Graphical Analysis of Multi-environmental Trials for Bread Wheat (Triticum aestivum L.) Grain Yield Based on GGE Bi-plot Analysis

Abstract

Genotypes by environment interaction and stability performance were investigated on grain yield per plot in seven environments (Year by location) during the main cropping season in 2021-22 and 2022-23 using 36 diverse and advanced bread wheat genotypes to evaluate the GEI by the graphical method of GGE biplot, and to identify the genotypes with high mean yield performance and stability. Field experiments were conducted at theAdet, Asasa, Kulumsa, and Sinana research centers in Ethiopia. The analysis of variance revealed that genotype, environment, and their interaction showed a highly significant effect on the yield as reflected in the GGE model~~.~~ and T~~t~~he GGE model indicated the suitability of the genotypes EBW202136 (33), Boru (1), and EBW202172 (12), with high mean yield and stability, whereas the genotypes EBW202185 (16) and Deka (36) produced high mean yield, but unstable. Likewise, the genotypes EBW202164 (27) and EBW202192 (29) produced low mean yield and unstable. The AMMI analysis of variance for grain yield across the environments showed that 17.26% of the total variation was attributed to genotypic effects, 64.03% to environmental effects, and 18.71% to GEI effects. Two mega environments were identified based on GGE biplot analysis and the which-won–model indicated the adaptation of genotypes Boru (1), EBW202159 (4), EBW202172 (12), EBW202171 (19), and EBW202136 (33) to first mega-environment and genotypes EBW202157 (3), EBW202166 (5), EBW202160 (6), EBW202162 (9), EBW202185 (16), Dursa (17) and Deka (36) in the second. These approaches allowed the identification of stable and high-yielding genotypes (EBW202136 (33) and EBW202172 (12)) which can be included in the national verification program, with a plan to release a new variety, and other genotypes with high yield could be utilized in breeding programs to further improve grain yield in bread wheat.

Keywords: AMMI, Environment,Genotype, GGE, Stability

1. Introduction

Ethiopia is one of the many countries in the world where wheat is a major food crop. Wheat is crucial for both nutrition and food security. The biggest nutritional demands of people are met by wheat, one of the most significant agricultural products [1]. With 12.1% protein, 1.8% fats, 1.8% ash, 2.0% reducing sugars, 6.7% pentosans, 59.2% starch, and 70% total carbs, it has a decent

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nutritional profile and offers 314 Kcal/100g of food [2]. It is an industrial crop since the grain, together with the stalk and chaff, is used as industrial raw materials and as mulch, building material, and animal bedding [3]. Due to its great importance as a stable staple that is mostly grown in rain-fed environments, wheat is one of Ethiopia's most farmed and significant crops [4]. The country can produce enough wheat grain under rainfed circumstances and with irrigation.

There are several restrictions on wheat breeding. The two biggest variables that limit agricultural output globally are drought and high temperatures [2,5]. Biological and abiotic elements, as well as socioeconomic issues, have complicated and interacting influences on Ethiopia's wheat production and productivity [6]. The main biological elements that affect Ethiopia's wheat yield are wheat rusts.Wheat stem rust and wheat stripe rust are the two primary biotic problems affecting wheat productivity in Ethiopia [7,8]. The low yield of wheat harvests in the country is a result of several factors, including the depletion of soil fertility, improper agronomic techniques, irregular rainfall, and drought [4]. Due to changeable environmental conditions, enhancing the yield stability of newly introduced cultivars while also boosting yield should be taken into account in rain-fed locations [9].

Multi-location trials are frequently used to examine how well genotypes adapt to various environments and to identify the optimal genotype for a given environment. Commercialization requires accurate and exact performance prediction of each advanced genotype in a variety of target contexts. Effective statistical approaches for assessing bread wheat breeding trials must be utilized to choose dependable types that contribute to agricultural productivity. The populations being studied must have a high level of genetic variation for stable variants to arise [3]. These populations enable the discovery of genotypes with a high degree of environmental stability [3]. This is accomplished through comprehending how the genotype and environment interact [10]. Inconsistent performance under various environmental conditions is a phenomenon known as genotype-by-environment interaction (GEI), and it has a significant impact on how genotypes function in various environments [11]. G x E interaction reduces the varietal recommendation accuracy and selection efficiency. Before introducing novel high-yielding genotypes with high stability in various environments, it is vital to research the genotype in the environment interaction due to this genotype by environment interaction [3]. Increasing stability and stabilizing crop productivity across a variety of environments is one of the main objectives of plant breeding initiatives [3]. The best techniques involve finding attractive cultivars with high genetic potential for production and assessing adaptation to a wide range of situations using multicondition tests in target locales [3].

