International Journal of Bio-resource and Stress Management https://ojs.pphouse.org/index.php/IJBSM

IJBSM June 2024, 15(6): 01-11 Article AR5375

Research Article Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2024.5375

Multi-environments Evaluation of Zn and Fe Enhanced Bread Wheat Genotypes in Optimum Areas of Ethiopia

Alemu Dabi[1], Gadisa Alemu[1], Berhanu Sime[1], Ruth Duga[1], Negash Geleta[1], Abebe Delessa[1], Tafesse Solomon[1], Habtemariam Zegaye[1], Cherinet Kasahun[1], Dawit Asnake[1], Bayisa Asefa[1], Abebe Getamesay[1], Demeke Zewudu[1], Ayele Badebo[2], Bekele Abeyo[2], Tilahun Bayisa[2], Endashaw Girma[2], Velu Govindan[2], and Zerihun Tadesse[2]

[1]Ethiopian Institute of Agricultural Research, Kulumsa Agricultural Research Center, Asella, Ethiopia
[2]CIMMYT Ethiopia Office, Addis Ababa, Ethiopia

Open Access

Corresponding alemudabi2009@gmail.com

0009-0006-1676-8294

ABSTRACT

A multi-location experiment was conducted during June, 2020–October, 2021 under rainfed condition at Kulumsa, Asasa, Adet, Holeta, and Sinana Research centers, Ethiopia to evaluate the genotype-by-environment interaction effect and grain yield stability of Zn and Fe enhanced bread wheat genotypes grown. The treatments constituted 21 advanced genotypes and two standard checks were evaluated in an alpha lattice design replicated three times and data analysis was carried using R software. The results showed that genotypes and genotype x environmental interaction had a significant (p<0.001) effect on days to 50% heading, days to 90% maturity, plant height, grain yield, and 1000 kernel weight. The bread wheat lines BW172862, EBW193416, BW172864, and EBW193414 were high-yielding across most test environments, whereas genotype EBW192455 and Hidasse were low-yielding ones. From stability analysis genotypes BW172862, and EBW193416 were identified to be the most adapted bread wheat genotypes. "BW172862 produced 24.43% and 86.38% yield advantage over the standard check (Lemu) and local check (Hidasse), respectively. The second candidate genotype EBW193416 also produced 23.58% and 85.1% yield advantage over the standard check (Lemu) and local check (Hidasse), respectively. EBW193416 and BW172862 have also exhibited lower Yellow and Stem rust severity compared to others across the test environments. Thus, BW172862 and EBW193416 were selected as best parent to recycle for bread wheat population improvement in 2023 for medium agro-ecology of Ethiopia.

KEYWORDS: Evaluation, genotype by environment interaction, stability, bread wheat

Citation* (VANCOUVER)*: Dabi et al., Multi-environments Evaluation of Zn and Fe Enhanced Bread Wheat Genotypes in Optimum Areas of Ethiopia. *International Journal of Bio-resource and Stress Management,* 2024; 15(6), 01-11. HTTPS://DOI.ORG/10.23910/1.2024.5375.

Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

Conflict of interests: The authors have declared that no conflict of interest exists.

RECEIVED on 12th April 2024 RECEIVED in revised form on 09th June 2024 ACCEPTED in final form on 27th June 2024 PUBLISHED on 29th June 2024

1. INTRODUCTION

Wheat (*Triticum* spp.) is the most important cereal crops cultivated in the world. Bread wheat and durum wheat are the most widely grown wheat species worldwide. In Ethiopia wheat is the top priority food, cultivated on 2.6 mha of land under rain-fed and irrigated systems, and with an annual total production of 8.2 mt in 2022. Ethiopia achieved a 100% wheat self-sufficiency with the surplus of more than 1 million tons for export, indicating that the new irrigated wheat initiative was found to be transformational and a game changer (Kefena et al., 2023). Rosegrant and Agcaoili (2010) reported that the demand for wheat in developing world is projected to increase 60% by 2050. The Ethiopian government is attempting to enhance production through land expansion, agro-clustering of wheat farmers and expansion of irrigation spatially to lowlands and temporally to dry season of the year. (Tadesse et al., 2022; Senbeta and Worku, 2023).

Wheat productivity is affected by complex and interwoven biophysical and socio-economic challenges (Nigus et al., 2022; Semahegn et al., 2021.). For long time the wheat productivity has remained stagnant at very low levels, and food production has lingered behind population growth (Hodson et al., 2020; Shiferaw et al., 2014; Belete et al., 1991). According to numerous studies (Tadesse et al., 2022; Negash et al., 2022), the most significant constraints are biotic and abiotic factors highly affecting the productivity of wheat in Ethiopia. Wheat diseases such as the rusts (YR, and SR), Sep, and FHB are the most prevalent yield reducing agents. The most difficult aspect of breeding diseases resistant and stable high yielding wheat varieties in Ethiopia is the frequent break down of diseases resistant genes in varieties. (Meyer et al., 2021).

Wheat, like many other staple cereals, contains low levels of essential micronutrients such as iron and zinc. Up to two billion people worldwide suffer from iron and zinc deficiencies, particularly in regions with predominantly cereal-based diets (Saha et al., 2017; Praharaj et al., 2021). Maintaining adequate mineral content in wheat (*Triticum aestivum* L.) grain is critically important for human nutrition. (Borrill et al., 2014). In Ethiopia, bread wheat research has recently started to focus on evaluating genotypes containing Zn and Fe in addition to high yielding and disease resistance traits.

Breeding wheat in Ethiopia is an ongoing attempt to develop new technologies that boost production and productivity as compared to cultivars in production. Since the start of Ethiopian's wheat research, improved bread wheat varieties and accompanied packages have been developed in an effort to boost production and productivity. As the result of the efforts made for the last 70 years more than 120 bread wheat varieties were released/registered (MoANR, 2020, 2021 and 2022). The wider adaptation of varieties for national release across a range of eco-geographical environments is confirmed by multi-location evaluation which involved a number of federal and regional research centers and higher learning institutions (Negash et al., 2022)

Evaluation of different genotypes in multi-environments is important to identify the adapted and stable genotypes under target environments (Yan, 2001). A genotype is considered stable if it is adapted for a trait of economic importance across diverse environments. Environmental component (E) generally represents the largest component in analyses of variance; only G and GE are relevant to meaningful genotype evaluation and must be considered simultaneously for making selection decisions (Yan & Kang, 2003). The objective of this study was to evaluate genotypes, and their (G × E) interaction and identify stable genotypes for grain yields in the test environments of Ethiopia.

