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

Crossref

IJBSM July 2023, 14(7):1089-1098 Print ISSN 0976-3988 Online ISSN 0976-4038 **Article** AR3570

Research Article *Stress Management*

DOI: HTTPS://DOI.ORG/10.23910/1.2023.3570

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

Alemu Dabi[1], Gadisa Alemu[1], Berhanu Sime[1], Negash Geleta[1], Abebe Delessa[1], Tafesse Solomon[1], Habtemariam Zegaye[1], Dawit Asnake[1], Bayisa Asefa[1], Ruth Duga[1], Yewubdar Shewaye[1], Abebe Getamesay[1], Demeke Zewudu[1], Bedada Girma[2], Ayele Badebo[2] and Bekele Abeyo[2]

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

Open Access

Corresponding alemudabi2009@gmail.com

0009-0006-1676-8294

ABSTRACT

A multi-location Experiment was conducted using 28 genotypes and two checks during the main cropping seasons of 2017 and 2018 at Kulumsa, Dhera, Melkasa, Asasa, Ilala, and Geregera in moisture-stress areas of Ethiopia to evaluate the genotype-Environment interaction effect and grain yield stability of bread wheat genotypes. The experiment was arranged in alpha lattice design replicated three times. The stability analysis was carried out for grain yield using R software. ANOVA showed a highly significant difference among genotypes and genotype×environmental interaction for traits; days to heading, days to maturity, plant height, grain yield, 1000 kernel weight. The average mean yield of the genotypes across the environments was 4.5 with the range of 3.5–5.3 t ha^{-1}. The genotypes ETBW 9578, ETBW 9565, ETBW 9570 and ETBW 9571 were top-yielding, ideal, and stable across the ten environments. However ETBW 9589 and Ogolcho were the low-yielding genotypes. The "which-won-where" graph categorizes the genotypes into four groups. The locations within the same group were closely correlated and share the same winning(vertex) genotype. E7 was ideal that has both discriminating abilities of the genotypes and representative of the other test environments. ETBW 9578 gave 37.7% and 39.1% yield advantage over the standard check Kingbird and local check Ogolcho, respectively. As a result the genotype ETBW 9578 was released in 2020 and designated by the variety name "Dursa". Thus, it was concluded that the Dursa variety could be used as a stable variety for cultivation.

KEYWORDS: Genotype×environment interaction, moisture stress, stability, *Triticum aestivum*

Citation* (VANCOUVER)*: Dabi et al., 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,* 2023; 14(7), 1089-1098. HTTPS://DOI.ORG/10.23910/1.2023.3570.

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 16th May 2023 RECEIVED in revised form on 02nd July 2023 ACCEPTED in final form on 18th July 2023 PUBLISHED on 29th July 2023

1. INTRODUCTION

Wheat is one of the first domesticated food crops and has been the basic staple food in the world (Curtis et al., 2002; Charmet, 2011; Haas et al., 2018). Wheat is one of the most important cereal crops widely cultivated in Ethiopia. Both bread wheat (*Triticum aestivum* L.) and durum wheat (*T. turgidum* L. var. *durum*) are are mainly cultivated by small-scale farmers in Ethiopia. The average wheat productivity is 3.0 t ha^{-1} (Anonymous, 2022) which is low as compared to that of the world Fisseha et al. (2020) reported 61%, 55%, and 46% wheat yield gap compared to the actual yield on the research station, farmers' plot, and potential yield in the highland areas of the country, respectively. The yield gap observed could be attributed to the Presence of significant GEI (genotype by environment interaction) (Gadisa and Abebe, 2020; Gadisa et al., 2021; Verma and Singh, 2021); lack of high yielding and stable varieties suitable to diverse agro-ecologies; biotic stresses (Olivera et al., 2015; Singh et al., 2015; Tolemariam et al., 2018); abiotic stresses; poor cultural practices; mono-cropping and socio-economic (Habte et al., 2014; Ayele et al., 2008; Hodson et al., 2020; Negash et al., 2022; Abate, 2023). Wheat diseases such as yellow rust (*Puccinia striifirmis* f.sp *tritici*) and stem rust (*P. graminis* f. sp. *tritici*) are among the major biotic factors which devastate wheat production in Ethiopia (Wubshet and Chemeda, 2016).

The development and release of crop varieties that are high yielding, stable, and stress tolerant are of the most importance to plant breeders (Akcura et al., 2006). According to Becker and Leon (1988); Fasahat et al. (2015) and Temesgen et al. (2015), a stable genotype is one that exhibits consistent performance regardless of changes in the environment. In addition to having a high yielding potential, a newly developed variety should be stable and generally adaptable across a variety of envirommemt (Akcura et al., 2006). For any breeding program, assessing performance stability and adaption range has become more crucial. The GEI study is particularly significant in nations like Ethiopia that have a variety of agro-ecologies (Fasahat et al., 2015).

Multi-environment trials are important in plant breeding for evaluating genotypes for their overall stability and adaptability in the presence of genotype by environment (GE) interaction. An understanding of GE interaction is important at all stages of plant breeding, including ideotype design, parent selection, selection based on traits, including grain yield (Yan et al., 1998). The G×E study is important in the presence of various agro-ecologies. Significant G×E interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (called qualitative or rank changes) or variations in the comparative ranking of the genotypes (called a quantitative or absolute difference between genotypes) (Falconer, 1952; Fernandez, 1991).