High performance has been attained in the region as wheat farming has increased in recent years. High-yielding cultivars are developed using the best genotypes. Numerous methods, each with benefits and drawbacks, have been put forth by scientists to ascertain the accuracy and consistency of genotypes as well as the characteristics of the G and E effects. The genotype effect (G) and genotype-environment interaction (GEI) of data from the multizone trials are displayed using the so-called GGE biplot approach [12, 13]. The genotype main effect and GE interaction of MET data are shown, interpreted, and explored using the GGE biplot visual tool [14]. The current study attempted to analyze the GEI in wheat genotypes using the graphical approach of the GGE biplot and to pinpoint the genotypes with the best performance and stability.

Materials and Methods

Experimental Location Description

The field experiments were carried out at seven environments in mid to highland mega wheat-growing regions in 2021-22 and 2022-23 main cropping season in Ethiopia, under rain-fed conditions. The agroecological main characteristics of testing locations are presented in Table 1.

Table 1: List of testing locations and their climatic characteristics

Code	Location	Geographic position Latitude (N)	Longitude (E)	Altitude (m)	Average rainfall (mm/year)	Temperature (°C)	Soil type
1	Kulumsa	08°01'10"	39°09'11"	2200	820	10.5-22.8	Luvisol
2	Asasa	07°07'09"	39°11'50"	2340	620	5.8-23.6	Clay loam
3	Adet	11° 16’	37° 29’	2216	1250		
4	Sinana	7°7’	39°49'	2450	791	10.0-22.0	Clay

Experimental Materials

Thirty-six bread wheat genotypes, including 33 advanced bread wheat breeding lines, were initially received from International Research Institutes (CIMMYT & ICARDA), and three nationally released varieties as checks, namely Boru, Dursa, and Deka were used for this multilocation yield trial. Detailed pedigree and selection history of the evaluated materials are presented in Table 2 for reference.

Experimental Design Layout

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The experiments were planted in an alpha lattice design replicated three times in six rows of 2.5m long. Row-to-row distance and distance between blocks were 0.2m and 1.5m, respectively. Depending on weather conditions, planting was carried out from mid-June to mid-July and harvested 115-135 days after planting (Table 1). Each plot was planted at a seed rate of 150 kg ha^{-1} Fertilizer applications and all necessary crop management practices were applied as per the local recommendations. Data were recorded on agronomic characters, major wheat diseases, quality parameters, and grain yield. However, sole grain yield was considered for stability analysis.

Statistical Analysis

Data were subjected to analysis of variance (ANOVA) for each environment separately; and a combined analysis of variance was conducted to determine the effect of environment (E), genotype (G), and their interaction on the expression of traits. The R Software was used for combined ANOVA and GGE biplots.

Stability analysis

The stability analysis among genotypes over environments was done using GGE biplot multivariate analysis methods as described below:

The GGE biplot is a biplot that displays the GGE part of MET data. The basic model for a GGE biplot is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

where Y_{ij} is the mean for the genotype in the j environment, μ is the grand mean β_j is the main effect of environment j, λ_1 and $\lambda_2$are the singular values of the 1st and 2nd principal components (PC1 and PC2), ξ_{i1} and $\xi_{i2}$are the PC1 and PC2 scores, respectively, for genotypeith, η_{j1} and η_{j2} are the eigenvectors for the jth environment for PC1 and PC2 and $\epsilon_{ij}$is the residual error term.

Table 2: Pedigree and selection history of materials tested across locations & years