2. MATERIALS AND METHODS

2.1. Experimental sites description

The experiment was conducted at five locations for two years (June, 2020 and october, 2021) and the trials were planted at, Kulumsa, Holeta, Adet, Sinana, and Asasa Agricultural research Centers. A description of the study sites is given below (Table 1).

2.2. Experimental design and field management

Twenty-one genotypes were grown in Alpha-Lattice Design

Table 1: List of test locations and their descriptions

Location	Geographic position		Altitude (m)	Temperature (°C)		Rainfall (mm)
	Latitude	Longitude		Min	Max	
Kulumsa	08°01'10"N	39°09'11"E	2200	10.5	22.8	820
Asasa	07°07'09"N	39°11'50"E	2340	5.8	24	620
Holeta	09°03'414" N	38°30'436"E	2400	6.1	22.4	976
Adet	11°16' N	37° 29' E	2216	9.2	25.5	1250
Sinana	7°7'N	39°49'E	2450	10	22	791

with three replications. Each experimental unit consisted of 3m^2 (with 1.2×2.5 m^2 length) plot size and 1.5 m alleys between reps. Non-experimental variables such as fertilizer rates and other crop management practices were done as per the recommendations of each test location uniformly. A seed rate of 125 kg ha^{-1} was used at all locations (Table 2).

Table 2: The list of bread wheat genotypes evaluated

S1. no.	Lemu	Check
1.	EBW193408	ZINCOL//SUP152/KENYA SUNBIRD/3/MAYIL
2.	EBW193410	DANPHE#1*2/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//SHA4/CHIL/4/WBLL1*2/KURUKU//KRONSTADF2004/3/WBLL1*2/BRAMBLING/5/MUTUS*2/HARIL #1
3.	EBW193411	NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/T.DICOCCONPI94624/AE.SQUARROSA(409)//BCN/6/WBLL4//BABAX.1B.1B*2/PRL/3/PASTOR/7/KINGBID #1//INQALAB 91*2/TUKURU/8/DANPHE/BAJ #1
4.	EBW193412	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA8600211//2*PBW343*2/KUKUNA/6/2*KACHU/SAUAL/4/ATTILA*2/PBW65//PIHA/3/ATTILA/2*PASTOR
5.	EBW193413	PAURAQ/4/SLM//AG/6*INIA66/3/SLM/5/PAURAQUE#1/6/BECARD#1/5/KIRITATI/4/2*SERI.1B*2/3/KAUZ*2/BOW//KAUZ
6.	EBW193414	VILLAJUAREZF2009/3/T.DICOCCONPI94625/AE.SQUARROSA(372)//3*PASTOR/4/WBLL1*2/BRAMBLING/5/2*WBLL1*2/BRAMBLING*2//BAVIS
7.	EBW193415	FRANCOLIN#1/7/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA(213)//PGO/4/HUITES/5/T.SPELTAPI348599/6/REH/HARE//2*BCN/3/CROC_1/AE.SQUARROSA(213)//PGO/4/HUITES/8/SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI/5/IWA 8600211//2*PBW343*2/KUKUNA/9/FRNCLN/DANPHE
8.	EBW193416	MELON//FILIN/MILAN/3/FILIN/8/NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/T.SPELTAPI348774/6/BACEU#1/7/WBLL1*2/4/YACO/PBW65/3/KAUZ*2/TRAP//KAUZ/9/KENYA SUNBIRD/KACHU/10/KENYA SUNBIRD/KACHU
9.	EBW193417	SHAKTI//FRANCOLIN #1*2/MUU
10.	EBW193418	C80.1/3*BATAVIA//2*WBLL1/3/ATTILA/3*BCN*2//BAV92/4/WBLL1*2/KURUKU/5/IWA8600211//2*PBW343*2/KUKUNA/6/2*KACHU/SAUAL/4/ATTILA*2/PBW65//PIHA/3/ATTILA/2*PASTOR
11.	EBW193419	ROLF07/YANAC//TACUPETOF2001/BRAMBLING/3/IWA8600211//2*PBW343*2/KUKUNA/4/BECARD/QUAU #1/5/WBLL1*2/BRAMBLING*2//BAVIS
12.	EBW192444	FRANCOLIN#1/3/IWA8600211//2*PBW343*2/KUKUNA/7/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
13.	EBW192455	SHAKTI/7/SERI.1B*2/3/KAUZ*2/BOW//KAUZ/4/KRONSTAD F2004/5/MUNAL/6/MUNAL #1/8/MP4010/MUNAL #1
14.	EBW192466	KOKILA/3/MUTUS*2//ND643/2*WBLL1/8/PSN/BOW//SERI/3/MILAN/4/ATTILA/5/KAUZ*2/CHEN//BCN/3/MILAN/6/WBLL1*2/SHAMA/7/IWA 8600211//2*PBW343*2/KUKUNA
15.	EBW192471	MANKU/6/WHEAR/KUKUNA/3/C80.1/3*BATAVIA//2*WBLL1/5/PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI
16.	EBW192477	MAYIL*2//SUP152*2/TECUE #1
17.	BW172862	BV2016\C8HPAN\37
18.	BW172864	BV2016\C8HPAN\38
19.	BW172936	BV2016\C8HPAN\160
20.	Hidasse	Check

2.3. Statistical analyses

2.3.1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) was performed using the R-software for Alpha-Lattice Design. ANOVA was done for each location and combined data over locations, Plot values were used for days to heading and maturity, grain yield, and thousand kernels weight while mean plants samples for height for analysis of variance. The Least Significant Difference (LSD) was used to compare means at 5% and 1% level of significance.

