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

IJBSM August 2023, 14(8):1141-1153 Print ISSN 0976-3988 Online ISSN 0976-4038 Article AR3574

Research Article Natural Resource Management

DOI: HTTPS://DOI.ORG/10.23910/1.2023.3574

Climate Smart Bread Wheat (*Triticum aestivum* L.) Variety Development for Optimum Moisture Areas of Ethiopia

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ABSTRACT

A study was undertaken during the 2017–18 to 2018–19 cropping seasons at at eleven locations and/or seventeen environments in optimum moisture areas of Ethiopian to identify stable genotypes with high grain yield and release as a variety for optimum-moisture environments. Alpha-lattice design with three replications was used. The combined ANOVA revealed very highly significant differences ($p \leq 0.001$) among genotypes, environments, and GEI for yield and its components. The environment sum of squares contributed more than the genotype and GEI sum of squares for the total variance of all traits. When we consider the overall mean for grain yield, genotype ETBW8751 (5.12 t ha^{-1}) the highest value followed by ETBW9554 (5.10 t ha^{-1}) whereas the lowest grain yield was obtained from the genotype ETBW8804 (3.67 t ha^{-1}). GGE and AMMI analysis explained almost similar amounts of variation; however, AMMI still show a slightly greater proportion than GGE during our study. According to AMMI and GGE analysis genotype 21 (ETBW9553) was more stable as well as high yielding followed by 22 (ETBW9554) and 2 (ETBW8751. Conversely, 15 (ETBW9547) was unstable, but high yielding. Hidasse had low yields but was unstable. ETBW9554 was validated on farmers' fields and recommended for registration as a commercial variety and finally released in 2020 with its designated local name "Boru" for commercial production for mid to highland agro-ecologies in Ethiopia.

KEYWORDS: AMMI, bread wheat, environment, genotype, GGE, grain yield

***Citation* (VANCOUVER):** Alemu et al., Climate Smart Bread Wheat (*Triticum aestivum* L.) Variety Development for Optimum Moisture Areas of Ethiopia. *International Journal of Bio-resource and Stress Management,* 2023; 14(8), 1141-1153. HTTPS://DOI.ORG/10.23910/1.2023.3574.

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 19th May 2023 RECEIVED in revised form on 14th July 2023 ACCEPTED in final form on 05th August 2023 PUBLISHED on 21st August 2023

1. INTRODUCTION

Bread or common wheat (*Triticum aestivum* L.) is the most widley cultivated cereal crop which has primary significance for human nutrition worldwide (Abdelaal et al., 2018; Hossainet et al., 2018). The yield of bread wheat should be increased in parallel with the increasing population (Karaman, 2019). In Ethiopia wheat is produced on a total area of 1.87 mha of land with a total production of 5.8 mt with average productivity of 3.1 t ha^{-1} under rain fed (CSA, 2022, which is relatively lower than the attainable yield of the crop, reaching up to 5 t ha^{-1} (Zegeye et al., 2020). On the other hand, Ethiopian government is determined to fill the demand gap through production of wheat during off-season in existing environments by using irrigation and expansion of wheat production in nontraditional wheat growing areas specially in lowlands (Abebe et al., 2023; Tadesse et al., 2022).

Biotic stress susch as diseases, insect pests, weedd soil fertility, erratic rainfall, sub-optimal use of agronomic practices, and increased costs of inputs are among limiting factors of wheat production in the low to mid altitude areas of Ethiopia (Habte et al., 2014; Shiferaw et al., 2014; Brasesco et al., 2019; Hodson et al., 2020; Adugnaw and Dagninet, 2020). Therefore, breeding for grain yield, disease resistance and wide adaptability has become priority of the national wheat improvement program in the country (Alemu et al., 2019; Gadisa et al., 2022). Bread wheat is the most widely adapted compared to other cultivated species and this situation favoured the crop to be one of the most cultivated food crops worldwide (Rajaram, 2005).

Grain yield is one of the traits of importance and breeders often seek to identify genotypes with high and stable yield across environments (Forgone, 2009). Wheat genotypes should be tested in multi-environment yield trials to determine grain yield, stability, GEI, adaptability, and to identify a potential candidate to release for commercial cultivation (Kaya et al., 2006). Stable and high yielding varieties under different environmental conditions would be the most important step in any breeding program before release as a variety (Gadisa et al., 2020). Determining the stability of genotypes helps in identifying potential genotypes to be released with broad and specific adaptability (Aktas, 2016 ; Husnu, 2016; Sajid and Mohammed, 2018).

For the development of stable varieties, there must be a presence of large genetic diversity in the populations under study (Gupta, et al., 2022). From these populations, one can identify genotypes showing wide stability under different environmental conditions (Gupta et al., 2022). This is performed by understanding the interaction of genotype with the environment (Regmi et al., 2021). Genotype by Environment Interaction (GEI) is a phenomenon related to the inconsistent performance under diverse environmental conditions, and it plays an important role in the performance of genotypes under different environments (Bhartiya et al., 2018). G×E interaction reduces the efficiency of selection and accuracy of varietal recommendation. Due to this interaction of the genotype by environment, it is necessary to study the genotype in the environment interaction before introducing new high-yielding genotypes with high stability in different environments (Gupta et al., 2022).