Genotype	Pedigree	Selection History
Boru	Check	Breeder Seed
EBW202163	SHAKTI/8/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/CMH75A.66/SERI/7/MUNAL #1	CMSS15B02055T-099TOPY-099M-099Y-14M-0WGY
EBW202157	KINDE*2/SOLALA/3/UP2338*2/KKTS*2//YANAC/4/UP2338*2/SHAMA//2*BAJ #1/5/FRANCOLIN #1/3/IWA 8600211//2*PBW343*2/KUKUNA	CMSS15B01614S-099M-099Y-10M-0WGY
EBW202159	MAYIL/5/PFAU/WEAVER*2/4/BOW/NKT//CBRD/3/CBRD/6/KINDE*2/SOLALA/3/UP2338*2/KKTS*2//YANAC/4/UP2338*2/SHAMA//2*BAJ #1	CMSS15B01658S-099M-099Y-11M-0WGY
EBW202166	KVZ/PPR47.89C//FRANCOLIN #1/3/2*PAURAQ/4/PBW343*2/ KUKUNA*2//FRTL/ PIFED*2/7/MELON//FILIN/MILAN/3/FILIN/5/CROC_1/AE.SQUARROSA (444) /3/T.DICOCCONPI94625/AE.SQUARROSA (372)//3*PASTOR/4/T.DICOCCON PI94625/AE.SQUARROSA (372)//3* PASTOR/6/AMUR	CMSS15B02164T-099TOPY-099M-099Y-3M-0WGY
EBW202160	IWA 8606686/MUCUY	CMSS15B01885S-099M-099Y-12M-0WGY
EBW202161	IWA 8606686/MUCUY	CMSS15B01885S-099M-099Y-28M-0WGY
EBW202175	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/CMH75A.66/SERI/7/MUNAL #1/8/KUTZ	CMSS15Y00161S-099Y-099M-099Y-23M-0WGY
EBW202162	SHAKTI//MUTUS*2/MUU/3/MUCUY	CMSS15B02036T-099TOPY-099M-099Y-15M-0WGY
EBW202173	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/CMH75A.66/SERI/7/MUNAL #1/8/KUTZ	CMSS15Y00161S-099Y-099M-099Y-19M-0WGY
EBW202180	MANKU//KACHU*2/CHONTE	CMSS14B01135S-099M-099Y-34M-0WGY
EBW202172	KOKILA/7/DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372) //SHA4/CHIL/6/WBLL1/3/STAR//KAUZ/STAR/4/BAV92/RAYON/5/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON	CMSS15Y00154S-099Y-099M-099Y-17M-0WGY
EBW202177	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU/5/IWA 8600211//2*PBW343*2/KUKUNA/6/INQALAB 91*2/TUKURU//WHEAR/3/IWA 8600211//2*PBW343*2/KUKUNA	CMSS15Y00171S-099Y-099M-099Y-2M-0WGY
EBW202168	KURKUT/8/TRCH/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/6/IWA 8600211//2*PBW343*2/KUKUNA/7/PBW343*2/KUKUNA*2//FRTL/PIFED	CMSS15Y00141S-099Y-099M-099Y-7M-0WGY
EBW202184	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/T.DICOCCON PI94624/AE.SQUARROSA (409)//BCN/6/WBLL4//BABAX.1B.1B*2/PRL/3/PASTOR/7/KINGBIRD #1//INQALAB 91*2/TUKURU/8/DANPHE/BAJ #1	CMSS14B01232S-099M-099Y-22M-0WGY
EBW202185	KVZ/PPR47.89C//TACUPETO F2001*2/BRAMBLING/3/2*TACUPETO F2001*2/BRAMBLING/5/2*ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE	CMSS14B01843T-099TOPY-099M-099Y-13M-0WGY
Dursa	Check	Breeder Seed
EBW202189	SHAKTI/7/2*TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1/6/TOBA97/PASTOR/3/T.DICOCCON PI94624/AE.SQUARROSA (409) //BCN/4/BL 1496/MILAN/3/CROC_1/AE.SQUARROSA (205)//KAUZ	CMSS14Y01169T-099TOPM-099Y-099M-099Y-21M-0WGY
EBW202171	KOKILA/7/DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372) //SHA4/CHIL/6/WBLL1/3/STAR//KAUZ/STAR/4/BAV92/RAYON/5/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON	CMSS15Y00154S-099Y-099M-099Y-6M-0WGY
EBW202176	NG8201/KAUZ/4/SHA7//PRL/VEE#6/3/FASAN/5/MILAN/KAUZ/6/ACHYUTA/7/PBW343*2/KUKUNA/8/IWA 8600211//2*PBW343*2/KUKUNA/9/TRCH/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/6/IWA 8600211//2*PBW343*2/KUKUNA/7/PBW343*2/KUKUNA*2//FRTL/PIFED	CMSS15Y00169S-099Y-099M-099Y-17M-0WGY
EBW202154	DANPHE #1*2/3/T.DICOCCON PI94625/AE.SQUARROSA (372) //SHA4/CHIL/6/WBLL1/3/STAR//KAUZ/STAR/4/BAV92/RAYON/5/TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/7/MUCUY	CMSS15B01547S-099M-099Y-4M-0WGY
EBW202179	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU/5/IWA 8600211//2*PBW343*2/KUKUNA/6/INQALAB 91*2/TUKURU//WHEAR/3/IWA 8600211//2*PBW343*2/KUKUNA	CMSS15Y00171S-099Y-099M-099Y-38M-0WGY
EBW202178	THB/KEA//PF85487/3/DUCULA/4/WBLL1*2/TUKURU/5/IWA 8600211//2*PBW343*2/KUKUNA/6/INQALAB 91*2/TUKURU//WHEAR/3/IWA 8600211//2*PBW343*2/KUKUNA	CMSS15Y00171S-099Y-099M-099Y-31M-0WGY
EBW202190	VALI/MAYIL//MANKU	CMSS14Y01192T-099TOPM-099Y-099M-099Y-7M-0WGY