Evaluation of different genotypes in a multi-environment and/or year is not only important to determine high-yielding cultivars but also to identify sites that best represent the target environment (Yan, 2001). Moreover, the new cultivar should have a stable performance and broad adaptation over a wide range of environments. A genotype or cultivar is considered stable if it has adaptability for a trait of economic importance across diverse environments. The environmental component (E) generally represents the largest component in analyses of variance, but it is not relevant to cultivar selection; only G and GE are relevant to meaningful cultivar evaluation and must be considered simultaneously for making selection decisions (Yan and Kang, 2003). The objective of this study was to evaluate the G×E interaction using GGE-biplot analysis for grain yield of bread wheat genotypes and identify stable genotypes under low moisture stress areas of Ethiopia.

2. MATERIALS AND METHODS

2.1. *Description of experimental sites*

The experiment was conducted at five locations. The list and descriptions of the study sites are shown in Table 1.

2.2. *Planting materials and experimental design*

Thirty genotypes were grown in Alpha-Lattice Design with three replications. Each experimental unit consisted of 3 m^2 (with 1.2 m width×2.5 m length) plot size 1.5 m alleys were left between reps. Non-experimental variables such as fertilizer rates and other crop management practices were

Table 1: List of testing locations and their descriptions

Location	Geographic position		Altitude	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	24.0	620
Dhera	08°19'10"N	39°19'13"E	1650	14.0	27.8	680
Melkasa	08°.24'N	39°.12'E	1550	13.6	28.6	763
Ilala	13°32'N	37°36' 0E	1965	11.4	26.6	530
Geregera	11°40' 0" N	38°48' 0" E	2900	9.6	22.3	931

done as per the recommendations of each test location. A seed rate of 125 kg ha^{-1} was used at all locations (Table 2).

2.3. Data collection and analyses

Data collection: Data on days to 50% heading, days to 50%

Table 2: List and pedigree of bread wheat elite lines and checks used in the experiment

Genotype Id	Genotype	Pedigree
1	Kingbird	Check
2	ETBW 9562	INQALAB91*2/TUKURU//T.SPELTAPI348599/3/2*INQALAB91*2/KUKUNA/4/2*KINGBIRD #1//INQALAB 91*2/TUKURU
3	ETBW 9563	SUP152/BAJ #1
4	ETBW 9564	CHIBIA//PRLII/CM65531/3/MISR2*2/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07
5	ETBW 9565	PREMIO/2*BAVIS
6	ETBW 9566	92.001E7.32.5/SLVS/5/NS732/HER/3/PRL/SARA//TSI/VEE#5/4/FRET2/6/SOKOLL/3/PASTOR//HXL7573/2*BAU
7	ETBW 9567	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/NAVJ07
8	ETBW 9568	MILAN/KAUZ//PRINIA/3/BAV92/4/BAVIS
9	ETBW 9569	SOKOLL/3/PASTOR//HXL7573/2*BAU/4/BECARD
10	ETBW 9570	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/BAV92/4/BERKUT/5/BAVIS
11	ETBW 9571	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/HUW234+LR34/PRINIA//PBW343*2/KUKUNA/3/ROLF07/5/WHEAR/SOKOLL
12	ETBW 9572	TRCH/SRTU//KACHU*2/3/KINGBIRD #1
13	ETBW 9573	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2/5/2*SOKOLL/3/PASTOR//HXL7573/2*BAU
14	ETBW 9574	PAURAQUE #1/3/PBW343*2/KUKUNA//PBW343*2/KUKUNA/4/BAJ #1
15	ETBW 9575	MILAN//PRL/2*PASTOR/4/CROC_1/AE.SQUARROSA(213)//PGO/3/BAV92/5/PAURAQ
16	ETBW 9576	FRANCOLIN #1/BAJ #1
17	ETBW 9577	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2*2/5/WHEAR/SOKOLL
18	ETBW 9578	NAVJ07/SHORTENED SR26 TRANSLOCATION/3/ATTILA/BAV92//PASTOR
19	ETBW 9579	W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1*2/5/WHEAR/SOKOLL
20	ETBW 9580	KFA/2*KACHU//WAXBI
21	ETBW 9581	KSW/SAUAL//SAUAL/3/REEDLING #1= KASUKO
22	ETBW 9582	KENYA WREN/KIRITATI/3/KINGBIRD #1//INQALAB 91*2/TUKURU
23	ETBW 9583	MUTUS*2/AKURI//MUTUS*2/TECUE #1
24	ETBW 9584	KFA/2*KACHU/3/KINGBIRD #1//INQALAB 91*2/TUKURU/4/KFA/2*KACHU
25	ETBW 9585	KFA/2*KACHU*2//QUELEA
26	ETBW 9586	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/5/GK ARON/AG SECO 7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
27	ETBW 9587	WHEAR/SOKOLL/5/GK\ARON/AGSECO7846//2180/4/2*MILAN/KAUZ//PRINIA/3/BAV92
28	ETBW 9588	SERI.1B//KAUZ/HEVO/3/AMAD/4/PFAU/MILAN
29	ETBW 9589	OPATA/RAYON//KAUZ/3/2*MILAN/DUCULA
30	Ogolcho	Check

maturity, plant height from randomly selected tillers, and grain yield, 1000 kernel weight,from harvested net plot were measured

2.3.1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) was performed using the R-software for Alpha-Lattice Design. Combined data over locations, analyses of variances, were done using the mean of sample plants for the characters plant height. However, plot values were used for the characters such as days to heading and maturity, grain yield, and thousand kernels weight for analysis of variance. The Least Significant Difference (LSD) was used to compare means at the 5% and 1% level of significance.

2.3.2. GGE model

A GGE biplot can simultaneously display 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 based on singular value decomposition (SVD) of the first two principal components is:

yij-μ-β_j=λ_1 £_i1 η_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, *μ*+β_j being the mean yield across all genotypes in environment j, β_1 and β_2 are the singular values (SV) for the first and second principal component (PCA1 and PCA2) respectively, ξ_i1 and ξ_i2 are 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, ε_ij is the residual associated with genotype i in the environment.