Improving the adaptability of crop varieties to a changing environment supported by appropriate crop management strategies is the working principle worldwide in ensuring crop productivity (Blum, 2011; Farooq et al., 2015; Stroosnijder et al., 2012; Wasson et al., 2012). The objective of this study was to identify stable genotypes with high grain yield and release as avariety for optimum moisture environments.

2. MATERIALS AND METHODS

2.1. Planting materials and test locations

Twentyeight advanced bread wheat genotypes were evaluated against two checks ('Wane' and Hidase') at eleven locations and/or seventeen environments in optimum moisture areas of Ethiopian in 2017–18 and 2018–19 cropping seasons. Sowing and harvesting of tested materials were carried out from first week of June to mid-July and from last week of October to last week of November, respectively. Description of eleven test locations and advanced bread wheat genotypes were presented in Tables 1 and 2 and figure 1, respectively.

2.2. Experimental layout

An alpha lattice design with three replications was used. Every plot had six rows of 2.5 m by 1.2 m (3m2) long with 0.2 m inter-row spacing. The seeding rate was 150 kg ha^{-1} while fertilizer and other agronomic practices were applied according the recommendation of each location.

Table 1: List of test locations and their description

Code	1	2	3	4	5	6	7	8	9	10	11
Location	Kulumsa	Arsi Robe	Asasa	Bekoji	Areka	Shambu	Debra Zeit	Holeta	Adet	Enawari	Aweli Gera
Altitude	2200	2420	2340	2780	2230	2503	1900	2400	2216	2650	2490
Rainfall (mm)	820	890	644	1020	1290	-	851	1044	1250	878	-

Table 2: List of bread wheat lines and varieties tested across locations

Code	Name	Pedigree
G1	Wane	SOKOLL/EXCALIBUR
G2	ETBW 8751	SUP152//ND643/2*WBLL1
G3	ETBW 8858	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
G4	ETBW 8870	WAXWING*2/TUKURU//KISKADEE #1/3/FRNCLN
G5	ETBW 8802	CHAM-4/SHUHA'S'/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB/4/BOW'S"
G6	ETBW 8991	SUP152//ND643/2*WBLL1
G7	ETBW 8862	C80.1/3*BATAVIA//2*WBLL1/3/C80.1/3*QT4522//2*PASTOR/4/WHEAR/SOKOLL
G8	ETBW 8804	TURACO/CHIL/6/SERI 82/5/ALD'S'/4/BB/GLL//CNO67/7C/3/KVZ/TI
G9	ETBW 8996	FALCIN/AE.SQUARROSA (312)/3/THB/CEP7780//SHA4/LIRA/4/FRET2/5/DANPHE #1/11/CROC_1/ AE.SQUARROSA(213)//PGO/10/ATTILA*2/9/KT/BAGE//FN/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA
G10	ETBW 8583	MINO/898.97/4/PFAU/SERI.1B//AMAD/3/KRONSTAD F2004
G11	ETBW 8668	BAVIS*2/3/ATTILA/BAV92//PASTOR
G12	ETBW 8595	BAVIS*2/3/ATTILA/BAV92//PASTOR
G13	ETBW 8684	PASTOR//HXL7573/2*BAU/3/WBLL1/4/1447/PASTOR//KRICHAUFF
G14	ETBW 9486	FRANCOLIN#1/3/PBW343*2/KUKUNA*2//YANAC/4/KINGBIRD#1//INQALAB 91*2/TUKURU
G15	ETBW 9547	MUTUS*2/AKURI//MUTUS*2/TECUE #1
G16	ETBW 9548	REEDLING #1//KFA/2*KACHU
G17	ETBW 9549	KFA/2*KACHU/3/KINGBIRD #1//INQALAB 91*2/TUKURU/4/KFA/2*KACHU
G18	ETBW 9550	KFA/2*KACHU*2//WAXBI
G19	ETBW 9551	KFA/2*KACHU/4/KACHU #1//PI 610750/SASIA/3/KACHU/5/KFA/2*KACHU
G20	ETBW 9552	KACHU#1/4/CROC_1/AE.SQUARROSA 205)//BORL95/3/2*MILAN/5/KACHU/6/KFA/2*KACHU
G21	ETBW 9553	MURGA/KRONSTAD F2004/3/KINGBIRD #1//INQALAB 91*2/TUKURU
G22	ETBW 9554	SAUAL/MUTUS/6/CNO79//PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7/7/CNO79 //PF70354/MUS/3/PASTOR/4/BAV92*2/5/FH6-1-7
G23	ETBW 9555	KFA/2*KACHU/5/WBLL1*2/4/BABAX/LR42//BABAX/3/BABAX/LR42//BABAX/6/KFA/2*KACHU
G24	ETBW 9556	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/PARUS/PASTOR
G25	ETBW 9557	SOKOLL/WBLL1/4/D67.2/PARANA 66.270//AE.SQUARROSA (320)/3/CUNNINGHAM
G26	ETBW 9558	BABAX/LR42//BABAX/3/ER2000/5/ATTILA/4/WEAVER/TSC//WEAVER/3/WEAVER/6/KA/NAC//TRCH
G27	ETBW 9559	CHIBIA//PRLII/CM65531/3/MISR *2/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07
G28	ETBW 9560	CHWINK/GRACKLE #1//FRNCLN
G29	ETBW 9561	TRAP#1/BOW/3/VEE/PJN//2*TUI/4/BAV92/RAYON/5/KACHU #1*2/6/KINGBIRD #1
G30	Hidasse	YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUAROSA(224)//OPATTA

2.3. Statistical analysis

Grain yield data were subjected to analysis of variance (ANOVA) for each environment separately, and combined analysis of variance was conducted to determine the effect of environment (E), genotype (G), and GEI. The SAS software version 9.3 and R Software were used for combined ANOVA, AMMI, and GGE biplot.