EBW202156	PICAFLOR #1/4/INQALAB 91*2/TUKURU//T.SPELTA PI348599/3/INQALAB 91*2/KUKUNA/5/ KINGBIRD #1//INQALAB 91*2/TUKURU/6/HOLO	CMSS15B01595S-099M-099Y-2M-0WGY
EBW202174	SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/PBW343*2/TUKURU/5/C80.1/3*BATAVIA//2*WBLL1/6/CMH75A.66/ SERI/7/MUNAL #1/8/KUTZ	CMSS15Y00161S-099Y-099M-099Y-22M-0WGY
EBW202164	KURKUT/8/2*TRCH/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES /6/IWA 8600211//2*PBW343*2/KUKUNA/7/PBW343*2/KUKUNA*2//FRTL/PIFED	CMSS15B02099T-099TOPY-099M-099Y-15M-0WGY
EBW202165	KURKUT/8/2*TRCH/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES /6/IWA 8600211//2*PBW343*2/KUKUNA/7/PBW343*2/KUKUNA*2//FRTL/PIFED	CMSS15B02099T-099TOPY-099M-099Y-28M-0WGY
EBW202169	KVZ/PPR47.89C//FRANCOLIN #1/3/2*PAURAQ/5/BAV92//IRENA/KAUZ/3/HUITES *2/4/MURGA/6/MAYIL/7/MANKU	CMSS15B02167T-099TOPY-099M-099Y-27M-0WGY
EBW202192	MELON//FILIN/MILAN/3/FILIN/8/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/T.SPELTA PI348774/6/BACEU #1/7/PAKHWA/9/KENYA SUNBIRD/KACHU/10/KENYA SUNBIRD/KACHU	CMSS14Y01264T-099TOPM-099Y-099M-099Y-8M-0WGY
EBW202167	KURKUT/8/TRCH/5/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/6/IWA 8600211//2*PBW343*2/KUKUNA/7/PBW343*2/KUKUNA*2//FRTL/PIFED	CMSS15Y00141S-099Y-099M-099Y-20M-0WGY
EBW202135	SHAKTI/MAYIL//MANKU	CMSS14B01826T-099TOPY-099M-099Y-21M-0WGY
EBW202136	FRANCOLIN #1/7/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/5/T.SPELTA PI348599/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA (213) //PGO/4/HUITES/8/TRAP#1/BOW/3/ VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1/6/TOBA97/PASTOR/3/T.DICOCCON PI94624/AE. SQ	CMSS14B01895T-099TOPY-099M-099Y-7M-0WGY
EBW202137	KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ/5/CMH81.530/6/MANKU	CMSS14Y00967S-099Y-099M-099Y-10M-0WGY
EBW202138	FRANCOLIN #1/3/IWA 8600211//2*PBW343*2/KUKUNA/4/MUCUY/5/MUCUY	CMSS14Y01258T-099TOPM-099Y-099M-099Y-8M-0WGY
Deka	Check	Breeder Seed

Results and Discussion

The Combined ANOVA presented given in Table 3 clarifies that the environment, genotype, and GEI revealed highly significant differences ($p < 0.001$) for grain yield across all studied environments. The total sum of squared factors explained (%) showed that bread wheat yield was influenced by environment (64.03%), genotype effect (17.26%), and genotype by environment interaction effect (18.71%) (Table 3). In agreement with these results, several authors reported that the environment is the most contributing, followed by the genotype by the environment interaction effect and the genotype effect [3, 15- 22]. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in grain yield, indicating that the environment has a strong influence on grain yield 18, 22] and the existence of mega-environments [23, 24]. Similarly, the significant interaction of the environments with genotypes indicates the presence of crossover of GE interaction as some genotypes outperformed other genotypes in different environments. The multiplicative variance of the treatment sum of squares due to interaction was partitioned into five significant interaction principal components. The first two PCs significantly explained 76.98% of the total variation, in which the contribution of PC1 was 63.19% and that of PC2 was 13.79% (Table 3).