3. RESULTS AND DISCUSSION

3.1. Analysis of variance

A combined analysis of variance was carried out for five traits recorded over the locations (Table 3). There was a highly significant difference among the genotypes for all traits including days to heading, days to maturity, plant height, grain yield, 1000 kernel weight confirming the presence of genotypic variability for yield and its components. The environment×genotype interaction was also significant for days to heading, days to maturity, grain yield, and 1000 kernel weight indicating the different performance of bread wheat genotype across locations or genotypes responded differently to the different environmental conditions. This infers the importance of genotype evaluation under different environments to identify better-performing genotypes for specific and wide adaptability. In accordance with Gadisa et al. (2020) and Alemu et al. (2019) who reported significant differences among genotypes for the traits; day to heading, days to maturity, plant height, 1000 kernel weight, and grain yield across environments.

Table 3: Combined analysis of variance of grain yield (unit?) and yield component for 30 bread wheat genotypes

Source of variation	GYLD (tonnes)		DTH		DTM		PHT (cm)		TKW (g)	
	Df	MS	Df	MS	Df	MS	Df	MS	Df	MS
ENV	9	400.77***	7	5205.1***	7	34353***	7	21342.5***	7	2217.55***
REP(ENV)	20	8.65***	16	7.5^{ns}	16	278***	16	704.4***	16	62.05***
GEN	29	5.59***	29	143***	29	54***	29	231.3***	29	130.55***
ENV: GEN	261	1.41***	203	8.3***	203	27***	203	47.1^{ns}	203	17.4***
Residuals	580	0.67	464	5.3	464	18	464	42.1	464	7.48

: Significant at $p\leq 0.01$, *: Significant at $p\leq 0.001$; Where, DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight, GYLD: Grain yield, DF: Degrees of freedom; MS: Mean of square; ***: highly significant difference exists; NS: Non-significant

3.2. Mean performance and range of grain yield and yield components

The mean performance of the 30 genotypes for 4 traits is presented in Tables 4 and for grain yield across location (Table 5). A range for days to heading was 54.5 to 64.5 days with minimum values in genotypes ETBW 9563 and the maximum in ETBW 9569 with an average value of 58.91 days. Days to maturity also ranged from 102.7 days (ETBW 9589) to 111 days (ETBW 9569) with an average value of 107.5 days indicating that the tested genotypes were early to medium maturing category. Plant height varied from 78.2 to 92.1 with a mean height of 84.2 cm. The 1000 kernel weight also ranged from 28.9 (Kingbird) to 39.4 (ETBW 9570) with an average value of 34.0 g.

The average mean yield of the genotypes across the environment was 4.5 with the range of 3.5 t ha^{-1} (ETBW 9589) and 5.3 t ha^{-1} **(**ETBW 9578). The highest grain yielding genotype was ETBW 9578 (5.3 t ha^{-1}), followed by ETBW 9565 (5.1 t ha^{-1}), ETBW 9570 (5.1 t ha^{-1}), ETBW 9571 (5.1 t ha^{-1}). The rank of the genotypes was changed

Table 4: Combined mean performance of important agronomic traits of 30 bread wheat genotypes

GID	Genotypes	DTH	DTM	PHT	TKW
G1	Kingbird	58.0	107.5	81.1	29.0
G2	ETBW 9562	56.6	106.5	83.1	33.3
G3	ETBW 9563	54.5	106.3	80.8	32.4
G4	ETBW 9564	57.3	107.1	88.8	32.6
G5	ETBW 9565	60.0	108.5	84.6	37.5
G6	ETBW 9566	59.3	106.8	83.4	32.9
G7	ETBW 9567	60.6	106.3	87.8	33.1
G8	ETBW 9568	57.4	106.3	84.6	35.2
G9	ETBW 9569	64.5	111.0	91.4	29.3
G10	ETBW 9570	57.0	107.3	87.4	39.4
G11	ETBW 9571	58.3	108.0	85.8	37.6
G12	ETBW 9572	60.0	106.8	82.5	33.7
G13	ETBW 9573	58.6	107.8	85.3	35.6
G14	ETBW 9574	60.5	107.5	84.5	34.6
G15	ETBW 9575	57.7	105.3	83.6	33.4
G16	ETBW 9576	55.0	106.4	86.3	34.3
G17	ETBW 9577	57.9	107.2	82.3	32.6
G18	ETBW 9578	57.0	108.1	84.1	35.3
G19	ETBW 9579	57.1	106.5	86.5	37.1
G20	ETBW 9580	58.1	109.2	82.2	34.2
G21	ETBW 9581	61.9	108.5	80.6	36.2
G22	ETBW 9582	59.9	108.4	84.9	33.6
G23	ETBW 9583	62.6	108.5	78.2	33.0
G24	ETBW 9584	62.3	109.3	82.8	32.7
G25	ETBW 9585	56.0	106.7	82.9	36.8
G26	ETBW 9586	59.8	107.5	82.3	33.4
G27	ETBW 9587	61.1	109.0	83.1	34.5
G28	ETBW 9588	59.8	108.2	81.8	31.7
G29	ETBW 9589	55.8	102.7	80.9	34.7
G30	Ogolcho	62.6	109.0	92.1	30.9
Mean		58.9	107.5	84.2	34.0
Range		54.5-64.5	102.7-111	78.2-92.1	28.9-39.4
LSD		1.3	1.8	3.0	1.5
CV		3.9	3.9	7.7	8.04