2.3.2. GGE model

A GGE biplot displays genotype main effects (G) and genotype × environment effects (GE) from a two-way data table (Yan et al., 2000). GGE biplot was used to identify high-yielding and adapted genotypes as well as suitable test environments. The model for the GGE biplot was based on singular value decomposition (SVD) of the first two principal components as:

yij-μ-βj = ʎ_1 ₤_i1 ŋ_j2+ε_ij

Where Y_{ij} is the measured mean of genotype i in environment j, μ is the grand mean, β_j is the main effect of environment j, $\mu + \beta$_j being the mean yield across all genotypes in environment j, λ_1 and λ_2 are the singular values (SV) for the first and second principal component (PCA1 and PCA2) respectively, ξ_i1 and ξ_i2 are eigenvectors of genotype I for PCA1 and PCA2 respectively, η_1j and η_2j are eigenvectors of environment j, for PCA1 and PCA2 respectively, εij is the residual associated with genotype i in the j environment.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

The ANOVA for individual site and across sites are presented (Table 3) and (Table 4) respectively. There were highly significant differences among genotypes for grain yield for each site and highly significant differences among genotypes, environments, and GEI for all traits that is; days to heading, days to maturity, plant height, 1000 kernel weight, hectoliter weight, and grain yield. The significances differences for GEI indicates the inconsistency of genotypes performance over locations and strong influence of environmental effects on bread wheat genotypes. Different researchers (Kaya et al., 2002; Ahmadi et al., 2012; Farshadfar and Sadeghi, 2014; Hassan et al., 2017; Singh et al., 2019, Gadisa et al., 2020 Alemu et al., 2021; Gadisa et al., 2022; Abebe et al., 2022; 2023; Alemu et al., 2023) reported the existence of strong environmental effects on bread wheat genotypes for most of the traits including grain yield.

Table 3: ANOVA for grain yield (t ha^{-1}) in bread wheat geneotypes at each location

Source of variation	Df	AA20	KU20	HL20	AD20	AD21	AA21	KU21	SN21	HL21
		MSq	MSq	MSq	MSq	MSq	MSq	MSq	MSq	MSq
Genotypes	20	5.38***	0.87*	3.51***	0.27*	0.58**	2.79***	1.55*	3.02***	1.48***
Rep	2	2.59*	0.11	0.62	0.34	1.73***	0.26	1	0.51**	0.8***
Block	6	0.64	0.21	0.37	0.08	0.31	0.15	0.33	0.31	0.27*
Rep: Block	12	0.14	0.49	0.14	0.08	0.24	0.44**	0.48	0.32	0.13
Residuals	22	0.41	0.32	0.36	0.11	0.16	0.11	0.57	0.44	0.08

Table 4: Combined ANOVA for agronomic, yield, and yield components in bread wheat genotypes

Source variation	Df	DTH	DTM	PTH	TKW	GYLD
		MS	MS	MS	MS	MS
Loc	8	973.11***	9755.7***	3331.4***	1297.89***	77.23***
Rep	2	8.04	2.6	26.3	1.71	1.25*
Block	6	79.45***	38.7***	92.4***	96.33***	2.84***
Genotypes	20	288.98***	98***	191.6***	239.08***	5.76***
LocxRep	16	3.81	5.2	50.8***	28.12**	0.84***
Locsxgenotypes	160	18.98***	21.4***	31.6***	45.82***	1.62***
Residuals	354	4.19	3.5	15.4	11.7	0.286

Note, Signif. Codes: 0 '***' 0.001 '**' 0.01 '*' 0.05. DTH: days to 50% heading, DTM: days to 90% maturity, PTH: Plant height, (cm); TKW: 1000 kernel weight (g), GYLD: grain yield (t ha^{-1})

3.2. Mean and range for grain yield and yield components

The genotypes' mean yields ranged from 2.35 t ha^{-1} (Hidasse) to 4.38 t ha^{-1} (BW172862), with a mean of 3.79 across all environments. BW172862 (4.38 t ha^{-1}) had the highest grain yield, followed by EBW193416 (4.35 t ha^{-1}) BW172864 (4.29 t ha^{-1}) and EBW193414 (4.27 t ha^{-1}). The rank of the genotypes changed as the test environments changed, indicating the existence of cross-over GEI. The result is consistent with the previous reports by (Gadisa et al., 2020; Gadisa et al., 2021; Alemu et al., 2021; Alemu et al., 2023) of varying genotype ranks across various environments. However, in most of the test environments, the genotypes viz. BW172862 (4.38 t ha^{-1}) and EBW193416 (4.35 t ha^{-1}) are the highest-yielding and the most stable Therefore, these advanced genotypes are the most adapted genotypes. Therefore, BW172862 and EBW193416 were chosen as the best parent for wheat population improvement in 2023 for medium agro-ecology of Ethiopia. "BW172862 (4.38 t ha^{-1})" outperformed the standard check (Lemu) and the locally susceptible check (Hidasse) in terms of yield by 24.43% and 86.38%, respectively. The second candidate genotype EBW193416 (4.35 t ha^{-1}) also produced 23.58% and 85.1% yield advantage over the standard check (Lemu) and rust susceptible local check (Hidasse), respectively. (Table 5).