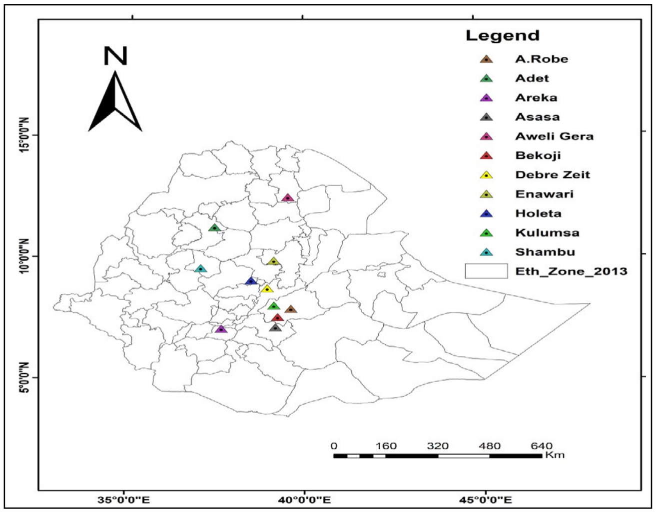

Figure 1: Location map of the study area

2.4. Stability analysis

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

2.5. AMMI analysis

The AMMI analysis was performed using the model suggested by Crossa et al. (1990):

$$Y_{ij}=\mu+G_i+E_j+\sum^{n}_{n=1}\lambda_n\alpha_{in}y_{jn}+e_{ijk}$$

Where is the yield of the genotype in the environment, μ is the grand mean, is the mean of the genotype minus the grand mean, is the mean of the environment minus the grand mean, is the square root of the Eigenvalue of the principal component analysis (PCA) axis, and are the principal component scores for PCA axis n of the genotype and environment and is the error term.

2.6. GGE biplot analysis

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

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

where is the mean for the genotype in the environment, is the grand mean is the main effect of environment j, and are the singular values of the 1st and 2nd principal components (PC1 and PC2), and are the PC1 and PC2 scores, respectively, for genotype, and are the eigenvectors for the environment for PC1 and PC2 and is the residual error term.

3. RESULTS AND DISCUSSION

The combined ANOVA given in Table 3 shows that the environment, genotype and GEI were highly significant (p<0.001) for all traits across environments in terms of grain yield, days to heading, days to maturity, plant height, thousand kernel weight, and test weight across.

The total sum of squares was divided into components to estimate the magnitude of GEI. For all measured traits, the explained percentage sum of the square for environments took the largest portion, accounting for 76.05% for grain yield, 80.72% for days to heading, 93% for days to maturity, 75.14% for plant height, 56.87% for thousand kernel weight and 81.58% for test weight (Table 4). An oversized sum of squares for environments indicated that the environment

Table 3: Combined analysis of variance of grain yield and agronomic traits for 30 bread wheat advanced genotypes evaluated at 17 environments

Source of variation	GYLD		DTH	DTM	TKW		PHT		HLW	
	Df	MS	MS	MS	Df	MS	Df	MS	Df	HLW
ENV	16	241.31***	4774.3***	20316.79***	12	10393.1***	11	8034.4***	10	2917.63***
REP(ENV)	34	3.900***	398***	99.2***	26	15.2***	24	71.3***	22	44.59***
GEN	29	6.57***	311.94***	252.2***	29	212.2***	29	620.5***	29	76.43***
ENV:GEN	464	2.21***	19.83***	36.97***	348	29.3***	319	41.3***	289	46.53***
PC1	44	6.96***	70.59***	267.70***	37	102.94***	39	111.54***	38	258.83***
PC2	42	4.56***	36.13***	95.55***	35	63.13***	37	59.58***	36	32.81***
PC3	40	3.46***	25.83***	45.18***	33	26.19***	35	46.17***	34	13.8^{ns}
PC4	38	2.63***	23.07***	40.75***	31	20.99***	33	40.00***	32	13.22^{ns}
Residuals	986	1.07	12.1	15.6	747	6.8	695	25.7	613	15.58
CV%	22.37		5.16	3.14	7.27		5.62		5.42	
Mean	4.62		67.36	125.9	35.89		90.27		72.78	

Where; ***: Very highly significant difference at p<0.001; GYLD: Grain yield; DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight; HLW: Hectoliter weight

Table 4: The contributions of the source of variation for tested characters

Source of variations	Contributions					
	GYLD	DTH	DTM	PHT	TKW	HLW
Environments	76.05	80.72	93	75.14	56.87	81.58
Genotype	3.75	9.56	2.09	15.26	17.19	3.40
Interactions	20.2	9.72	4.91	9.59	25.94	15.02