DTH: Days to heading; DTM: Days to maturity; PHT: Plant height; TKW: Thousand kernel weight; CV: Cofietient of variation; LSD: Least significant difference

with the change of the test environments indicating the existence of cross-over GEI due to variation among the testing environments. The result is in line with Gadisa et al. (2020) who reported different ranks of genotype over the different environment. But the genotypes ETBW 9578 and ETBW 9565 top-yielding at most of the test environments. Accordingly, the genotype ETBW 9578 (5.3 t ha^{-1}) and ETBW 9565 (5.1 t ha^{-1}), were selected as candidate bread wheat varieties for variety release due to their high yielding ability over locations (Table 5). The candidate bread wheat varieties are high-yielding varieties across wide environments. Among the two selected genotypes; the genotype ETBW 9578 was released as a variety for the end-user or large production designated by the variety name Dursa. The variety was adaptable for different bread wheat-growing in low moisture areas of Ethiopia. This released new variety ETBW 9578 (Dursa), produced 37.7% and 39.1% yield advantage over the standard check (Kingbird) and local check (Ogolcho), respectively. Likewise, the variety (Dursa) had bold seed than checks i.e. had 22% and 14.3% TKW advantage than Kingbird and Ogolcho, respectively (Table 5).

3.3. Genotype and genotype by environment interaction (gge) biplot analysis

The partitioning of GGE through GGE biplot analysis showed that PCA1 and PCA2 accounted for 47.6% and 13.3% of the GGE sum of squares respectively for grain yield. The first two principal components for this model explained a proportion as high as 60.91% of the data variability as shown in Figure 2. The polygon is drawn by joining the genotypes (G4 (ETBW 9564), G18 (ETBW9578), G14 (ETBW 9574), G22 (ETBW 9582), G29 (ETBW 9589), and G30 (Ogolcho)) that are located farthest from the biplot origin so that all other genotypes are contained in the polygon. The genotypes at the corner of the polygon can be called the vertex genotypes. The vertex genotypes are either the best or poorest in one or more environments. The genotype at the vertex of the polygon performs best in the environment falling within the sectors (Yan, 2002; Yan and Tinker, 2006). The which-won-where graph revealed that the environments fall into three quadrants while the genotypes fall into four quadrants (Figure 1). Environments within the same sector share the same winning genotype, the five environments E8 (Melkasa 2018), E6 (Dhera 2018), E2 (Dhera 2017), E1 (Melkasa 2017) and E5 (Assasa 2018) fall in the first quadrant which contains eight genotypes G14 (ETBW 9574), G22 (ETBW 9582), G16 (ETBW 9576), G17 (ETBW 9577), G21 (ETBW 9581), G18 (ETBW9578), G8 (ETBW 9568) and G6 (ETBW 9566). The genotype G18 (ETBW9578) and G22 (ETBW 9582) were the vertexes and the high-

Table 5: Mean performance for grain yield (t ha^{-1}) of 28 genotypes and 2 checks tested across 10 environments (2017–2018 cropping seasons)

GID	Genotypes	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Mean
G1	Kingbird	2.5	3.8	6.4	4.9	4.7	1.7	6.3	1.4	3.5	3.3	3.9
G2	ETBW 9562	2.4	3.7	6.4	5.6	5.5	2.0	6.6	1.2	4.2	3.4	4.1
G3	ETBW 9563	3.3	3.9	6.5	5.0	5.9	2.3	7.3	1.8	4.7	3.4	4.4
G4	ETBW 9564	2.4	4.2	8.9	7.1	3.3	1.3	6.9	2.1	4.6	3.5	4.4
G5	ETBW 9565	3.1	4.7	8.4	7.5	6.7	2.4	8.4	2.8	3.3	3.5	5.1
G6	ETBW 9566	4.8	3.5	8.4	7.1	6.6	2.7	7.9	2.3	3.2	2.9	4.9
G7	ETBW 9567	4.2	3.5	6.6	6.8	4.8	1.9	5.9	1.6	3.0	3.5	4.2
G8	ETBW 9568	4.0	3.0	8.5	6.8	7.2	2.5	8.1	2.6	3.1	3.4	4.9
G9	ETBW 9569	4.2	3.5	7.5	7.7	4.5	2.1	7.5	1.6	3.9	3.7	4.6
G10	ETBW 9570	5.3	4.6	7.9	7.7	5.2	1.9	8.8	2.2	4.0	3.2	5.1
G11	ETBW 9571	4.5	3.8	7.7	8.2	6.4	2.2	8.8	1.8	4.0	3.4	5.1
G12	ETBW 9572	4.0	5.3	7.2	5.5	5.2	2.7	6.9	2.2	3.2	2.4	4.5
G13	ETBW 9573	3.3	4.7	8.1	7.7	5.8	2.0	8.8	1.3	4.1	3.8	5.0
G14	ETBW 9574	3.9	4.1	7.6	6.1	6.3	2.1	7.5	2.6	2.6	2.9	4.6
G15	ETBW 9575	3.8	4.7	7.6	7.9	5.9	1.4	7.6	1.7	3.0	3.8	4.7
G16	ETBW 9576	4.5	4.2	6.9	7.8	7.2	2.3	7.3	2.5	4.7	3.3	5.1
G17	ETBW 9577	3.0	3.3	7.3	6.7	7.1	1.4	7.9	2.0	2.9	3.2	4.5
G18	ETBW 9578	4.0	4.4	8.8	7.2	7.0	2.1	9.5	2.6	4.4	2.9	5.3
G19	ETBW 9579	3.5	4.7	7.7	7.5	6.0	1.5	7.5	1.9	4.4	3.1	4.8
G20	ETBW 9580	3.3	3.6	6.4	5.4	5.7	1.9	6.3	1.4	4.1	3.0	4.1
G21	ETBW 9581	4.1	3.8	7.7	6.9	6.6	2.3	8.4	1.9	3.4	3.5	4.9
G22	ETBW 9582	4.6	4.3	8.1	7.2	7.1	1.9	7.9	1.6	2.8	3.3	4.9
G23	ETBW 9583	3.1	4.5	7.7	5.7	5.8	2.1	7.6	1.5	3.1	2.9	4.4
G24	ETBW 9584	4.0	5.7	7.2	5.3	6.6	2.2	7.0	1.9	3.6	2.1	4.6
G25	ETBW 9585	2.7	4.5	7.3	7.2	6.8	2.0	7.5	2.2	4.1	3.1	4.7
G26	ETBW 9586	2.3	3.1	7.4	7.2	6.6	1.5	7.6	3.3	4.3	2.7	4.6
G27	ETBW 9587	2.7	4.2	8.0	6.2	5.9	1.7	8.3	2.4	4.4	3.0	4.7
G28	ETBW 9588	1.8	2.8	7.6	6.0	6.0	1.4	6.3	1.7	3.9	3.0	4.1
G29	ETBW 9589	2.8	2.3	6.6	4.0	4.8	1.1	5.5	1.3	4.1	2.8	3.5
G30	Ogolcho	3.8	4.5	5.9	4.8	4.8	1.6	4.4	1.6	3.4	3.3	3.8
Mean		3.5	4.0	7.5	6.6	5.9	1.9	7.4	2.0	3.7	3.2	4.6
LSD		1.38	1.02	0.73	2.02	0.92	0.75	0.86	1.16	1.67	0.82	
CV		23.8	15.4	5.96	8.92	9.5	23.6	7.1	36	27.24	15.62	