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Table 3. Combined ANOVA of grain yield for 36 advanced bread wheat genotypes evaluated at seven environments

Source of variation	DF	SS	PERCENT	MS	F	PROBF
ENV	6	1037.64	64.03	172.94	482.76	0.00
GEN	35	279.70	17.26	7.99	22.31	0.00
ENV*GEN	210	303.17	18.71	1.44	4.03	0.00
PC1	40	367.14	63.19	9.18	32.36	0.00
PC2	38	80.16	13.79	2.11	7.44	0.00
PC3	36	63.12	10.86	1.75	6.18	0.00
PC4	34	35.67	6.14	1.05	3.70	0.00
PC5	32	19.19	3.30	0.60	2.11	0.00
Residuals	756	270.82	0.00	0.36		

Asasa-2022 recorded the highest location mean yield (5.66 t/ha), followed by Asasa-2021 (4.77 t/ha), Kulumsa-2022 (4.57 t/ha) and kulumsa-2021 (4.54 t/ha), while Adet-2021 recorded the lowest location mean yield (2.64 t/ha), followed by Sinana-2021 (3.03 t/ha), and Sinana-2022 (3.3 t/ha) (Table 4). The mean grain yield of the genotypes ranged from 2.72 t/ha to 4.94 t/ha, with an overall genotype mean of 4.08 t/ha. This indicates the inconsistent performance of the tested genotypes across the tested environments, justifying the interaction between genotype and environment. Accordingly, Boru produced the maximum grain yield (4.94 t/ha), followed by EBW202136 (4.87 t/ha) and EBW202172 (4.81 t/ha) whereas the minimum grain yield was produced by EBW202164 (2.72 t/ha) (Table 4).

Table 4: Mean grain yield (t/ha) of 36 bread wheat genotypes in seven environments

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SN	Genotype	Adet - 2021	Asasa - 2021	Asasa - 2022	Kulumsa - 2021	Kulumsa - 2022	Sinana - 2021	Sinana - 2022	Mean
1	Boru	2.80	5.35	7.17	5.83	6.45	3.65	3.34	4.94
2	EBW202163	3.14	5.79	4.70	5.60	5.69	2.62	2.40	4.27
3	EBW202157	2.91	4.80	6.08	5.00	5.42	2.72	4.07	4.43
4	EBW202159	2.58	5.19	7.12	4.62	5.83	3.42	3.56	4.62
5	EBW202166	3.09	5.73	5.59	4.96	5.25	3.16	3.65	4.49
6	EBW202160	2.84	4.48	5.73	4.59	4.79	3.68	4.39	4.36
7	EBW202161	2.93	4.70	3.92	4.80	3.94	2.29	3.16	3.68
8	EBW202175	1.84	4.86	5.12	3.82	4.05	2.48	2.18	3.48
9	EBW202162	2.61	4.89	5.75	4.58	5.99	3.55	4.09	4.49
10	EBW202173	2.59	5.12	5.79	3.43	4.48	3.06	3.30	3.97
11	EBW202180	3.10	4.16	5.67	4.84	2.73	2.78	3.04	3.76
12	EBW202172	2.81	5.38	7.66	5.08	5.86	3.46	3.43	4.81
13	EBW202177	2.47	5.36	5.61	4.62	4.16	3.05	4.38	4.23
14	EBW202168	2.47	4.85	5.17	3.51	3.83	2.84	2.57	3.60
15	EBW202184	3.20	4.07	5.44	4.95	3.85	2.69	3.32	3.93
16	EBW202185	3.03	4.78	6.05	5.01	4.94	3.83	5.02	4.67
17	Dursa	3.08	4.99	4.25	5.53	5.26	3.28	3.53	4.27
18	EBW202189	2.60	4.18	5.20	3.55	3.60	2.62	2.83	3.51
1	EBW202	2.70	4.88	6.79	4.92	5.61	3.09	3.31	4.4

9	171								7
20	EBW202176	2.71	5.15	5.99	4.60	4.52	3.05	3.34	4.19
21	EBW202154	2.41	4.04	4.77	5.25	4.17	3.15	3.53	3.90
22	EBW202179	2.65	4.15	4.76	4.03	3.53	2.06	2.29	3.35
23	EBW202178	2.56	4.84	5.97	4.20	3.42	3.30	3.53	3.97
24	EBW202190	2.63	4.47	6.37	5.05	4.30	3.31	3.22	4.19
25	EBW202156	2.18	5.28	7.22	4.75	4.98	3.77	4.08	4.61
26	EBW202174	2.15	5.01	6.03	3.37	4.95	2.92	2.91	3.90
27	EBW202164	2.59	3.89	2.54	3.47	2.77	1.84	1.96	2.72
28	EBW202165	2.00	4.54	5.32	3.55	3.76	3.15	2.93	3.61
29	EBW202169	2.39	3.95	3.71	3.46	2.25	2.01	2.56	2.90
30	EBW202192	3.24	5.12	6.50	4.21	5.35	3.38	2.15	4.28
31	EBW202167	2.25	4.37	5.31	4.19	4.11	2.30	2.95	3.64
32	EBW202135	2.34	4.94	5.18	5.00	2.46	3.54	3.17	3.80
33	EBW202136	2.21	5.15	7.28	4.93	7.09	3.46	3.98	4.87
34	EBW202137	2.34	3.77	6.09	3.75	4.90	2.08	2.53	3.64
35	EBW202138	2.97	5.11	5.98	5.30	5.07	3.38	3.05	4.41
36	Deka	2.84	4.55	6.14	5.13	5.29	4.28	5.18	4.77
	Mean	2.64	4.77	5.66	4.54	4.57	3.03	3.30	4.08
	CV	14.50	11.09	13.21	10.06	15.98	17.70	17.85	14.26
	LSD	0.54	0.74	1.05	0.64	1.02	0.75	0.85	0.31