Where; GYLD: Grain yield, DTH: Days to heading, DTM: Days to maturity, PHT: plant height, TKW: Thousand kernel weight, and HLW: Hectoliter weight

was diverse, with large variations among environmental means causing most of the variation in grain yield and yield components of the bread wheat genotypes and contributing in large to the GEI. Similar findings have been reported on different crops including wheat by several authors (Kaya et al., 2002; Asrat et al., 2009; Farshadfar and Sadeghi, 2014; Yasin et al., 2014; Verma et al., 2015 Dawit et al., 2017; Jeberson et al., 2017; Gadisa et al., 2021; Abebe et al., 2022, Abebe et al., 2023), indicating environments and interaction effects are much more than the effect of genotypes. The highly significant environmental effect and its high variance component could be attributed to the large difference between the test locations in altitude, daily temperature, and a difference in both amount and distribution of rainfall. Similarly Abebe et al. (2023) indicated that the presence of GEI mainly attributed to different factors such as soil type, pests, altitude, rainfall, temperature and humidity. Dawit et al., 2017, Gadisa et al., 2019, Gadisa et al., 2020, Abebe et al., 2022, Abebe et al., 2023 reported that bread wheat grain yield was significantly affected by the environment. The amount of variance contributed by GEI (20.2%) was larger than that contributed by the genotype (3.75%) main effect. This result indicated that there was a noticeable GEI effect present in bread wheat multi-environment data, leading to a substantial difference in genotypic responses across the test environments. This result was in agreement with the reports of Somayeh et al. (2019) and Assefa et al. (2020). The presence of significant G×E interaction showed the differential performance of bread wheat genotypes across environments and unstable performance of genotypes across the different testing locations and complicates the selection and recommendation of genotypes in a specified environment. This implies a selected thirty bread wheat genotype might not exhibit constant phenotypic performance underneath totally different environmental conditions or different genotypes might respond otherwise to a particular environment.

3.1. *Mean performance of advanced bread wheat genotypes*

Kulumsa-2017 had the highest location mean yield (7.7 t ha^{-1}), followed by Kul-2018 (7.4 t ha^{-1}) and Asasa-2018 (6.6 t ha^{-1}), while Robe Arsi-2018 had the lowest location mean yield (2.5 t ha^{-1}), Robe Arsi-2017 (2.9 t ha^{-1}), and Bekoji-2017 (3.0 t ha^{-1}), indicating sub-seasonal variations among test environments (Figure 2). Thus, diverse climates across locations and years demonstrated the existence of significant heterogeneity in wheat productivity within the country's optimum moisture and highlands regions. Robe Arsi is a soggy environment with limited pre-season and seasonal rainfall, but Kulumsa is a high-yielding environment with plenty of pre-season and seasonal rainfall. Among the testing locations, eight yielded more than the location mean (4.6 t ha^{-1}). The remaining sites all produce less than the average yield (4.6 t ha^{-1}).

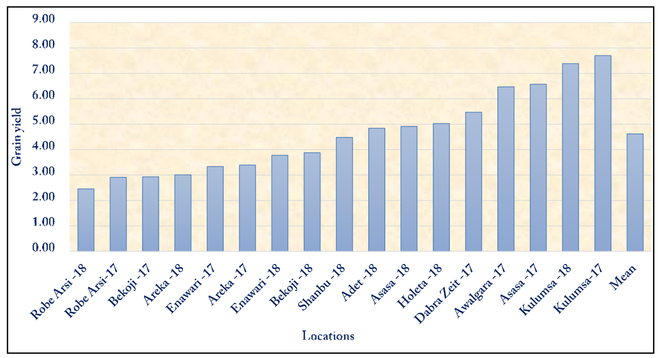

Figure 2: The mean performance of grain yield over environments

The genotype's average yield of grains varied with environment, ranging from 3.67 t ha^{-1} for ETBW8804 to 5.12 t ha^{-1} for ETBW8751 (Figure 3). Only two genotypes were ranked first in two locations: ETBW9557 in Enawari-2017 and Awaligara-2017 and ETBW9560 in the Robe Arsi-2017 and Bekoji-2017. This suggests that the genotypes' performance in terms of grain yield and other parameters showed more cross-over interaction (Kaya et al., 2006). According to Yan and Hunt (2001), differential yield ranking of genotypes across environments revealed that the G E interaction effect was of the crossover type

3.2. *Reaction to the foremost wheat diseases*

Foliar fungal diseases may cause important losses on yield and quality of (Simon et al., 2020). Despite the high stripe rust disease pressure, the genotype ETBW9554, and ETBW9553 exhibited adequate level of resistance to yellow rust disease (Table 5). Genotypes with slow rusting resistance would be quite important to achieve effective breeding for durable resistance to stripe rust (Nzuve et al., 2012). The standard check variety, *Wane* which was released in 2016 showed moderately susceptible reaction response to both yellow and stem rust while the the other local check,

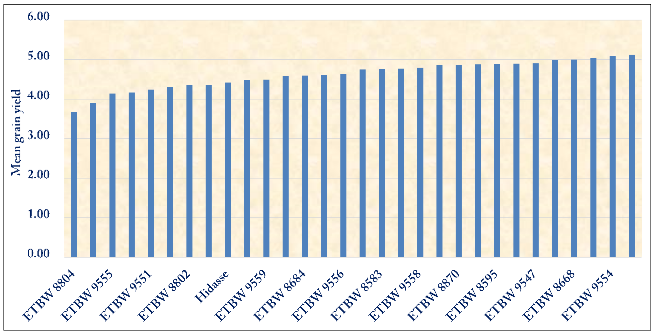

Figure 3: Mean performance of advanced bread wheat genotypes

Hidasse exhibited susceptible reactions to both yellow and stem rust (Table 5). The newly released bread wheat varieties are moderately resistant to stem rust, and septoria leaf blotch compared to the checks as well (Table 5).