Days to 50% heading ranged from 60.2 (EBW193417) to 70.7 days (EBW192444) with an average value of 64.6 days (Table 6). Days to 90% maturity likewise ranged from 120 days to 126 days for EBW193412 and EBW192444, respectively, with an average value of 122.54 days indicating that the tested genotypes were early to medium maturing. According to Goodwin et al. (2018), plant height has a

Table 5: Mean grain yield (t ha^{-1}) of 19 genotypes and 2 checks tested in 2020 and 2021 cropping seasons

Entry	Genotype	AD20	AD21	AA20	AA21	HL20	HL21	KU20	KU21	SN21	Mean
1	Lemu	2.72	3.29	4.62	2.02	5.06	3.48	3.89	3.40	3.20	3.52
2	EBW193408	3.34	3.82	6.98	3.66	2.30	2.51	3.27	4.13	2.76	3.64
3	EBW193410	2.85	4.11	7.06	4.99	3.39	2.86	3.66	4.59	4.20	4.19
4	EBW193411	3.74	3.77	5.75	3.24	2.34	1.38	3.22	4.08	1.95	3.27
5	EBW193412	3.18	3.82	7.29	4.45	1.93	2.59	4.11	4.58	3.56	3.94
6	EBW193413	3.11	3.63	6.40	3.69	2.67	2.47	3.98	4.26	2.84	3.67
7	EBW193414	3.65	4.17	7.08	4.59	2.96	3.51	4.04	4.33	4.10	4.27
8	EBW193415	3.54	3.86	7.43	3.54	1.81	1.88	2.35	4.62	4.18	3.69
9	EBW193416	3.84	3.98	7.80	4.97	2.71	2.92	4.07	5.09	3.79	4.35
10	EBW193417	3.21	3.13	5.79	3.70	2.56	2.20	4.43	3.58	2.87	3.50
11	EBW193418	3.43	3.39	7.15	4.60	3.19	2.49	4.66	5.03	4.11	4.23
12	EBW193419	3.24	3.81	4.87	4.84	3.31	2.35	3.27	3.51	4.00	3.69
13	EBW192444	3.26	3.60	5.80	3.89	4.14	3.20	3.65	4.79	2.57	3.88
14	EBW192455	2.88	3.50	3.70	2.68	4.44	1.56	3.15	3.41	2.77	3.12
15	EBW192466	3.25	3.39	6.11	4.22	5.19	3.45	4.23	3.97	2.63	4.05
16	EBW192471	3.39	3.90	5.37	2.81	4.17	2.10	4.20	4.09	1.48	3.50
17	EBW192477	3.04	3.12	6.96	3.29	4.30	3.12	3.95	4.64	2.74	3.90
18	BW172862	3.53	3.75	8.20	4.70	2.12	2.76	3.80	5.48	5.08	4.38
19	BW172864	3.52	4.01	8.67	4.24	2.50	3.21	4.49	3.82	4.14	4.29
20	BW172936	3.59	3.98	7.92	4.84	2.26	2.70	3.62	4.98	3.68	4.17
21	Hidasse	3.63	2.24	4.34	1.62	1.47	0.91	3.48	2.39	1.03	2.35
	Mean	3.33	3.63	6.44	3.84	3.09	2.55	3.79	4.23	3.22	3.79
	CV (%)	9.99	10.88	10. 04	8.45	19.49	11.25	15.1	17.87	20.59	14.11
	LSD (5%)	0.56	0.67	1.09	0.55	1.02	0.48	0.96	1.28	1.12	0.28

20AA: Asasa 2020; 21AA: Asasa2021; 20AD: Adet 2020; 21AD: Adet 2021; KU20: Kulumsa 2020; KU21: Kulumsa 2021; SN20: Sinana 2020; SN21: Sinana 2021 significant impact on wheat's plant architecture and yields potential. Low yields can be caused by both high and short wheat plants. Tall plants can result in lodging, which reduces yields directly, while short plants can crowd canopy leaves, slow photosynthetic rate, and have insufficient biomass to serve as an adequate "source" (Hedden, 2003). With a mean height of 89.41 cm, the semi-dwarf genotypes examined in this study had height ranging from 84.71 to 92.77 cm. The 1000 kernel weight also ranged from 29.34 g (EBW193408) to 36.04 g (EBW192444) with an average value of 32.98 g.

The grain Zn and Fe content for the advanced bread wheat genotypes are presented in Table 6. Grain Zn content ranged from 28.8 ppm to 48.1ppm. The grain Fe content also ranged from 31.5 ppm to 44.7 ppm. This result is in line with Joshi et al. (2010) who reported the range 32.6–34.8 ppm grain Zn content on the advanced bread wheat lines. The average Fe concentration was 36.07 ppm, and Zn concentration was 36.06 ppm for the test genotypes. More than 76.19% of tested genotypes exhibited grain Zn above the standard checks 32.1 ppm. But the standard check Lemu were scored highest grain Fe among the test genotypes. Oury et al. (2006) also reported that Zn values of 15–35 ppm and Fe concentrations of 20–60 ppm for a set of high-yielding genotypes though the lines were slightly different from the current study. This may be due to the processing (milling differences or the mode of application in respect to soil micronutrient contents). A huge number of wheat germplasm are being tested for grain Zn concentration and

Table 6: Average agronomic performance of 19 bread wheat genotypes and 2 standard checks tested across 5 locations in 2020 and 2021 cropping seasons

Sl. No.	Genotype	DTH (Days)	DTM (Days)	PHT (cm)	TKW (g)	GYLD (t ha^{-1})	Zn (PPM)	Fe (PPM)
1.	Lemu	66.8	124.01	89.49	29.80	3.52	31.5	46.0
2.	EBW193408	63.4	120.66	88.44	29.34	3.64	33.8	37.0
3.	EBW193410	64.0	122.38	89.73	35.70	4.19	33.6	33.2
4.	EBW193411	66.4	122.63	90.90	32.46	3.27	32.1	33.8
5.	EBW193412	60.7	120.37	84.71	32.53	3.94	37.8	32.6
6.	EBW193413	61.8	121.57	90.20	31.04	3.67	41.4	32.3
7.	EBW193414	65.5	123.26	86.73	33.26	4.27	34.5	32.1
8.	EBW193415	64.3	122.04	89.84	33.17	3.69	34.4	36.1
9.	EBW193416	64.8	121.12	88.97	30.07	4.35	37.2	44.7
10.	EBW193417	60.2	121.04	88.50	34.63	3.5	40.3	32.5
11.	EBW193418	63.7	123.19	88.52	34.33	4.23	31.9	31.5
12.	EBW193419	68.6	124.39	90.67	33.82	3.69	33.8	33.0
13.	EBW192444	70.7	126.30	92.77	36.04	3.88	38.9	33.0
14.	EBW192455	61.4	121.48	87.77	33.11	3.12	36.4	38.5
15.	EBW192466	65.3	123.88	91.23	35.71	4.05	43.4	39.4
16.	EBW192471	63.7	123.02	88.31	31.84	3.5	48.1	37.6
17.	EBW192477	64.0	122.63	89.73	35.13	3.9	32.8	36.9
18.	BW172862	63.4	122.58	86.62	34.26	4.38	28.8	35.5
19.	BW172864	67.1	123.00	90.23	31.69	4.29	35.2	35.9
20.	BW172936	65.6	122.03	89.72	31.67	4.17	39.2	37.7
21.	Hidasse	65.1	121.88	92.50	33.21	2.35	32.1	38.2
	Mean	64.6	122.54	89.41	32.98	3.79	36.06	36.07
	CV (%)	3.16	1.52	4.39	10.37	14.11	-	-
	LSD (5%)	1.09	0.99	2.10	1.83	0.28	-	-