Where, CV = Coefficient of variation, LSD = Least significant difference

GGE Biplot Analysis

Which-Won-Where Model

The GGE biplot method has become an increasingly popular data visualization tool in analyzing MET data, as it allows visualizing the -won-where pattern of the MET data, the interrelationship among the test environments, and the ranking of genotypes based on mean yield performance and stability [25, 26]. The GGE biplot is a data visualization tool that allows an evaluation of environments due to the discriminative ability and representativeness of the GGE view, which is an advantage over the AMMI biplot analysis [17, 22, 25, 27], and the most effective way for a precise and useful interpretation of genotype-environment interactions as well as interrelationships among various test environments and genotypes and identifies the best line of each environment [22, 28]. The most attractive feature of GGE biplots is the ‘which won-where’ analysis, in which crossover GE interaction, mega-environment differentiation, and specific genotype adaptation are graphically represented [29]. The vectors were connected furthest from the origin of the biplot, and a polygon was obtained. The vertex genotypes were the most responsive for being located at the greatest distance from the biplot origin. These vertex genotypes were the most responsive, located at the greatest distance from the biplot origin [22, 23, 24, 25, 27, 28, 30, 31]. In this biplot, genotypes EBW202136 (33), EBW202137 (34), EBW202135 (32), EBW202164 (27) and Deka (36) were the most responsive genotypes (Figure 1), with crossover GE interaction, mega-environment differentiation, and specific genotype adaptation [32]. In the biplot, the equality line divides the graph into six sectors, and seven environments were retained in two sectors (Figure 1), probably due to climatic variations and variability related to soil characteristics. The test locations could be partitioned into two mega environments, one with Asasa-2021, Asasa-2022, and Kulumsa-2022, and the second with Adet-2021, Kulumsa-2021, sinana-2021, and Sinana-2022. In the first mega environment, the genotype EBW202136 (33) was the winning genotype, and Deka (36) in the second. There were strong correlations between environments located within the same sector, and variation in genotype performance within environments indicated a strong environmental influence and the existence of a mega environment [18, 28, 29, 33].

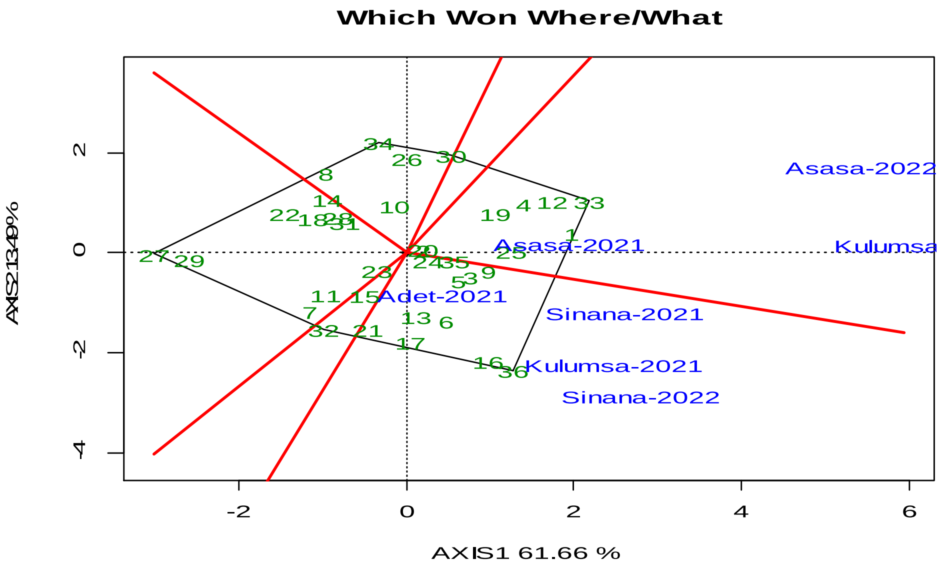

Figure 1: Polygon view of GGE (genotype plus genotype by environment interaction) biplot (Which-Won-Where) showing 36 advanced bread wheat genotypes in seven environments