E1: Melkasa 2017; E2: Dhera 2017; E3: Kulumsa 2017; E4: Assasa 2017; E5: Assasa 2018; E6: Dhera 2018; E7: Kulumsa 2018; E8: Melkasa 2018; E9: Ilala 2018; E10: Garagara 2018; CV: cofietient of variation; LSD: Least significant difference

yielding genotype for the section at those environments. None of the environments fall in the second quadrant which contains vertex genotypes G14 (ETBW 9574) and G30 (Ogolcho). These genotypes were not performed in any of the test environments indicates that the genotypes were the poorest in some or all of the environments since they had the longest distance from the origin of the biplot on the opposite side of the environments. The third quadrant contains

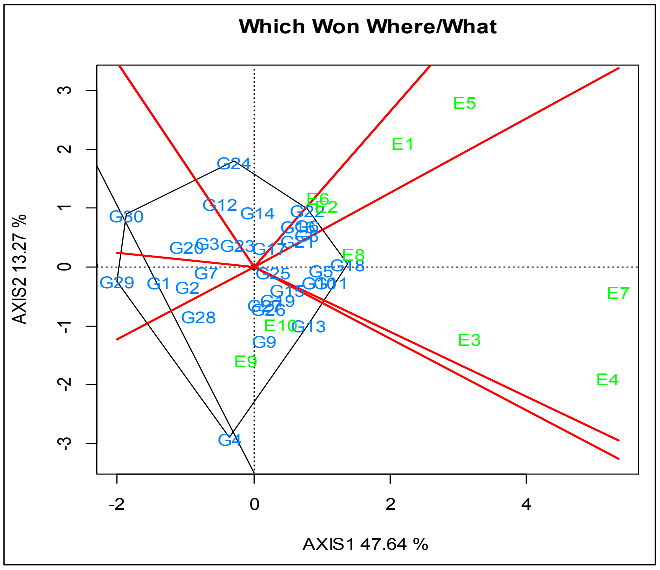

Figure 1: Which genotype won where view of the GGE biplot; E1: Melkasa 2017; E2: Dhera 2017; E3: Kulumsa 2017; E4: Assasa 2017; E5: Assasa 2018; E6: Dhera 2018; E7: Kulumsa 2018; E8: Melkasa 2018; E9: Ilala 2018; E10: Garagara 2018

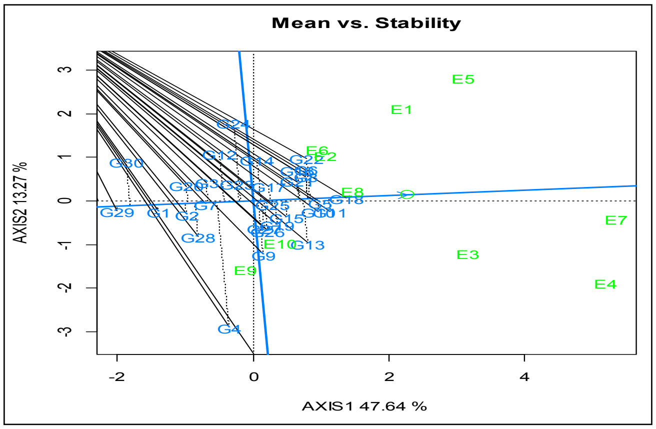

Figure 2: The average-environment coordination (AEC) view to show the mean performance and stability of the genotypes

one environment E9 (Ilala, 2018) and six genotypes. The Genotype G4 (ETBW 9564) and G29 (ETBW 9589) were vertex and high yielding and low yielding for this section respectively. The two environments E10 (Garagara, 2018) and E3 (Kulumsa, 2017) fall in the fourth quadrant which contains about ten genotypes. The vertex genotype G18 (ETBW9578) was nearly common for the first and fourth quadrant which implies the best performance of this genotype at the environments fall in these two quadrants.

