by Agarfa-2024, showed greater representativeness of the overall target environment due to their smallest angular deviations from the AEC axis.

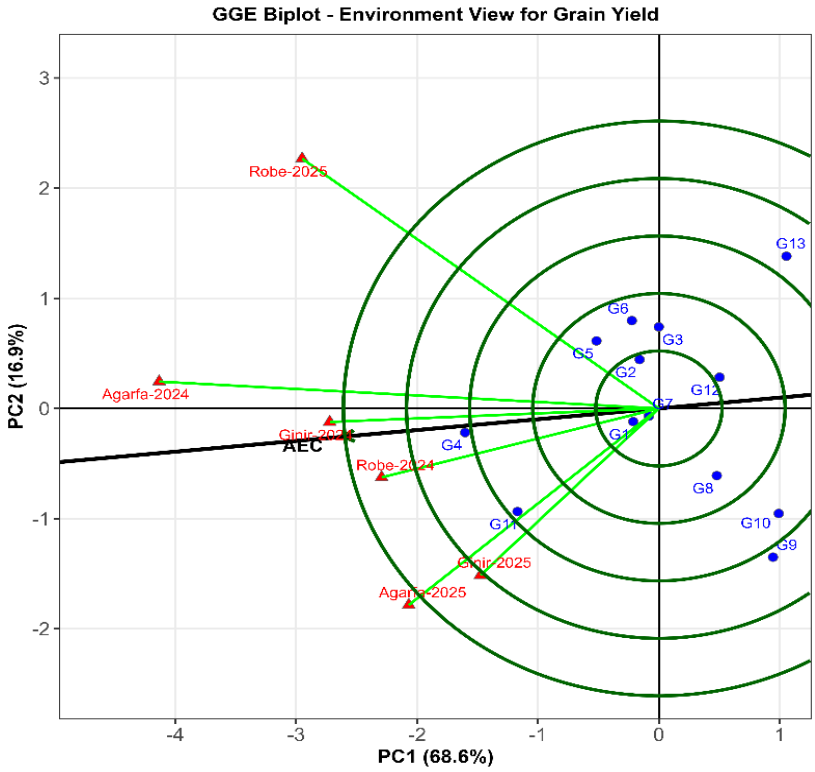

Figure 4. Environment view of GGE biplot for the 13 bread wheat genotypes evaluated at three locations over two seasons (six environments)

3.6.4. Evaluation of the Genotype Relative to the Ideal Genotype

In addition to identifying the best testing environments, GGE biplot analysis also plays a crucial role in selecting and releasing the best genotypes. In the GGE biplot presented in the current study (Fig. 5), G4 falls within the first concentric circle, indicating the most favorable combination of high grain yield and stability among the 13 tested genotypes. Genotype G11 exhibited relatively greater proximity to the ideal genotype (G4); consequently, it was considered the next most preferred genotype among the tested bread

wheat genotypes after G4. Genotype G13, which recorded the lowest grain yield, was identified as the least desirable genotype because of its considerable distance from the ideal-genotype target. Similarly, G9 and G10 are far away in the lower-right region.