Mean Performance and Stability of Genotypes Using GGE Biplot

The GGE biplot can be applied to visualize the position of ideal bread wheat genotypes. In this diagram, the desirability of a genotype depends on its distance from the assumed ideal genotype. In other words, the genotypes closest to the assumptive ideal genotype are the most desired genotypes. The best genotype can be defined as the one with the highest yield and stability across environments. Within a single mega-environment, genotypes should be evaluated on both mean performance and stability across environments [16, 23, 25, 34, 35]. The ranking biplot shows the average grain yield and stability performance of 36 bread wheat genotypes across seven environments (Figure 2). Therefore, in the present study, the ranking biplot showed that genotypes Boru (1), EBW202136 (33), EBW202172 (12), Deka (36), EBW202185 (16), EBW202159 (4), EBW202156 (25), EBW202166 (5), EBW202162 (9), EBW202171 (19), EBW202138 (35), EBW202160 (6), EBW202192 (30), EBW202163 (2), Dursa (17), EBW202177 (13), EBW202176 (20) and EBW202190 (24) produced a high mean grain yield compared to the overall mean yield of all genotypes. Whereas, genotypes EBW202164 (27),

EBW202169 (29), EBW202179 (22), EBW202175 (8), EBW202189 (18), EBW202168 (14), EBW202165 (28), EBW202137 (34), EBW202167 (31), EBW202161 (7), EBW202180 (11), EBW202135 (32), EBW2021674 (26), EBW202154 (21), EBW202184 (15), EBW202178 (23) and EBW202173 (10) were characterized by low mean grain yield. Meanwhile, in addition to the genotypic mean grain yield performance, the stability of genotypes across the testing environments is very crucial [16, 18, 24 35, 36]. A genotype that has a shorter absolute length of projection in either of the two directions of AE Coordinates (located closer to AEC abscissa), represents a smaller tendency of GEI, which means it is the most stable genotype across different environments or vice versa. Hence, genotypes Boru (1), EBW202136 (33), and EBW202172 (12) were identified as the most stable and high-yielding genotypes. The genotypes EBW202164 (27), EBW202169 (29), EBW202179 (22), and EBW202189 (18) were identified as stable, but low-yielding genotypes across the environments. Genotypes Deka (36) and EBW202185 (16) and were high-yielding but unstable (Figure 2). Similar findings have been reported by several authors [18, 24, 25, 30, 31, 35, 37].