3.4. *Grain yield performance and stability of bread wheat genotypes*

GGE of genotypes for both average yield and stability performance over environments were indicated in figure 2 for thirty genotypes using the average environment coordination (AEC) method. 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. In the GGE biplot, genotypes with high PC1 scores have high mean yield and those with low PC2 scores have stable yield across environments (Yan and Tinker, 2006). Accordingly, the genotypes G18 (ETBW 9578), G5 (ETBW 9565), G10 (ETBW 9570), and G11 (ETBW 9571) were relatively closer to the concentric circle and had the short projection from the AEC x-axis indicating the highest mean yield and stability across test environments. Similarly, the genotypes, G29 (ETBW 9589), G1 (Kingbird), G2 (ETBW 9562), and G7 (ETBW 9567) were recorded below the mean grain yield (low yielding) and stable across the test environment. On the other hand, the genotypes, G4 (ETBW 9564), G9 (ETBW 9569) G24 (ETBW 9584) which had the longest projection from the AEC x-axis were highly unstable indicating the highest interaction of genotypes with the environment. The genotypes ETBW 9589 (G29) and Ogolcho (G30) were recorded the lowest average mean yield across the test environments. However, the two genotypes differ in their stability level i.e. ETBW 9589 (G29) was low yielder and stable but Ogolcho was low yield and unstable. Generally, genotype G18 (ETBW9578) gave the highest average yield (largest PCA1 scores), and highly stable genotype, due to its lower absolute PCA2 scores. The average yield of genotypes G 4 (ETBW 9564), G14 (ETBW 9574), G29 (ETBW 9589), and G30 (Ogolcho) were below the mean average (PCA1 scores <0), as shown in Figure 2, and were thus classified as the non-adaptable genotypes. On the other hand, genotypes G18 (ETBW 9578) and G5 (ETBW 9565) with PCA1 scores >0 were detected as the genotypes of interest (i.e. adaptable or higher-yielding).

3.5. *Ranking genotypes relative to the ideal genotype*

An ideal genotype should have both high mean performance and high stability (Yan and Tinker, 2006) across environments. Yan and Kang (2003) also stated that the ideal genotype is one that with the highest mean performance and stability. In this study, Figure 3 shows a GGE-biplot based on genotype-focused scaling for comparison of the genotypes with the ideal genotype. This is assumed to be in the center of the concentric circles the arrow pointing to it (Figure 3). Such an ideal genotype is defined by having the

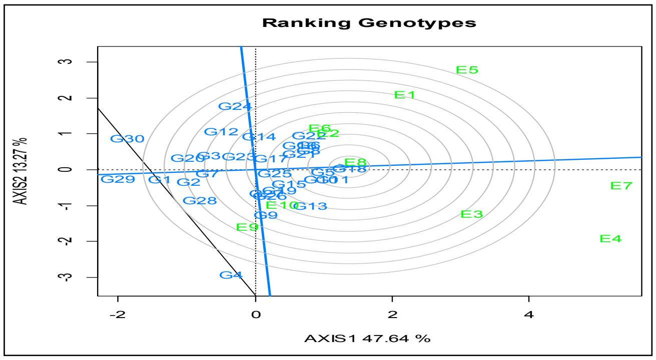

Figure 3: The average-environment coordination (AEC) view to rank genotypes relative to an ideal

greatest vector length of the high-yielding genotypes and with zero GEI. An ideal genotype should have an invariably high average yield in all environments concerned. This ideal genotype is graphically defined by the longest vector in PC1 and without projections in PC2. The concentric circles in Figure 3 help visualize the distance between each genotype and the ideal genotype. The genotypes located closer to the 'ideal genotype' are more desirable than others. Accordingly, the genotypes G18 (ETBW9578), and G5 (ETBW 9565) followed by G 10 (ETBW 9570) and G 11 (ETBW 9571) were ideal and more desirable relative to other genotypes in terms of higher-yielding ability and stability. On the other hand; the genotypes G29 (ETBW 9589) and the standard check G30 (Ogolcho)) were the poorest genotype as they are far from the ideal genotype.

3.6. Evaluation of environments relative to the ideal environments

An ideal environment should have a high PC1 score (greatest power of genotype discrimination in terms of main genotype effects) and zero scores for PC2 (greatest representativeness of all other environments). Similar to the ideal genotype, the ideal environment is only an estimate and serves as a reference for site selection for multi-environment trials. The most desirable is the one closest in the graph of the ideal environment (Yan et al., 2000; Yan and Rajcan, 2002). In figure 4, all environments are ranked relative to the ideal environment which is E7 (Kulumsa, 2018) based on the performance of genotypes across all environments and most important to select widely adapted bread wheat genotypes. E4 (Kulumsa 2017) and E3 (Assasa 2017) are also one of the most desirable environments because of their closeness to the ideal environment in the graph of the ideal environment. In contrast; E9 (Ilala 2018) was far from the ideal environment and can be referred to as not representative for the environments included in the study.

3.7. The relationship among test environments

The cosine of the angle between the vectors of two environments approximates the correlation between them (Diriba, 2019). Less than 90° indicates a positive correlation, more than 90° a negative correlation, and close to 90° no correlation (Yan and Kang, 2003). Accordingly, E2 (Dhera 2017), E1 (Melkasa 2017), E5 (Assasa 2018), and E6 (Dhera 2018) were shown a strong positive correlation. E4 (Kulumsa 2017) and E3 (Assasa 2017 also have a strong positive correlation while E9 (Ilala 2018) and E6 (Dhera 2018) were showed a negative correlation which indicates a strong crossover GE (Figure 5). The presence of close associations among test environments suggests that the same information about the genotypes could be obtained from fewer test environments, and used to reduce testing cost by reducing one of the test environments.