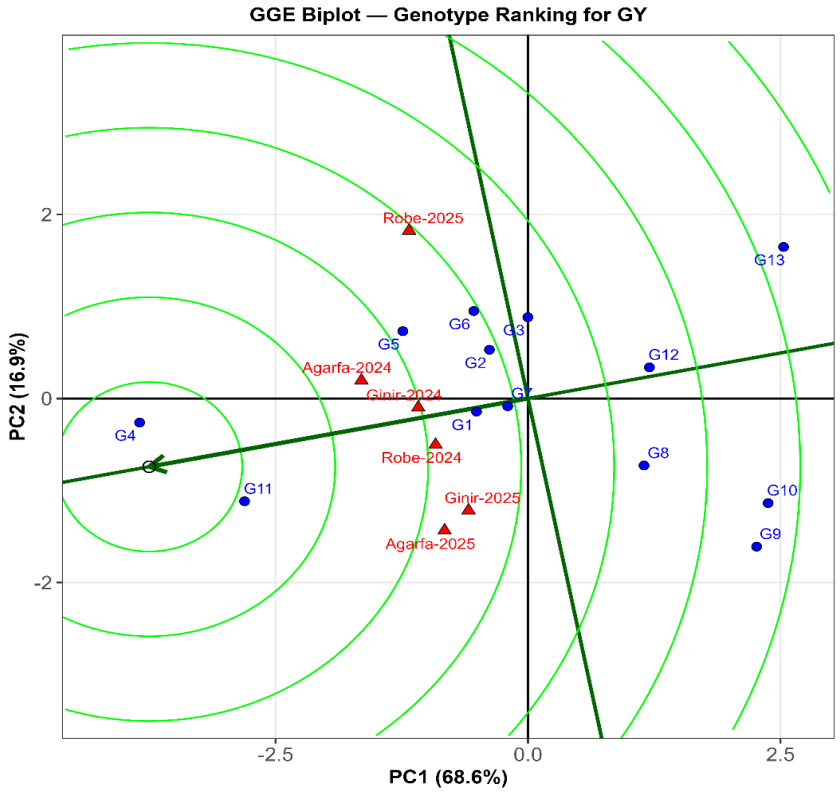

Figure 5. The ideal genotype view of GGE biplot for the 13 bread wheat genotypes evaluated across three locations and two seasons, comprising six test environments

3.6.5. Mean Grain Yield and Stability Performance of the Genotypes

An average environment coordination (AEC) is an important method in plant breeding and variety selection, as it is a useful approach for assessing genotype stability based on its performance across diverse environments [57]. In the present study, there is a horizontal axis that runs from the lower-left toward the upper-right, with the arrowhead toward the lower-left (Fig. 6). This axis represents increasing mean performance and is termed the AEC abscissa. Another line, extending through the biplot origin and perpendicular to the AEC abscissa, is referred to as the AEC ordinate. Varieties on the positive side of the AEC abscissa, which are located furthest from the origin, are associated with higher mean grain yield, while those on the negative side of the AEC abscissa, which are located furthest from the origin, are associated with lower mean grain yield. Accordingly, G4 recorded the greatest mean grain yield, with G11, G5, G1, and G7 ranking successively thereafter. Genotypes G1 and G7 are the stable genotypes with yield performance closer to the average grain yield, while G12 is the stable genotype with yield

performance below the average grain yield. The biplot also reveals that G9, G10, and G13 are identified as unstable genotypes with poor grain yield. Overall, based on their stability and satisfactory yield performance, G4 and G11 were the preferred genotypes among the 13 tested bread wheat (Fig. 6).