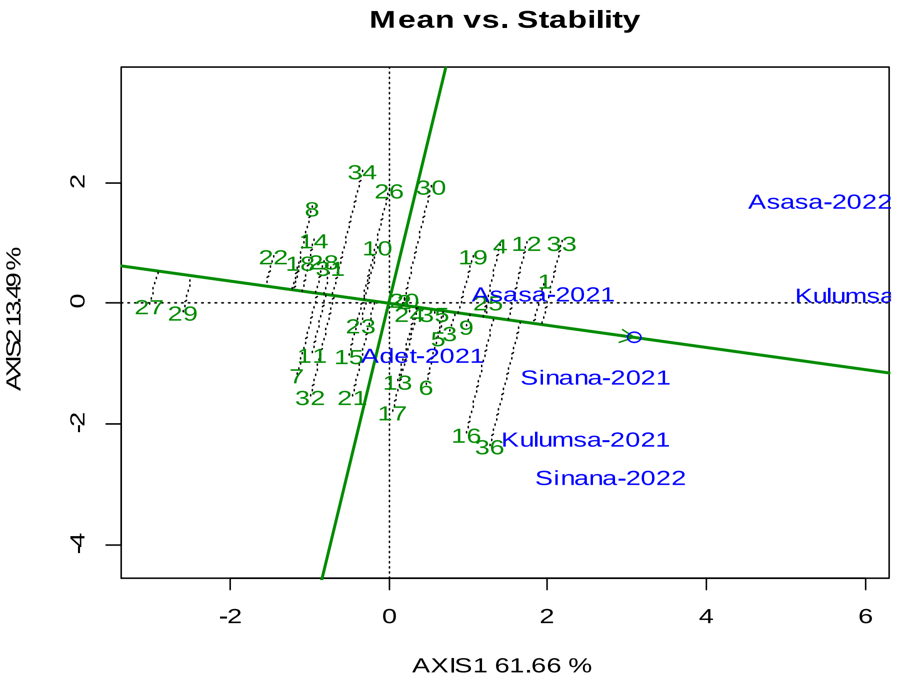

Figure 2: Mean Performance and Stability of Genotypes Using GGE Biplot

GGE-biplot for comparing the environments with the ideal environment

The assumptive ideal environment was drawn according to the average data for two years of an experiment in the most appropriate and most inappropriate environment (Figure 3). Based on this diagram, each environment close to the assumptive ideal environment is more desired than other environments. The main characteristic of correlation among the environments is the environment vector's length, which estimates the standard deviation inside each environment and indicates the environments' discrimination ability (large PC1 scores) and representativeness (small absolute PC2 scores) [25, 30, 35, 38, 39]. A greater length indicates a high standard deviation and more discriminability. The discriminatory and representativeness of the trial environments from the grain yield results obtained at seven environments where the yield experiments of the bread wheat genotypes are carried out are given in Figure 3. The concentric circles on the biplot help to visualize the length of the vectors. This relates to the standard deviation of the relevant environment and is an indication of the distinctive features of the environment. Accordingly, the environments Kulumsa-2022 and Asasa-2022 are the most discriminating environments whereas the environment Adet-2021 shows the least discriminating ability. The average environment axis (represented by the small circle at the end of the arrow) has the average coordinates of all test environments. Environmental coordination passes through the environment average and biplot origin. A test location with a smaller environmental angle than the average environmental coordinate has the ability to represent more than other test locations. Asasa-2021, Adet-2021, and Sinana-2021 were the most representative environments, while environments Asasa-2022 and Sinana-2022 depicted the lowest representativeness. Test environments that are both discriminatory and representative are good test environments in the selection of genetically adapted genotypes.

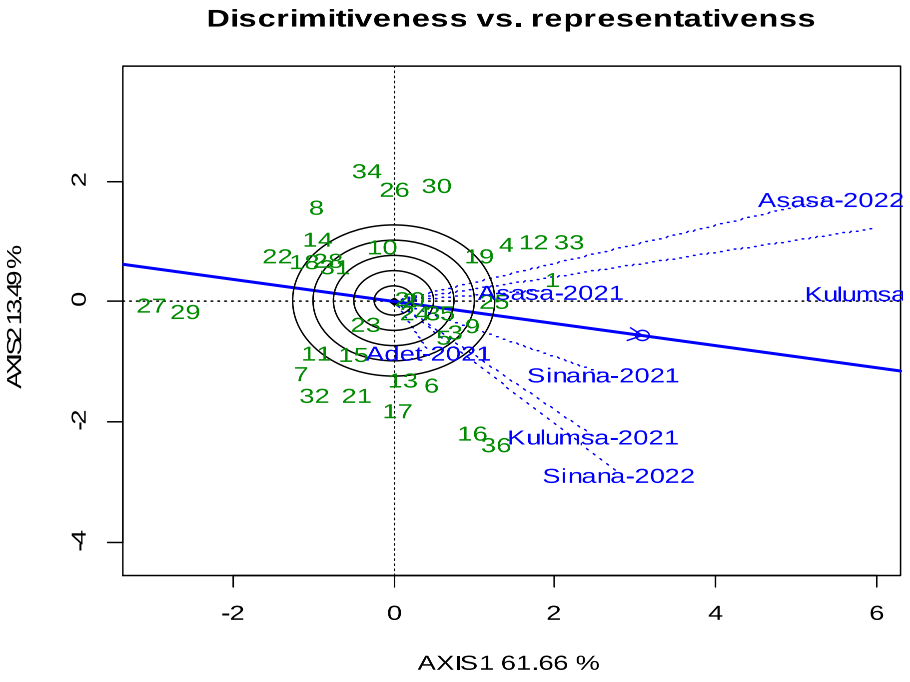

Figure 3. GGE-biplot for comparing the environments with the ideal environment

Conclusion

Thirty-six bread wheat genotypes were planted and evaluated according to the GEI-based GGE Graphical biplot technique in four research stations. A significant variation was observed among the bread wheat for mean yield, performance and stability, indicating that the bi-plot method facilitated the discrimination of genotypes in different environments. Both PC1 and PC2 explained more than 75% of the yield performance variation. GGE biplot analysis showed thatA study of grain yield and stability of bread wheat genotypes using the biplot of average environment coordinates showed that ETB202136 (33) and Boru depicted superior stability and mean grain yield performance than other genotypes. On the other hand, EBW202164 (27) and EBW202169 (29) genotypes had minimum stability on grain yield. Hence, genotype ETB202136 (33) shall be verified and released for large-scale production in major bread wheat-growing regions of Ethiopia.

Comment [H4]: 1.Acknowledgement
2. Declare here any conflict of interest

Data availability

Available from the first author upon request

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