DTH: Days to 50% heading; DTM: Days to 90% maturity; PHT: Plant height (cm); TKW: Thousand kernel weight (g); GYLD: Grain Yield (t ha^{-1})

their environmental interactions. Based on a range of reports and survey studies, the average grain Zn concentration of wheat in various countries ranges between 20–35 ppm, with high genetic variations and heritabilities for both grain Zn and Fe (Whitneyy and Rolfes, 2019). Therefore, based on disease resistance and agronomic superiority combined with grain Zn, grain Fe and grain yield the genotypes EBW193416 (Fe, 44 ppm; Zn, 37.20 ppm) and BW172862 (Fe, 35.50ppm; Zn, 28.80ppm), were selected as parents for cross breeding. Since the majority of the minerals (Fe and Zn) were eliminated during the milling process with wheat bran, future research should be done on the milling effect on the Fe and Zn concentration for a better suggestion.

3.3. GGE biplot pattern for elucidation of multivariate analysis in grain yield

The GGE biplot analysis used to partition the data in to PCA1 and PCA2 contributed 57.18% and 21.84% respectively, of the GGE sum of squares. The first two principal components for this model explained 79.02% of the data variability (Figure 1). The polygon is drawn by joining the genotypes # 8 (EBW193415), # 18 (BW172862), # 15 (EBW192466), # 1 (Lemu), # 14 (EBW192455), and # 21 (Hidasse) that are located farthest from the biplot origin so that all other genotypes are contained in the polygon. The vertex genotypes are the genotypes found at the polygon's corners. The vertex genotypes are either the best or poorest in one or more environments. According to Yan 2002; Yan and Tinker, 2006, the genotype at the vertex of the polygon performs best in the environment falling within the sectors. Environments and genotypes that lie within the same two dotted lines on which-won-where biplots share similar environmental and genotypic effect (Yan, 2014). The genotype # 18 (BW172862), # 9 (EBW193416), # 19 (BW172864) and # 20 (BW172936) performed best at environment KU20, SN21, AA21 and, AA20. Genotype # 21 (Hidasse), was performed worst in every testing environment. In environment HL20, genotypes # 1 (Lemu), # 15 (EBW192466), and # 14 (EBW192455) performed best.

GGE of genotypes for both average yield and stability performance over environments were indicated for twenty-one genotypes using the average environment coordination (AEC) method in Figure 2. The line passing through the biplot origin is called the average environment coordinate (AEC). Closer to concentric circle indicates higher mean yield. The line which passes through the origin and is perpendicular to the AEC with double arrows represents the stability of genotypes. A genotype that has a shorter absolute length of projection in either of the two directions of AEC ordinate (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. The best genotype can be defined as the one with the highest yield and stability across environments. As Yan and Tinker (2006), explained the GGE biplot shows that genotypes with high PC1 scores have high mean yield and whereas those having low PC2 scores have stable yield across environments. The genotypes (# 18) BW172862, **(#19)** BW172864, (#9) EBW193416**,** (#3) EBW193410, (# 7) EBW193414 and (# 11) EBW193418 had the short projection from the AEC x-axis indicating the highest mean yield and stability across test environments, as a result of which they were comparatively closer to the concentric circle. On the other hand the genotypes, (# 10) EBW193417, (# 6) EBW193413, and (# 12) EBW193419 were stable across the test environments and scored below the mean grain yield (poor yielding). The genotypes, (# 8)

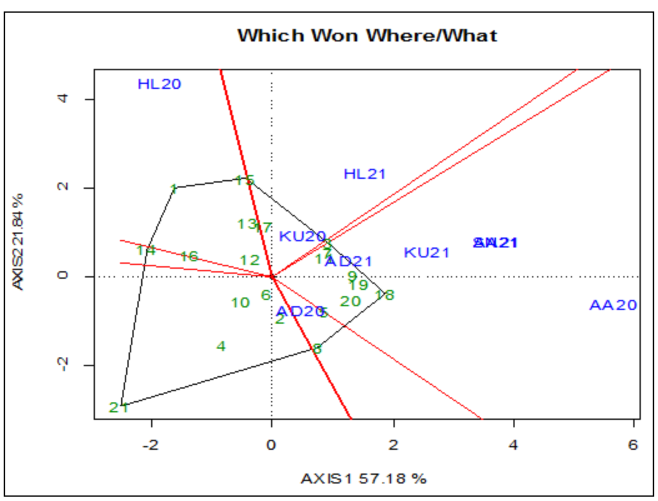

Figure 1: GGE biplot analysis of the polygon view of the environments and genotypes for the PC1 and PC2 (the candidate varieties are #9 and # 18)