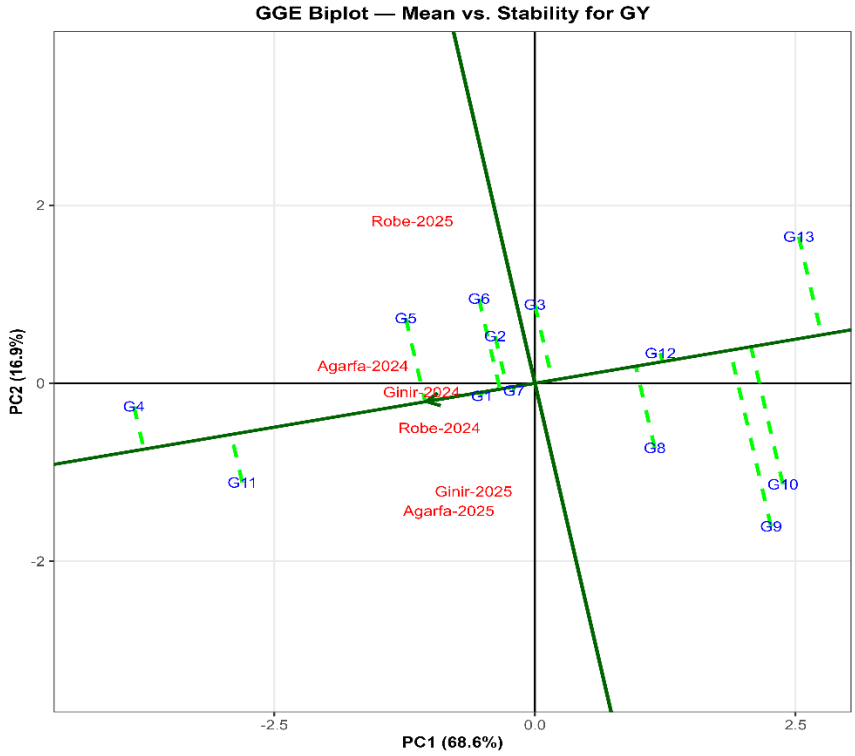

Figure 6. Mean Versus stability view of GGE biplot for the 13 bread wheat genotypes evaluated at three locations over two seasons (a total of six environments)

4. Discussion

The present study integrated the assessment of grain yield, disease response, and genotype stability. Such integration is eminent for understanding the adaptive performance of our test genotypes and identifying promising lines for further breeding and cultivar development. The key findings have practical implications for selecting high-yielding, disease-resistant, and broadly adapted genotypes under the heterogeneous growing conditions of Ethiopia in general and southeastern Ethiopia in particular. The findings are contextualized and presented in the following sections.

4.1. Patterns and Implications of the Genotypic Variation, Yield Performance and GEI

In the present study, the tested advanced bread wheat genotypes showed a significant variation for agronomic, yield-related, and disease-response traits suggesting a substantial genetic diversity within the genotypes. For example: the wide range observed in grain yield (4.63 to 7.18 t ha^{-1} with grand mean of 5.71 t ha^{-1}) suggest a good opportunity for selecting superior materials. Similar results have been reported on bread wheat tested across diverse environments in the country [43–45,47,48]. The existence of such

wealth of variations is fundamental to breeding as it provides the basis for improving productivity, adaptation, and resistance to major production constraints including disease.

On the other hand, the significant environmental effects observed for grain yield and most other traits indicate substantial differences among the six test environments. In this regard, the spatial and temporal variations observed have a particular relevance in southeastern Ethiopia, where differences in rainfall, temperature, altitude, soil conditions, and growing-season characteristics can influence wheat performance. The significant GEI further demonstrated the inconsistency of genotype rankings across environments. For example, grain yield scored 48.79% for genotype, 22.66% for environment, and 28.55% for GEI of the total variation suggesting substantial contribution of GEI that signpost importance of considering environmental responsiveness while selecting superior genotypes regardless of the genotype being the largest component. Similar results have been reported on Ethiopian bread wheat trials [43–45,54,58].

Moreover, the present study revealed wide variation in phenology and plant architecture which further suggest differences in adaptation among the genotypes considered. For example: the wide variation in days to heading (61.22 to 74.89 days) and days to maturity (120.39 to 138.39 days) could provide a good opportunity for matching genotypes with environments differing in growing-season length and terminal moisture availability. Other considerable variations in plant height, spike length, grains per spike, thousand-seed weight, biomass yield, and harvest index also offer opportunity for further breeding activities targeting improvement. From among the genotypes considered, G4 combined the highest grain yield with relatively short plant height (86.52 cm), while G11 combined high yield with intermediate plant height. The shorter plant height of G4 could be favored where lodging is a concern and vice versa for G11.