3.3. AMMI analysis

The results of the analysis of variance of the AMMI model revealed that grain yield is significantly (p<0.001) affected by environment, genotype and genotype by environment interaction (Table 3) which explained 76.05%, 3.75% and 20.2% of the occurred variation, respectively (Table 4). Furthermore, Only 4 PCs out of the 16 components included in the AMMI model's breakdown of the GEI are significant, accounting for 73.45% of the square's overall amount. Several authors reported similar observations in bread wheat (Kaya et al., 2002, Ahmadi et al., 2012, Farshadfar and Sadeghi, 2014, Hassan et al., 2017, Singh et al., 2019, Gadisa et al., 2020, Gadisa et al., 2021, Abebe et al., 2022, Abebe et al., 2023, Gupta et al., 2023), durum wheat (Mohammadi et al., 2007), barley (Zerihun, 2012), maize (Haruna et al., 2017), sorghum (Rakshit et al., 2012), soybean (Asrat, 2009), mungbean (Thangavel et al., 2011), field pea (Tamene et al., 2013), chickpea (Assefa et al., 2017), cowpea (Tariku, 2018), linseed (Adane and Abebe, 2018), and cassava (Boakye et al., 2013) suggesting the existence of wide variability among environments, among genotypes and the possibility of selection for high yielding, best performing and stable genotypes. Results showed variability within the bread wheat grain yield of various genotypes at different locations and located that it would be ideal to decide on a bread wheat genotype with higher grain yield and higher stability. There are two basic AMMI biplots, the AMMI 1 biplot (Figure 4), and the AMMI 2 biplot (Figure 5).

Table 5: Reaction to the major wheat diseases

Disease	ETBW9554	ETBW9553	Wane (standard check)	Hidasse (local check)
Stem rust (%+ reaction)	5MR	TR	10MS	80S
Yellow rust (%+reaction)	5R	TMR	5MS	60S
Leaf rust (%+ reaction)	0	0	0	0
Septoria (00-99)	21	32	12	56

3.4. AMMI 1 biplot analysis

In AMMI 1 biplot, the differences among genotypes in terms of direction and magnitude along with the X-axis (yield) and Y-axis (IPCA 1 scores) are important. In the biplot display, genotypes or environments that appear almost on a perpendicular line of the graph had similar mean yields and those that fall almost on a horizontal line had similar interaction. The score and sign of IPCA1 reflect the magnitude of the contribution of both genotypes and environments to GEI, where scores near zero are characteristic of stability, whereas higher scores (absolute value) are considered unstable and specifically adapted to a certain environment. The characterization of each promising genotype to mean grain yield and contribution to GEI

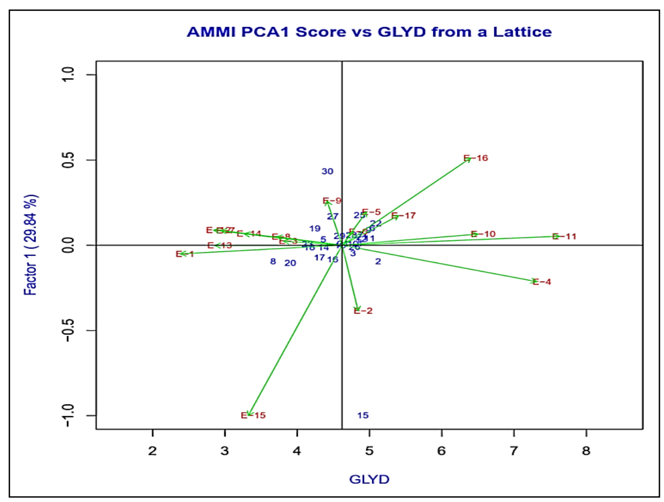

Figure 4: AMMI 1 biplot analysis for the mean grain yield (t ha^{-1}) with first IPCA score in 30 bread wheat genotypes from seventeen environments

by mean of IPCA1 (Figure 4) indicates that Genotype 11 (ETBW8668), 4 (ETBW8870), 3 (ETBW8858), 13 (ETBW8684), 23 (ETBW9555), 24 (ETBW9556), 19 (ETBW9551), 1 (Wane), 18 (ETBW9550), and 10 (ETBW8583) were near to zero IPCA1 by which was shown to have higher stability for yield than other genotypes and were the overall winner with less variable yield across the environments explaining its suitability as one of the