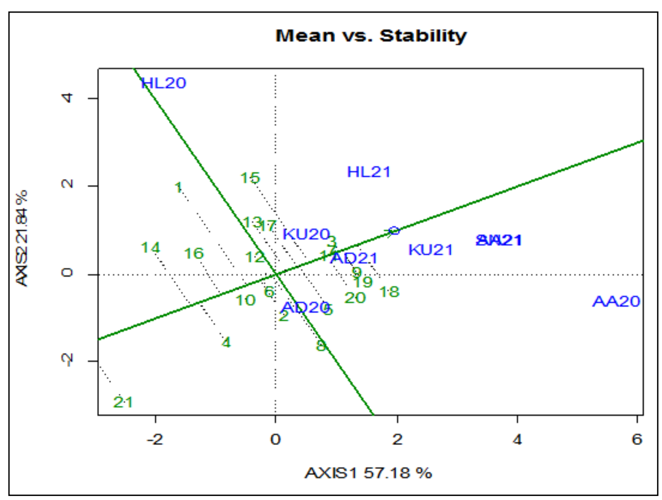

Figure 1: GGE biplot analysis of the polygon view of the environments and genotypes for the PC1 and PC2 (the candidate varieties are #9 and # 18)

EBW193415, (# 1) Lemu, and (# 15) EBW192466 which had the longest projection from the AEC x-axis which indicate highly unstable or there is high interaction of genotypes with the environment. In all test environments, the genotypes EBW192455 (# 14) and Hidasse (# 21) had the lowest average mean yield and unstable. Based on high yield and stability; the genotypes (# 18) BW172862 and **(#** 19**)** BW172864, were selected as the genotypes of interest (i.e., adaptable or higher-yielding).

3.4. The reaction of bread wheat genotypes against yellow and stem rusts

Mean severity and reaction of advanced wheat genotypes against yellow and stem rusts, were given in Tables 7 and 8. The severity and reaction of the genotypes were slightly different for each environment for the two rusts. The degree of susceptibility to yellow rust varied across locations due to variation in virulence spectra of the pathogen and climatic

Table 7: severity (%) and reaction of bread wheat genotypes against yellow rust at different environment

Genotype	Entry	20SN	20KU	20AA	21HL	21SN	AA21	21KU
Lemu	G1	30S	50S	60S	50S	40S	40S	50S
EBW193408	G2	50S	5MR	20MRMS	30S	30S	40S	20MSS
EBW193410	G3	10MS	5MR	15MR	30S	30S	30S	20MSS
EBW193411	G4	20MS	50S	40MS	50S	40S	50S	20MSS
EBW193412	G5	20S	10MS	10MR	20MS	40S	30S	10MSS
EBW193413	G6	50S	5MR	15MR	20MS	30S	30S	20MSS
EBW193414	G7	20MS	10MS	15MR	40S	15S	40S	10MSS
EBW193415	G8	30S	60S	10MR	20MS	10MSS	60S	5MRMS
EBW193416	G9	20MS		20MR	10MS	30S	20MSS	1MRMS
EBW193417	G10	15MS	10MRMS	30MS	40S	50S	50S	25MS
EBW193418	G11	30S	40S	25MRMS	30S	40S	50S	20MSS
EBW193419	G12	30S	60S	50S	80S	30S	30S	50S
EBW192444	G13	10S	1MR	25MRMS	40S	30S	40S	30S
EBW192455	G14	10MS	60S	50MSS	60S	60S	60S	50S
EBW192466	G15	10MS	1MR	15MR	20MS	30S	20S	5MSS
EBW192471	G16	20S	5MS	30MS	40S	50S	40S	15MSS
EBW192477	G17	30S	1MR	10MR	20MS	30S	20MSS	10MSS
BW172862	G18	20MS	1MR	20MR	20MS	10MSS	20MSS	5MRMS
BW172864	G19	10MS	5MR	20MR	20MS	10MSS	30S	5MRMS
BW172936	G20	30S	1MR	10MR	10MS	20S	20MSS	5MRMS
Hidasse	G21	10MS	40S	40S	60S	60S	70S	40S

20AA: Asasa 2020; 21AA: Asasa 2021; KU20: Kulumsa 2020; KU21: Kulumsa 2021; SN20: Sinana 2020; SN21: Sinana 2021

Table 8: Severity (%) and reaction of bread wheat genotypes against stem rust at different environments

Genotype	Entry	20SN	20KU	20AA	21SN	AA21	21KU
Lemu	1	30S	15MSS	20MSS	40S	40S	5MS
EBW193408	2	70S	15S	15MS	25S	30S	10S
EBW193410	3	60S	10S	10MSS	10MS	10MSS	5MSS
EBW193411	4	50S	1MRMS	20MSS	20S	20MSS	10MRMS
EBW193412	5	60S	0	20MS	30S	15MS	15S
EBW193413	6	80S	5MR	10MSS	30S	20MSS	5MRMS
EBW193414	7	60S	20S	30MSS	30S	30S	10MSS

Table 8: Continue...

Genotype	Entry	20SN	20KU	20AA	21SN	AA21	21KU
EBW193415	8	50S	1MR	70S	60S	20MSS	20S
EBW193416	9	25MS	5MS	10MSS	20S	10MSS	1MS
EBW193417	10	60S	15MS	10MS	30S	30S	10MSS
EBW193418	11	70S	0	40MSS	40S	30MSS	20MSS
EBW193419	12	70S	0	30MSS	25S	10MRMS	1MR
EBW192444	13	70S	30S	50S	40S	40S	5MS
EBW192455	14	70S	5MS	20MSS	30S	30S	0
EBW192466	15	70S	10MRMS	80S	60S	50S	10MSS
EBW192471	16	70S	30S	70S	80S	50S	30S
EBW192477	17	70S	30S	70S	50S	30S	20S
BW172862	18	20MS	5MS	10MSS	30S	20MSS	5MRMS
BW172864	19	25S	30S	30MSS	80S	30S	10MSS
BW172936	20	40S	5MS	5MS	15S	15MS	5S
Hidasse	21	70S	80S	90S	80S	70S	50S

20AA: Asasa 2020; 21AA: Asasa 2021; KU20:Kulumsa 2020; KU21: Kulumsa 2021; SN20: Sinana 2020; SN21: Sinana 2021

conditions for the disease pressure (Wubishet et al., 2015). In this study, high yellow and stem rust rates were recorded for most of the genotypes at each experimental site. The findings indicate that the yield potential of the genotypes were influenced by the disease pressure at each location. Hence emphasis should be given to resistance to these diseases during wheat genotype selection or screening for yield at the respective location. Genotypes EBW193416 and BW172862 relatively showed lower severity rates at each testing environment.