From among the traits considered, grain yield clearly showed differences in the genotypes. For example: G4 produced the highest mean yield (7.18 t ha^{-1}), followed by G11 (6.94 t ha^{-1}), G5 (6.12 t ha^{-1}), and G1 (5.98 t ha^{-1}), whereas G13 produced the lowest yield (4.63 t ha^{-1}). Such relatively superior performance of G4 and G11 is important as the good performance of both genotypes is supported by stability and GGE analyses which represent a more meaningful breeding signal. The result further supports the reports indicating the importance of evaluating productivity together with adaptation and stability rather than relying on mean yield alone[43,48,54,59].

4.2. Patterns of Disease Response and its Implications for Genotype Selection

The present study revealed a wide range of variation in stem rust and yellow rust severities among the genotypes tested which could be used as additional evidence for the presence of considerable genetic

variations among the genotypes. For example, the broad range of variation in stem rust severity (7.28 to 76.67%) and yellow rust severity (3.29 to 74.44%) indicates substantial differences in disease response. The variation provides good opportunities for selection and incorporation of favorable resistance into wheat improvement programs.

With regards to the genotypes tested, G4 which showed a superior grain yield was again accompanied by low stem rust (7.28%) and yellow rust (6.72%) severities. Similarly, G11 showed relatively favorable stem rust (19.18%) and yellow rust (17.06%) responses. Such combinations of productivity and disease response further increase the breeding value of G4 and G11 as compared to genotypes having good performance in only one of those parameters. Hence, the result provides an additional reason to prioritize G4 and G11 for further evaluation. On the other hand, G5 which is the third top for grain yield (6.12 t ha^{-1}) a contrasting performance for disease response (very low yellow rust severity or 3.29% but relatively high for stem rust severity or 46.11%). Such contrasting response could evidence the fact that favorable performance against one rust disease cannot necessarily be interpreted as broad-spectrum rust resistance.

In general, the results support the argument suggesting the importance of considering multiple traits together while selecting genotypes for further advancements. Based on the present supportive evidence, further dedicated disease-screening experiments under controlled or high-pressure conditions are needed to confirm the resistance of promising genotypes.

4.3. Implications of AMMI, Stability Analysis and Identification of Adapted Genotypes

In the present study, AMMI analysis again confirmed genotype, environment, and GEI as significant sources of variation in grain yield, one of the important traits. In this regard, the first three interaction principal component axes explained 91.38% of the GEI, with IPCA1, IPCA2, and IPCA3 accounting for 52.31%, 24.35%, and 14.71%, respectively. IPCA1 took the largest share and contain a substantial proportion of the interaction supporting the usefulness of AMMI for interpreting differential genotype responses. There are similar reports suggesting usefulness of IPCA1 [48,54,60,61]

The AMMI1 analysis further showed the association of several genotypes (some are identified as good yielding) such as G4, G11, G5, G1, and G7, with relatively favorable environments. On the contrary, several lower-yielding genotypes such as G13, G10, G9, G8, and G12 were found associated with less productive environments. The observed pattern clearly shows the relatedness of environmental productivity and genotype responsiveness which further confirms the limitation of identifying best genotype from overall mean yield alone. On the bases of AMMI2 and ASV, which further differentiated genotypes according to stability, G1 scored the lowest ASV (0.229), followed by G12 (0.327) and G7

(0.352), indicating comparatively small interaction effects and relatively stable performance across environments. There are similar reports indicating the ability of AMMI2 and ASV in identifying stable genotypes [52,60,61].

However, the most stable genotype, G1 had a moderate mean yield (5.98 t ha^{-1}) as compared to G4 which showed the highest yield but intermediate ASV (0.810). The result once again confirms the loose paralalessim between stability and productivity and the limitation of selecting genotypes using stability alone. Thus, using YSI analysis which provides a more integrated assessment by considering both yield and stability is eminent. In this regard, five genotypes: G1, G11, G4, G7, and G2, in that order, were among the best genotypes, with G11 showing an especially favorable balance (second for mean yield, fourth for ASV, and second for YSI). The first ranked G4 was third for YSI. In general, the results are in agreement with several reports suggesting the use of complementary stability approaches rather than relying on a single statistical criterion [48,54,58,61].