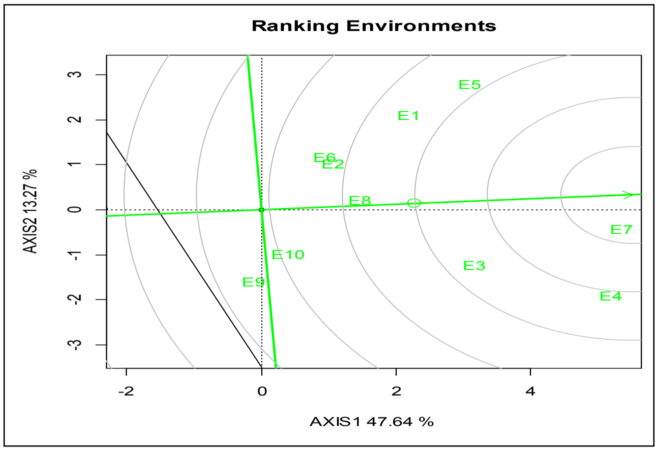

Figure 4: Ranking environments in relative to ideal environment based on the performance of genotype

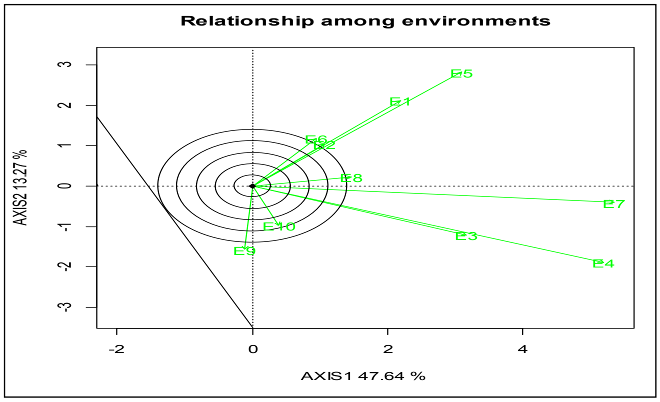

Figure 5: The relationship among test environments

3.8. Discriminating power and representativeness of environments

The discriminating power versus representativeness view of the GGE biplot showed that test environments E4 (Assasa 2017), E7 (Kulumsa 2018), and E5 (Assasa 2018), with the longest projection from the biplot origin, were found to be the environments with more discriminating power that they provided much information about the differences among genotypes. On the other hand, E10 (Garagara) with its shortest vector from the biplot origin, was found less discriminating of the test genotypes and provide little information on the genotypes and, therefore, should not be used as test environments. The test environments E9 (Ilala 2018), E6 (Dhera 2018), E10 (Garagara 2018) E2 (Dhera 2017) and E1 (Melkasa 2017) were less representative due to the largest angle from the Average Environment Axis (AEA). Test environment E7 (Kulumsa 2018) was found to be more representative of other test environments because they have smaller angles with the Average Environment Axis (AEA) (Figure 6). Hence, E7 (Kulumsa 2018) was well-known as an ideal environment that has both discriminating abilities of the genotypes and representative of the other test environments. The environment E7 (Kulumsa 2018) can be used to select superior wheat genotypes that have stable performance across environments (generally adapted genotypes).

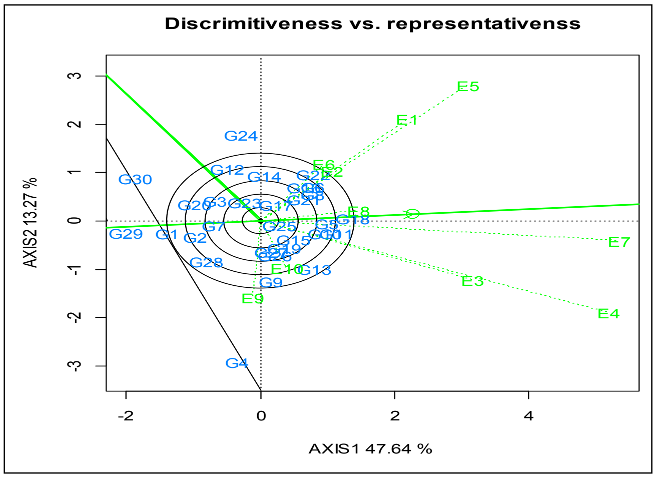

Figure 6: Discrimitiveness and representativeness of the test environments

4. CONCLUSION

The genotypes ETBW 9578, ETBW 9565, ETBW 9570 and ETBW 9571 were top-yielding, ideal, and stable across the ten environments and detected as the genotypes of interest. ETBW 9578 outperformed the standard check "Kingbird" and the local check "Ogolcho" by 37.66% and 39.1%, respectively. As a resut the genotype ETBW 9578 was released in 2020 and designated by the variety name "Dursa". Thus, it was concluded that the Dursa variety could be used as a stable variety for large scale wheat cultivation.

5. ACKNOWLEDGEMENT

The authors would like to thank the Ethiopian Institute of Agricultural Research (EIAR) and Kulumsa Agricultural Research Center (KARC) for offering facilities to carry out this research

6. REFERENCE

Abate, M., 2023. Agroecology-specific varietal matching to achieve self-sufficiency in wheat production in Ethiopia. Heliyon 9 e14127

Akcura, M., Kaya, Y., Taner, S., Ayranci, R., 2006. Parametric stability analyses for grain yield of durum wheat. Plant Soil Environment 52(6), 254–261.