4. CONCLUSION

BW172862, BW172864, EBW193416, EBW193410, EBW193414 and EBW193418 were identified as the top-yielding, and stable genotypes across the ten environments. However, in most test situations, BW172862 and EBW193416 are the highest-yielding and most stable genotypes. So they were proposed as parent genotypes advanced for crossing block. "BW172862 outperformed the standard check (Lemu) and the locally susceptible check (Hidasse) in yield by 24.43% and 86.38%, respectively. EBW193416 likewise produced 23.58% and 85.1% yield advantage over the standard check (Lemu) and rust disease susceptible local check (Hidasse), respectively.

5. ACKNOWLEDGMENT

We acknowledge EIAR for their grateful role in facilitating the study, CIMMYT for providing the planting materials, and the Harvest Plus project for providing financial support.

6. REFERENCE

Abebe, D., Gadisa, A., Negash, G., Alemu, D., Habtemariyam, Z., Tafesse, S., Rut, D., Dawit, A., Zerihun, T., Bayisa, A., Abebe, G., 2022. Stability and performance evaluation of advanced bread wheat (*Triticum aestivum* L.) genotypes in optimum areas of Ethiopia. International Journal of Bio-resource and Stress Management 14(1), 019–032.

Ahmadi, J., Mohammadi, A., Mirak, T.N., 2012. Targeting promising bread wheat (*Triticum aestivum* L.) lines for cold climate growing environments using AMMI and SREG GGE biplot analyses. Journal of Agricultural Sciences and Technology 14(3), 645–657.

Alemu, D., Gadisa, A., Berhanu, S., Negash, G., Abebe, D., Tafesse, S., Habtemariam, Z., Dawit, A., Bayisa, A., Ruth, D., Yewubdar, Sh., Abebe, G., Demeke, Z., Bedada, G., Ayele, B., Bekele, A., 2023. Genotype×Environment interaction and stability analysis using GGE biplot for grain yield of bread wheat (*Triticum aestivum*) genotypes under low moisture stress areas of Ethiopia. International Journal of Bio-resource and Stress Management, 14(7), 1089–1098. HTTPS://DOI.ORG/10.23910/1.2022.3570.

Alemu, G., Geleta, N., Dabi, A., Delessa, A., Solomon, T., Duga, R., 2021. Stability models for selecting adaptable and stable bread wheat (*Tritium aestivum* L.) varieties for grain yield in Ethiopia. Journal of Agricultural Science and Engineering 7(1), 14–22.

Anonymous, 2012. The World Health Report. Geneva, 668 Switzerland. Available at http://www.who.int/about/licensing/copyright_form/en/index.html. Accessed on

24th January, 2024.

Badebo, A., Bekele, E., Bekele, B., Hundie, B., Degefu, M., Tekalign, A., Ayalew, M., Ayalew, A., Meles, K., Abebe, F., 2008. Review of two decade of research on diseases of small cereal crops in Ethiopia. In: Abreham Tadesse (Ed.), Increasing crop production through improved plant protection. Proceedings of the 14th annual conference of the plant protection society of Ethiopia (ppse). 19–22. December 2006. Addis Ababa Ethiopia. Pp. 375–429.

Belete, A., Dillon, J.L., Anderson, F.M., 1991. Development of agriculture in Ethiopia since the 1975 land reform. Agricultural Economics 6(2), 159–175.

Dabi, A., Alemu, G., Geleta, N., Delessa, A., Solomon, T., Zegaye, H., Asnake, D., Asefa, B., Duga, R., Getamesay, A., Zewudu, D., Tadesse, Z., Girma, B., Badebo, A., Abeyo, B., 2021. Genotype×environment interaction and stability analysis for grain yield of bread wheat (*Triticum aestivum*) genotypes under low moisture stress areas of Ethiopia. American Journal of Plant Biology 6(3), 44–52. doi: 10.11648/j.ajpb.20210603.12.

Delesa, A., Dabi, A., Alemu, G., Geleta, N., Solomon, T., Zegeye, H., Duga, R., Asnake, D., Asefa, B., Tadesse, Z., Getamesay, A., 2023. Stability and performance evaluation of advanced bread wheat (*Triticum aestivum* L.) genotypes in low to mid altitude areas of Ethiopia. International Journal of Bio-resource and Stress Management 14(1), 019–032.

Effa, K., Fana, D.M., Nigussie, M., Geleti, D., Abebe, N., Dechassa, N., Anchala, C., Gemechu, G., Bogale, T., Girma, D., Berisso, F.E., 2023. The irrigated wheat initiative of Ethiopia: a new paradigm emulating Asia's green revolution in Africa. Environment, Development and Sustainability. https://doi.org/10.1007/s10668-023-03961-z.

Farshadfar, E., Sadeghi, M., 2014. GGE biplot analysis of genotype×environment interaction in wheat-agropyron disomic addition lines. Agricultural Communications 2(3), 1–7.

Gadisa, A., Alemu, D., Negash, G., Tafesse, S., Abebe, D., Rut, D., Habtemariam, Z, Dawit, A., Abebe, G., Bayisa, A., Demeke, Z., Bekele, G.A., Ayele, B., Bedada, G., 2020. Development of bread wheat (*Triticum aestivum* L.) varieties for high moisture areas of Ethiopia: A G×E Interaction and stability analysis for grain yield. Ethiopian Journal of Crop Sciences 8(1), 87–104.

Goodwin, A.W., Lindsey, L.E., Harrison, S.K., Paul, P.A., 2018. Estimating wheat yield with normalized difference vegetation index and fractional green canopy cover. Crop, Forage & Turfgrass Management 4(1), 1–6.

Hassan, K., Ali, A.A., Mohtasham, M., Hassan, G., Tahmasb, H., Mohammad, A., 2017. Evaluation of adaptability in bread wheat genotypes under dryland conditions in tropical and subtropical locations. Journal of Research in Ecology 5(2), 948–957.