The combined AMMI, ASV, and YSI analysis were used to distinguish between genotypes suitable primarily as candidate cultivars and those that may be valuable as breeding parents. Accordingly, the combined analysis identified two genotypes, G4 and G11, were identified as promising materials for further improvement programs. On the other hand, the combined analysis signaled G1 and G7 as broadly adapted genotypes and hence potential materials for targeted advancements. The exceptionally low ASV revealed by G1 could be valuable in breeding populations where predictable performance across environments is an important objective.

4.4. GGE Biplot Analysis, Mega-environments and Genotype Adaptation

GGE biplot analysis was made to get complementary information on genotype performance and GEI. Accordingly, the largest variation (85.5% of the G+GE variation) was explained on the first two principal components (PC1 = 68.6% and PC2 = 16.9%) suggesting that the two-dimensional biplot captured most of the relevant variation for interpreting genotype adaptation. There are similar reports on wheat suggesting ability of the first two biplots in capturing the largest variation [48,50,54,55].

The which-won-where analysis identified two major genotype-response sectors: G4 as the winning genotype in Robe-2025, Agarfa-2024, Ginir-2024, and Robe-2024 and G11 as the winner in Ginir-2025 and Agarfa-2025. The result further confirmed the superiority of G4 and G11 in their overall means as well as in different environmental groups and hence promising candidates for further targeted improvement activities. Moreover, this finding suggests the practicability of genotype recommendations by taking into account environmental differentiation rather than assuming that one genotype will be

optimal across all production conditions. Similar use of GGE biplots for identifying winning genotypes and delineating mega-environments has been reported in wheat and other crops [48,50,54,59].

Furthermore, the relationships among environments also revealed similarities in genotype responses. In this regard, strong associations were observed between Ginir-2025 and Agarfa-2025, Agarfa-2024 and Ginir-2024, and Ginir-2024 and Robe-2024. The discriminating ability of environments showed variations with Agarfa-2024 and Robe-2025 showing relatively strong capacity to differentiate genotypes, unlike Ginir-2025 that showed comparatively weak discrimination. However, according to reports, test environment is said to be useful if it is being both discriminating and representative of the target production region [48,54,62]. In this regard, Ginir-2024 and Robe-2024, followed by Agarfa-2024 (all the three test locations along with the climatic conditions of 2024), appeared relatively representative of the overall target environment and may therefore provide useful testing conditions in future trials.

The pattern of the GGE biplot or the convergence of the GGE analyses observed further strengthened the identification of the two genotypes, G4 and G11 for further improvement. G4 being closest to the ideal genotype in the GGE ideal-genotype analysis, followed by G11 reveal its combined high productivity, favorable interaction behavior, and broad environmental performance. The pattern observed in G11 also provided a strong alternative with particularly favorable performance in its associated environments. However, the result is weak to be considered as permanent mega-environments as the experiment covered only two seasons. Hence, additional test years and environments are eminent to determine whether these genotype–environment relationships are sufficiently consistent to support differentiated cultivar recommendations.

4.5. Implications and Prospects for Breeding and Cultivar Development

In the present study, the overall results demonstrate that the tested bread wheat advanced lines possess useful genetic variation for productivity, phenology, plant architecture, and disease response though the variation is strongly under environmental influence. The complementary analyses performed using AMMI, ASV, YSI, and GGE biplot used in this study provided different but converging evidence that could be used as baseline information for further targeted breeding.