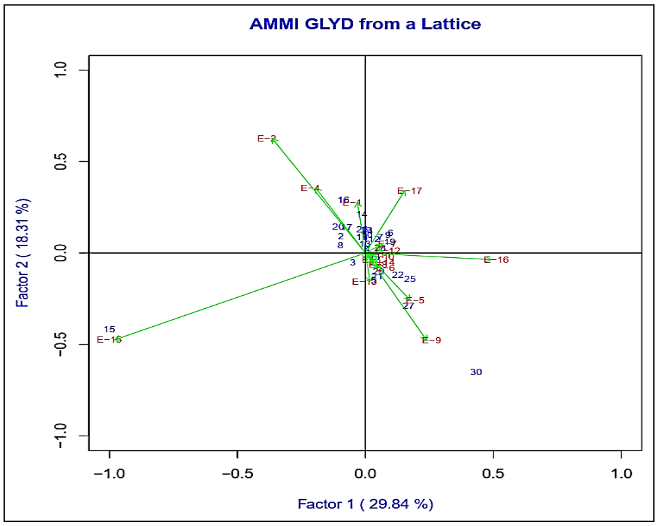

Figure 5: AMMI 2 Biplot of IPCA 1 against IPCA 2 for grain yield of 30bread wheat genotypes tested across seventeen locations

leading promising advanced genotypes for such trials (Figure 4). This finding was in agreement with Kadhem and Baktash (2016), Verma et al. (2016), and Jeberson et al. (2017). The genotypes 6 (ETBW8991), 9 (ETBW8996), 22 (ETBW9554), and 25 (ETBW9557) were specifically adapted to high yielding environments with grain yield more than grand average yield (Figure 4). However, genotype 30 (Hidasse) was adapted to low yielding environment but not stable

3.5. *AMMI 2 biplot analysis*

AMMI2 analysis positioned the genotypes in numerous sections containing different locations, indicating the interaction pattern of the genotypes. On the opposite, the IPCA scores of a genotype in the AMMI analysis are reported as an indication of the stability of a genotype across environments (Purchase et al., 2000). Accordingly, the nearer the IPCA scores are to zero (origin), the more stable the genotypes are across all their testing environments (Purchase et al., 2000). The genotypes on the upper and the right side of the graph had a positive interaction between the two IPCA1 and IPCA2 axes and the genotypes located on the lower and the left side of the graph had a negative interaction between the two axes. Since the IPCA2 explained interactions were lower than IPCA1, genotypes that had a positive or negative interaction with the IPCA1 axis compared to the IPCA2 axis are going to be recognized as high-interactions genotypes. During this study, the AMMI model was able to identify high-yielding and stable genotypes to some extent. The genotypes in the middle of the graph had less interaction with each IPCA1 and IPCA2 axes. Genotypes close to the origin are non-sensitive to environmental interactive forces and those distant from the origin are sensitive and have large interactions (Samonte et al., 2005). Accordingly, genotypes ETBW8668 (G11), ETBW8870 (G4), ETBW8858 (G3), ETBW8684 (G13), ETBW9555 (G23), and ETBW9556 (G24) showed lesser differential response to the changes in the growing environments as compared to the other genotypes and were recognized as stable genotypes based on AMMI-II biplot while ETBW9547 (G15), Hidasse (G30), and ETBW9559 (G27) were highly influenced by the interactive force of environment and sensitive to environmental changes, scored the highest IPCA-1; they are considered as non-stable and showed the highest levels of interaction (Figure 5).

3.6. *GGE biplot analysis*

One of the best interesting features of a GGE biplot is its ability to point out the which-won-where model of a GEI dataset and the vertex genotype(s) for each sector has a higher (sometimes the highest) yield than the others in all environments that fall in the sector. According to Yan and Tinker (2006) and Hagos and Abay (2013), the vertex genotypes were the most responsive genotypes as they had the longest distance from the origin in their direction. The vertex genotypes could be either best performing or poorest at one or many environments (Yan and Rajcan, 2002; Yan et al., 2007; Mehari et al., 2015). The sectors that received environments, the vertex genotypes are specifically suitable to those environments. Therefore, according to Figure 6, 17 environments were grouped into 4 sectors as mega environments, and genotypes were also grouped into 5 sectors. Areka-2018 (E-7), Aweli Gera-2017 (E-16), and Debre Zeit-2017 (E-17) fall into the first mega-environments correlated in genotypic ranking, and these environments genotypes did not differ significantly from each other, with the vertex genotype of this mega-environment being 30 (Hidasse) and the high-yielding genotype of these

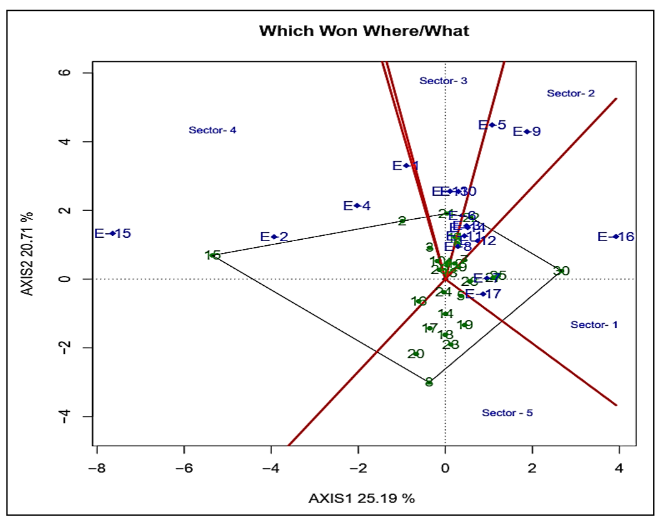

Figure 6: Which-won-where pattern of GGE biplot based on the mean yield of 30 wheat genotypes evaluated across seventeen environments

