

*Full Length Research Paper*

# **Adaptability and yield stability of bread wheat (*Triticum aestivum*) varieties studied using GGE-biplot analysis in the highland environments of South-western Ethiopia**

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The objectives of this study were to evaluate released Ethiopian bread wheat varieties for yield stability using the GGE biplot method and identify well adapted and high-yielding genotypes for the highland environments of South-western Ethiopia. Twenty five varieties were evaluated in a randomized complete block design with three replications at Dedo and Gomma during the main cropping season of 2016 and at Dedo, Bedelle, Gomma and Manna during the main cropping season of 2017, generating a total of six environments in location-by-year combinations. Combined analyses of variance for grain yield indicated highly significant ( $p < 0.001$ ) mean squares due to environments, genotypes and genotype-by-environment interaction. Yield data were also analyzed using the GGE (that is, G, genotype + GEI, genotype-by-environment interaction) biplot method. Environment explained 73.2% of the total sum of squares, and genotype and genotype X environment interaction explained 7.16 and 15.8%, correspondingly. The first 2 principal components (PC1 and PC2) were used to create a 2-dimensional GGE biplot and explained 63.88 and 15.71% of GGE sum of squares, respectively. The GGE biplot identified two wheat growing mega-environments. The first mega environment consisted of environments E1 (Gomma-2016), E2 (Dedo-2016), E3 (Bedele-2017), E4 (Manna-2017) and E5 (Gomma-2017) with G6 (Ogolcho) as a vertex genotype. The second mega environment consisted of E6 (Dedo-2017) with G8 (Hulluka) as its vertex genotype. Genotypes (G10) Mekelle-4, (G7) Hoggana, (G16) Danda'a and (G14) Ga'ambo did not fit in any of the mega-environments. Genotypes (G5) Hidasse, (G15) Kakaba, (G21) Sofumar, (G11) Shorima, (G20) Tay, (G14) Ga'ambo, (G17) Gassay and (G4) Millan were found to be the most stable genotypes with mean grain yield exceeding the grand mean. Genotypes (G14) Ga'ambo and (G20) Tay were found to be benchmarks/ideal genotypes and could be used as checks to evaluate the performance of other genotypes and also can be recommended for wider cultivation in the highland environments of South-western Ethiopia. However, bread wheat breeding research should be started to identify higher yielding genotypes for these environments with testing sites established at Bedelle and Dedo to address the two mega environments.

**Key words:** GGE biplot, GXE interaction, Ideal genotypes/environments, mega-environments.

## **INTRODUCTION**

Wheat (*Triticum aestivum*) is one of the major cereals grown for use as food and industrial raw materials in

Ethiopia. It is an important staple food in the diets of many Ethiopians, providing an estimated 12% of the daily

per capita caloric intake for the country's over 90 million population (FAO, 2017). It is annually grown in 1.7 million hectares of land which is 13.38% of the total area of land used for cereal production (CSA, 2018). It ranks second after maize contributing 15.17% of the total annual cereal production. Among the nine National Regional States of the country, Oromia and Amhara, respectively, account for 898,455.57 ha (52.9%) and 554,284.49 ha (32.7%) of the total national wheat production area, while the remaining 14.4% is accounted for by the Southern Nations Nationalities and Peoples Regional State (SNNPR) and other regional states (CSA, 2018). When production is considered, 58.7% (26,699,177.73 quintals(Qts)) and 29.1% (14,047,074 Qts) of the total national wheat production are, respectively, contributed by Oromia and Amhara regions with an additional 12.2% coming from SNNPR and other regional states (CSA, 2018).

In the highlands of South-western Ethiopia, including Jimma and Illubabore zones, wheat is grown in 3% of the national and 5% of the regional total wheat production area (CSA, 2018). Tef, high land pulses, maize, wheat and barley are the major crops grown in both zones. Wheat is, however, becoming an important crop because of its higher yield potential and higher market price compared to other crops. In 2017, meher season annual production of wheat in Jimma and Illubabore zones was 701,047.43 and 170,327.59 Qts with productivity of 20.56 and 25.70 Qts/ha, respectively. Though the average productivity in both zones is less than both the national (26.75 Qts/ha) and the regional (29.65 Qts/ha) average productivity (CSA, 2018). It shows potential of the zones in wheat production, which can be improved further if improved varieties and management practices are applied.