Alemu, D., Firew, M., Tadesse, D., 2019. Genetic variability studies on bread wheat (*Triticum aestivum* L.) genotypes. Journal of Plant Breeding. Crop Science 11(2), 41–54

Anonymous, 2022. Central statistical agency. Agricultural sample survey of area and production of major crops. Available from: https://www. statsethiopia.gov.et/. Accessed on September, 2022.

Ayele, B., Eshetu, B., Berhanu, B., Bekele, H., Melaku, D., Asnakech, T., Melkamu, A., Amare, A., Kiros, M., Fekadu, A., 2008. Review of two decade of research on diseases of small cereal crops in Ethiopia, 375–429. In: Abreham Tadesse (Eds.). 2008. Increasing crop production through improved plant protection. Proceedings of the 14th annual conference of the plant protection society of Ethiopia (ppse). Addis Ababa, Ethiopia, 19–22.

Becker, H.B., Leon, J., 1988. Stability analysis in plant breeding. Plant Breeding 101, 1–23.

Charmet, G., 2011. Wheat domestication: Lessons for the future. Comptes Rendus Biologies 334, 212–220.

Curtis, B.C., Rajaram, S., Gomez, M.H., 2002. Bread wheat improvement and production. FAO Plant Production and Protection Series No. 30. https://fao.org/3/y4011e/y4011e00.htm accessed on July 22, 2021.

Diriba, T., 2019. Stability analysis using GGE biplot and linear mixed model analysis by R. Ethiopian institute of agricultural research, Addis Ababa, Ethiopia. http://www.eiar.gov.et

Falconer, D.S., 1952. The problem of environment and selection. The American Naturalist 86, 293–298.

Fasahat, P., Rajabi, A., Mahmoudi, S.B., 2015. An overview on the use of stability parameters in plant breeding. Biometrics and Biostatistics International Journal 2(5), 149–159.

Fernandez, G.C.J., 1991. Analysis of genotype×environment interaction by stability estimates. Horticulrual Science 26, 947–950.

Fisseha, Z., Bamlaku, A., Degefa, T., 2020. Analysis of wheat yield gap and variability in Ethiopia. International Journal of Agricultural Economics 5(4), 89–98. doi: 10.11648/j.ijae.20200504.11

Gadisa, A., Alemu, D., Negash, G., Tafesse, S., Abebe, D., Rut, D., Habtemariam, Z., Dawit, A., Abebe, G., Bayisa, A., Demeke, Z., Bekele, G., 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. Journal of Plant Breeding and Genetics 07(2) 87–94

Gadisa, A.W., Abebe, D.A., 2020. Evaluation of grain yield stability analysis in bread wheat (*Triticum aestivum* L.) genotypes using parametric method. American Journal of Life Sciences 8(6), 189–195

Haas, M., Schreiber, M., Mascher, M., 2018. Domestication and crop evolution of wheat andbarley: Genes, genomics, and future directions. Journal of Integrative Plant Biology 61(3), 204–225.

Habte, D., Tadesse, K., Admasu, W., Desalegn, T., Mekonen, A., 2014. Agronomic and economic evaluation of the N and P response of bread wheat growing in the moist and humid mid highland vertisols areas of Arsi zone, Ethiopia. African Journal of Agricultural Research 10, 89–99.

Hodson, D.P., Jaleta, M., Tesfaye, K., 2020. Ethiopia's transforming wheat landscape: tracking variety use through DNA fingerprinting. Scientific Reports 10, 18532.

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. Addis Ababa, Ethiopia, 25–26.

Olivera, P., Newcomb, M., Szabo, L.J., Rouse, M., 2015. Phenotypic and genotypic characterization of race TKTTF of Puccinia graminis f. sp. tritici that caused a wheat stem rust epidemic in southern Ethiopia in 2013–14. Phytopathology 105(7), 917–928.

Singh, R.P., Hodson, D.P., Jin, Y., 2015. Emergence and spread of new races of wheat stem rust fungus: continued threat to food security and prospects of genetic control. Phytopathology 105(7), 872–884.

Tolemariam, A., Jaleta, M., Hodson, D., Alemayehu, Y., Yirga, C., Abeyo, B., 2018. Wheat varietal change and adoption of rust resistant wheat varieties in Ethiopia from 2009/10 to 2013/14. Socioeconomics Program Working Paper 12. Mexico, CDMX: CIMMYT.

Verma, A., Singh, G.P., 2021. Combining AMMI and mean yield of wheat genotypes evaluated under rainfed conditions of northern hills zone for stability analysis. International Journal of Bio-resource and Stress Management 11(6), 590–600. DOI: HTTPS://DOI.ORG/10.23910/1.2020.2162b

Wubshet, A., Chemeda, F., 2016. Effects of environment on wheat (*Triticum aestivum* L.) varieties' yellow rust resistance, yield and yield related traits in South-Eastern Ethiopia. Plant 4(3), 14–22; https://www.sciencepublishinggroup.com/j/plant;

Yan, W., 2002. Singular value partitioning for biplot analysis of multi-environment trial data. Agron Journal 4, 990–996

Yan, W., Kang, M.S., 2003. GGE biplot analysis: a graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton

Yan, W., Rajcan, I., 2002. Biplot analysis of test sites and trait relations of soybean in Ontario. Crop Science 42, 11–20.

Yan, W., Tinker, N.A., 2006. Biplot analysis of multi-environment trial data: principles and applications. Canadian Journal of Plant Science 86, 623–645.

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, 1111–1118.

Yan, W., Hunt, L.A., 1998. Genotype by environment interaction and crop yield. Plant Breeding Reviews 16, 135–178.

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.