four environments being 30 (Hidasse). Other five genotypes 7 (ETBW8862), 25 (ETBW9557), 27 (ETBW9559), 28 (ETBW9560) and 29 (ETBW9561)) were fell under sector one. The second mega environment contained environments of Bekoji-2018 (E-3), Kulumsa-2018 (E-4), Holeta-2018 (E-5), Enawari-2018 (E-8), Kulumsa-2017 (E-11) and Robe Arsi-2017 (E-12) and included genotype 22 (ETBW9554) as vertex and genotype 6 (ETBW8991), 9 (ETBW8996), 12 (ETBW8595), 13 (ETBW8684) as the genotype member. The third Mega-environment contained two environments Asasa-2017, and Bekoji-2017 with winning genotype 21 (ETBW9553), and the other three genotypes are grouped under this sector namely genotype 1 (Wane), 4 (ETBW8870), and 11 (ETBW8668). Similarly, four environments, Robe-Arsi-2018, Asasa-2018, Kulumsa-2018, and Robe Arsi-2017 fell into the fourth mega environments with vertex genotype 15 (ETBW9547) and genotype 2 (ETBW8751), 3 (ETBW8858), 16 (ETBW9548), and 26 (ETBW9558) as the genotype member for this sector. No environment fell in sector five and the sector includes genotype 8 (ETBW8804) as vertex genotypes and genotype 5 (ETBW8802), 14 (ETBW9486), 17 (ETBW9549), 18 (ETBW9550), 19 (ETBW9551), 20 (ETBW9552), 23 (ETBW9555) and 24 (ETBW9556) as the genotype members and demonstrating that these genotypes were the lowest yielding genotypes, they were poorly performed in all environments.

3.7. Mean performance and stability of genotypes using GGE biplot

In Figure 7 X-axis is an indicator of grain mean yield, while Y-axis exhibits stability of genotypes. Therefore it is possible to identify simultaneously genotypes with high yield with stability. This is further demonstrated using average PC1 and PC2 scores for all environments and is indicated by a small circle. The ordinate of the AEC is the line that passes through the origin and is perpendicular to the AEC abscissa (Figure 7). Unlike the AEC abscissa, which has one direction, with the arrow pointing to greater genotype main effect, the AEC ordinate is indicated by double arrows, and either direction away from the biplot origin indicates greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from those with above-average means. The biplot displayed the pattern of variability of genotypes, environment, and their interactions and stability. According to Figure 7, genotypes with above-average means were from 21 (ETBW9553), 22 (ETBW9554), 2 (ETBW8751), 11 (ETBW8668), 9 (ETBW8996), 6 (ETBW8991) and 3 (ETBW8858) were near to ideal genotypes while genotypes below-average means were from 8 (ETBW8804), 20 (ETBW9552), 23 (ETBW9555), 18 (ETBW9550), 17 (ETBW9549), 19 (ETBW9551) and 14 (ETBW9486). However, the

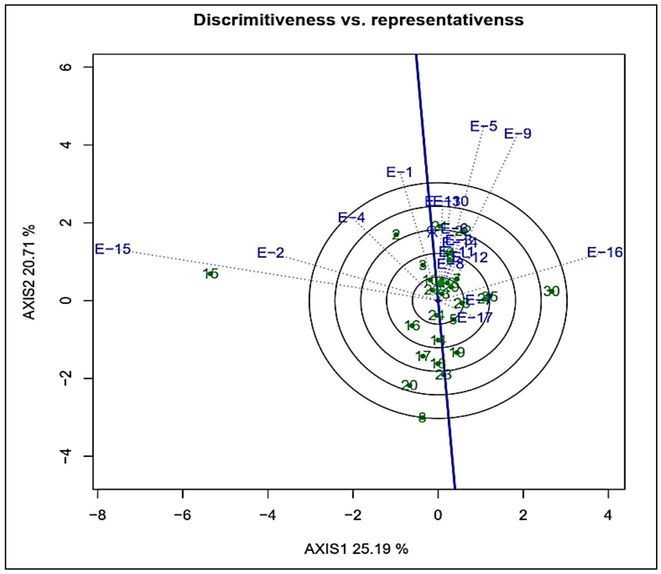

Figure 7: Mean Performance and stability of genotypes using GGE Biplot

length of the average environment vector was sufficient to select genotypes based on yield mean performances. Genotypes with above-average means 21 (ETBW9553), 22 (ETBW9554), 2 (ETBW8751), 11 (ETBW8668), 9 (ETBW8996), 6 (ETBW8991) and 3 (ETBW 8858) could be selected, whereas the rest were discarded. On the other hand, genotypic stability is quite crucial in addition to the genotype yield mean. A longer projection to the AEC ordinate, regardless of the direction, represents a greater tendency of the GE interaction of a genotype, which means it is more variable and less stable across environments or vice versa. For instance, genotype 21 (ETBW9553) was more stable as well as high yielding followed by 22 (ETBW9554) and 2 (ETBW8751. Conversely, 15 (ETBW9547) was unstable, but high yielding.