Among the tested lines, G4 and G11 emerged as the strongest candidates for further evaluation. G4 was appeared as the most outstanding line combining the highest mean grain yield, favorable stability, superiority in four of the six test environments, and showed closeness to the GGE ideal genotype, and low severity of both stem and yellow rust. Its scored a higher yield advantage (26.68%) over the standard check Lemu (5.67 t ha^{-1}) followed by G11 (22.61% advantage) with favorable stability, high YSI ranking, superiority in two environments, and relatively low disease severity. Such combined attributes make both

genotypes strong candidates for advanced verification. Moreover, G1 showed exceptional stability regardless of its moderate yield and could be valuable as a parent for developing broadly adapted lines. Using such complementary traits as high-yielding and high stability could strengthen future breeding populations.

However, additional seasons, locations, farmer-managed trials representing the major target production environments, and additional agronomic traits are important before considering G4 and G11 for cultivar-development and immediate release. Repeated testing is recommendable because the magnitude and direction of GEI can change with seasonal variation in rainfall, temperature, soil moisture, and disease pressure [28,29].

In general, the present study underscores the value of integrating multi-environment testing with complementary stability and adaptation analyses for wheat improvement in southeastern Ethiopia. The evidence supports prioritizing G4 and G11 for further verification together with G1 and G7 that provide useful sources of stability for breeding. If further confirmation across broader environments and seasons is carried out, these materials could contribute to improved wheat productivity and cultivar deployment in the region as continued evaluation of genetically diverse materials and timely replacement of cultivars are important issues for maintaining wheat productivity under increasingly variable production environments [28,29].

5. Conclusion and Recommendation

The present study assessed grain yield stability and genotype × environment interaction among 13 bread wheat genotypes evaluated across six environments, comprising two seasons and three locations in southern Ethiopia. The result indicated that there is significant variability in mean grain yield across environments, genotypes, and the GEI interaction. Based on the AMMI and GGE biplot assessment of genotype × environment interaction and grain-yield stability in bread wheat genotypes, it can be inferred that genotype performance was significantly influenced by environmental conditions. Furthermore, the AMMI and GGE biplot results indicated that G4 and G11 were the most stable, high-yielding genotypes across the evaluated environments. The genotypes produce an average mean grain yield of 7.18 t/ha and 6.94 t/ha compared to the standard check, producing 5.67 t/ha. This makes the genotype have a yield advantage of 26.68% and 22.61% over the standard check, respectively. Conversely, genotype G5 demonstrated high yield potential but relatively lower stability across the environments. Thus, two genotypes, G4 andG11, were identified as candidate genotypes and proposed to the Ethiopian Agricultural Authority for further verification trials and potential release. The authority will verify the candidate based on their yield advantages over the checks, their stable performance across the testing sites, and their

tolerant reaction to major diseases across Ethiopian wheat-growing agro-ecologies, with the other candidates proposed by different research institutions across the country.

Similarly, G5 was a high-yielding genotype but was not selected and advanced to the variety verification trail due to its poor adaptation across tested environments. On the other hand, G1 revealed broad adaptation across testing environments but produced moderate yields. As a result, these types of genotypes are critical in other breeding programs, such as backcrossing, to benefit from their desirable characteristics. It is also recommended that future studies employing multiple locations and seasons with a high number of agronomic and yield component traits be carried out to create more credible information.

Declaration

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests

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Authors' contributions

Koricho Lemma: Conceptualization, Methodology, Investigation, Formal analysis, Data curation, Visualization, Validation, Writing – original draft, Writing – review and editing, Project administration, Supervision, Software, Resources, **Solomon Debele**: Conceptualization, Project administration, Supervision, Writing – review and editing. **Fekadu Gadissa**: Conceptualization, Project administration, Supervision, Writing – original draft, Writing – review and editing, **Diriba Tesfaye**: Conceptualization, Data curation, Project administration, Supervision, Writing – review and editing**. Kami Ahmed:**

Conceptualization, Investigation, Supervision, and Writing – review and editing. **Gosaye Kebebew:** Conceptualization, Investigation, Supervision, Writing – review and editing. All authors reviewed and approved the final manuscript.

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