Hedden, P., 2003. The genes of the Green Revolution. Trends Genet 19(1), 5–9.

Hodson, D.P., Jaleta, M., Tesfaye, K., Yirga, C., Beyene, H., Kilian, A., Carling, J., Disasa, T., Alemu, S.K., Daba, T., Misganaw, A., Negisho, K., Alemayehu, Y., Badebo, A., Abeyo, B., Erenstein, O., 2023. Ethiopia's transforming wheat landscape: tracking variety use through DNA fingerprinting. Science Reports 10(1), 18532. doi: 10.1038/s41598-020-75181-8.

Joshi, A.K., Crossa, J., Balasubramaniam, A., Chand, R., Trethowan, R., Vargas, M., Ortiz-Monasterio, I., 2010. Genotype×environment interaction for zinc and iron concentration of wheat 529 grain in eastern Gangetic plains of India, Field Crops Research 116(3), 268–277.

Kaya, Y., Palta, C., Taner, S., 2002. Additive main effects and multiplicative interactions analysis of yield performances in bread wheat genotypes across environments. Turkish Journal of Agriculture and Forestry 26, 275–279.

Negash, G., Gadisa, A., Alemu, D., Tafesse, S., 2022. Review on restrospects and prospects of breeding and genetics research in Ethiopia. In: Negash, G., Taye, T., Diriba G. (Eds.), Revitalizing the Ethiopian wheat sector: progresses and challenges of wheat research and seed production. Proceeding of national wheat research workshop, 25-26 may 2021, EIAR HQ, Addis Ababa, Ethiopia.

Nigus, M., Shimelis, H., Mathew, I., Abady, S., 2022. Wheat production in the highlands of Eastern Ethiopia: opportunities, challenges and coping strategies of rust diseases. Acta Agriculturae Scandinavica, Section B-Soil & Plant Science 72(1), 563–575.

Oury, F.X., Leenhardt, F., Remesy, C., Chanliaud, E., Duperrier, B., Balfouriera, F., Charmet, G., 2006. Genetic variability and stability of grain magnesium, zinc and 564 iron concentration in bread wheat. European Journal of Agronomy 25(2), 177–185.

Borrill, P., Connorton, J.M., Balk, J., Miller, A.J., Sanders, D., Uauy, C., 2014. Biofortification of wheat grain with iron and zinc: integrating novel genomic resources and knowledge from model crops Front. Plant Science 5, 53. doi: 10.3389/fpls.2014.00053.

Praharaj, S., Skalicky, M., Maitra, S., Bhadra, P., Shankar, T., Brestic, M., Hejnak, V., Vachova, P., Hossain, A., 2021. Zinc biofortification in food crops could alleviate the zinc malnutrition in human health. Molecules 26(12), 3509. https://doi.org/10.3390/molecules26123509.

Rosegrant, M.W., Agcaoili, M., 2010. Global food demand, supply, and price prospects. International food policy research institute, Washington DC, mimeographed.

Saha, S., Chakraborty, M., Padhan, D., Saha, B., Murmu, S., Batabyal, K., Seth, A., Hazra, G.C., Mandal, B., Bell, R.W., 2017. Agronomic biofortification of zinc in rice: Influence of cultivars and zinc application methods on grain yield and zinc bioavailability. Field Crops Research 210, 52–60. https://doi.org/10.1016/j.fcr.2017.05.023.

Semahegn, Y., Shimelis, H., Laing, M., Mathew, I., 2021. Farmers' preferred traits and perceived production constraints of bread wheat under drought-prone agro-ecologies of Ethiopia. Agriculture and Food Security 10(18).

Senbeta, A.F., Worku, W., 2023. Ethiopia's wheat production pathways to self-sufficiency through land area expansion, irrigation advance, and yield gap closure. Heliyon 9 e20720. 2405–8440. DOI: 10.1016/j.heliyon.2023.e20720.

Shiferaw, B., Kassie, M., Jaleta, M., Yirga, C., 2014. Adoption of improved wheat varieties and impacts on household food security in Ethiopia. Food Policy 44, 272–284.

Singh, C., Gupta, A., Gupta, V., Kumar, P., Ramadas, S., Tyagi, B.S., Singh, G., Chatrath, R., Singh, G.P., 2019. Genotype×environment interaction analysis of multi-environment wheat trials in India using AMMI and GGE biplot models. Crop Breeding and Applied Biotechnology 3, 309–318.

Tadesse, W., Zegeye, H., Debele, T., Kassa, D., Shiferaw, W., Solomon, T., Negash, T., Geleta, N., Bishaw, Z., Aseffa, S., 2022. Wheat production and breeding in ethiopia: Retrospect and prospects. Crop Breeding, Genetics and Genomics 4(3), e220003. https://doi.org/10.20900/cbgg20220003.

Whitney, E., Rolfes, S.R., 2019. Understanding nutrition (15th Edn.). Thomson Wadsworth, USA, IBSN-10: 1-337.

Yan, W., 2002. Singular value partitioning for biplot analysis of multi-environment trial data. Agronomy Journal 94, 990–996.

Yan, W., 2001. GGE biplot-A windows application for graphical analysis of multi-environment trial data and other types of two-way data. Agronomy Journal 93(5), 1111–1118.

Yan, W., 2014. Crop variety trials: data management and analysis; John Wiley & Sons, Blackwell: Hoboken, NJ, USA; ISBN 978-1-118-68856-4.

Yan, W., Tinker, N.A., 2006. Biplot analysis of multi-environment trial data: principles and applications. Canadian Journal of Plant Science 86, 623–645. http://dx.doi.org/10.4141/P05-169.

Yan, W., Hunt, L.A., Sheng, Q., Szlavnics, Z., 2000. Cultivar evaluation and mega environment investigation based on the GGE biplot. Crop Science 40, 597–605.

Yan, W., Kang, M.S., 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton, ISBN: 978-0-8493-1338-4.