3.8. Ranking of environments based on differentiation and representative of environments

Genotype and GEI biplot analysis was also used to classify and identify the most discriminative and representative locations. The line connecting each location to the origin in the biplot is called the vector. Locations with longer and shorter vectors are considered more and less discriminative, respectively, of the genotypes. Most locations were discriminative for genotypes, as shown by their position away from the biplot origin. However, locations differed greatly in their discriminative ability, as shown by their proximity to the origin of the biplot and different vector lengths. For grain yield, among the seventeen environments, Areka-2017 (E-15), Aweli Gera-2017 (E-16), Shambu-2017 (E-9), Holeta-2018 (E-5), and Asasa-2018 (E-2) were the most discriminating (informative) as depicted by the longest vector, whereas Areka-2018 (E-7), Enawari-2018 (E-8) and Debra Zeit-2017 (E-17) were the least discriminating, having the shortest vector (Figure 8). The representativeness of the test environments with a small angle to the average environmental axis (AEA) is more representative than other test environments. The environment Asasa-2017(E-10) and Bekoji-2017(E-13) were more representative than other environments for grain yield. Test environments, which were consistently non-discriminating (non-informative), provided little information on the genotypes and, therefore, can be omitted as test locations. However, the locations with long vectors and large angles with AEC abscissa cannot be used to select superior genotypes, but are effective to eliminate unstable genotypes.

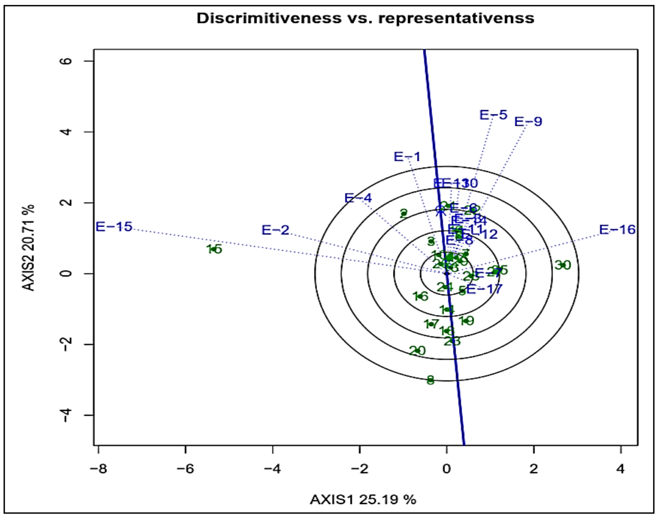

Figure 8: Ranking of 17 environments based on differentiation and representative of environments

3.9. *Comparison of AMMI and GGE biplot analyses*

The two sources of variation that are very important for mega-environment analysis, genotype evaluation, and test-environment evaluation are G and GE; they need to be considered simultaneously for these purposes. These two sources of variations are combined instead of separate by AMMI analysis and GGE biplot analysis in mega-environment analysis and genotype evaluation; AMMI graphs for these purposes also are "GGE" graphs. In our study, AMMI explained 48.15% of the total variation in the first two components while GGE explained 45.90% of the total variation in the first two components. GGE and AMMI analysis explained almost similar amounts of variation; however, AMMI still show a slightly greater proportion than GGE during our study. Similar to this result (Hongyu et al.,2015) also reported that AMMI explains a slightly greater amount than GGE. The same author also compared AMMI and GGE analysis in a similar way to that presented in this study, showing the advantages of including both models in the analysis to exploit their strengths. In the GGE biplot, it is easy to construct which-won-where which is easier to visualize the which-won-where patterns than AMMI1graph for mega-environment analysis in that it explains more G+GE. The mean vs. stability view of the GGE biplot is explain more about G+GE than the AMMI1 biplot for genotype evaluation so, it is superior to the AMMI1 biplot. The discriminating power vs. representativeness view of the GGE biplot is an efficient tool for test-environment evaluation, which may lead to the identification of a minimum set of discriminating and representative test environments. The G and GE are specific to the environments during which they are estimated, and G and GE are interchangeable, counting on the scope of the environments. This understanding is the basis and justification for mega-environment analysis and GE analysis. While genotypes are often considered to represent wide adaptation, it is only as wide because that range of the test environments allows; specific adaptation to be determined by both G and GE rather than by GE alone. Both models identify similar genotypes as stable and high-yielding genotypes. According to AMMI and GGE analysis genotype 21 (ETBW9553) was more stable as well as high yielding followed by 22 ETBW9554) and 2 (ETBW8751. Conversely, 15 (ETBW9547) was unstable, but high yielding.

4. CONCLUSION

The study has identified promising genotypes, ETBW9554 and ETBW9553 as most resistant to wheat rust which also combines high yield and other useful agronomic traits, indicating that these traits can be combined in wheat as preferred by farmers. Finally, ETBW9554 has been officially released by the National Variety Releasing Committee (NVRC) of the country, with the common name Boru for large-scale production and ETBW9553 genotype was including in crossing block as parents.

5. ACKNOWLEDGMENT

The author wishes to acknowledge the help provided by the Ethiopian Institute of Agricultural Research (EIAR), AGGW project, and Kulumsa Agricultural Research Center (KARC) for financial support to conduct these research and other collaborating centers and support staff in the national wheat research program. The author also acknowledges CIMMYT and ICARDA for providing germplasm. Finally, the author acknowledges Mr. Abu Tolcha Climate and Geospatial Research Process for his kindly support of the location map.

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