Even though research on wheat has been going on for a long time in the country, the highland environments of Jimma and Illubabore zones have not been considered among the target agroecologies. This was mainly due to the fact that priorities were given to the central highlands and varieties which are currently in production were bred and selected specifically for their adaptation to the central highlands where combined use of those improved varieties and their improved production packages have played an immense role in significantly improving wheat productivity. Contrary to this, in parts of South-western highland, wheat is still grown following traditional practices using low yielding and low quality mixed seed obtained from local market owing to lack of well adapted and high yielding varieties. Therefore there is an urgent need to identify well adapted and high yielding improved varieties and avail to the farming communities to promote production and productivity of wheat in these areas within

the possible short time. Evaluating adaptation of the already existing nationally released varieties is the best cost effective and time efficient approach to identify those varieties before starting breeding program from the grass root level.

Looking at the diversity of the highland environments of the South-western Ethiopia, it is not obvious whether to make varietal recommendation for the whole region from variety performance evaluation conducted in a single environment or test at specific environment and make site specific varietal recommendation. Furthermore, no information is available regarding how many wheat mega-environments are available in the regions. Multi-location performance evaluation trial (MLPET) of the nationally released bread wheat varieties was proposed to identify varieties for specific and broad adaptation and also to characterize the environments and group homogenous environments into a single and more representative one in terms of discrimination ability. In order to identify best performing adapted genotypes for specific or wider adaptation, genotype-by-environment (GXE) interaction and stability analysis are the major methodologies employed in plant breeding.

A number of statistical packages are available for effective analyses of yield data obtained from MLPET and identifying genotypes for specific and wider adaptation by generating information on the degree of GXE interaction. The Wricke (1962) ecovalence, Finlay and Wilkinson (1963) regression coefficient, Eberhart and Russell (1966) regression coefficient and deviation from regression, Shukla (1972) stability variance parameter, Pinthus (1973) coefficient of determination, Lin et al. (1986) Cultivar superiority measure (Pi), GGE biplot (Yan et al., 2000), AMMI Stability Value (ASV) (Purchase et al., 2000), Yield stability index (YSI) (Farshadfar et al., 2011), Multivariate analysis methods (principal component analysis, principal coordinate analysis, factor analysis, cluster analysis and additive main effects and multiplicative interaction (AMMI) are some of the packages available to date.

Yan et al. (2000) proposed the methodology known as genotype and genotype-by-environment (GGE) biplot for graphical display of GXE interaction pattern of MLPET data with many advantages. GGE biplot analysis considers both genotype (G) and genotype-by-environment interaction effects and graphically displays GXE interaction in a two way table (Yan et al., 2007). GGE biplot is an effective method based on principal component analysis (PCA) to fully explore MLPET data. It allows visual examination of the relationships among the test environments, genotypes and the GXE interactions. GGE Biplot is an effective tool for; environmental evaluation (the power to discriminate among genotypes

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**Table 1.** Background information of bread wheat varieties used in the study.

No	Entry code	Varieties	Year of release	Area of adaptation(*masl)	Source
1	G1	ETBW 5879	2011	2200-2600	KARC
2	G2	ETBW 6095	2011	1800-2400	KARC
3	G3	Worrakatta	2014	-	KARC
4	G4	Millan	2015	-	KARC
5	G5	Hidasse	2012	2200-2600	KARC
6	G6	Ogolcho	2012	1600-2100	KARC
7	G7	Hoggana	-	-	KARC
8	G8	Hulluka	2012	2200-2600	KARC
9	G9	Mekelle-3	-	-	KARC
10	G10	Mekelle-4	-	-	KARC
11	G11	Shorima	2011	2100-2700	KARC
12	G12	Mekelle-1	-	-	KARC
13	G13	Mekelle-2	-	-	KARC
14	G14	Ga'ambo	2011	750	KARC
15	G15	Kakaba	2010	1500-2200	KARC
16	G16	Danda'a	2010	2000-2600	KARC
17	G17	Gassay	2007	1890-2800	KARC
18	G18	Alidoro	2007	2800-3100	KARC
19	G19	Digelu	2005	2000-2600	KARC
20	G20	Tay	2005	1900-2800	KARC
21	G21	Sofumar	2000	2300-2800	KARC
22	G22	Mada-Wolabu	2000	2300-2800	KARC
23	G23	Pavon-76	1982	750-2500	KARC
24	G24	Geferson	-	-	KARC
25	G25	King bird	-	-	KARC

KARC: Kulumsa Agricultural Research Center; \*masl: Meters above the mean sea level

in target environment), genotype evaluation, mega environment analysis (e.g., "which- won- where" pattern), where by specific genotype can be recommended to specific mega environment and ranking of genotypes (based on their mean performance and stability). The objectives of this study were, therefore, to evaluate released Ethiopian bread wheat varieties for yield stability using the GGE biplot method, and identify well adapted and high-yielding genotypes for the highland environments of South-western Ethiopia.

## MATERIALS AND METHODS

### Experimental materials and test environments

Twenty five nationally released bread wheat varieties (Table 1) were obtained from the National Bread Wheat Research Coordinating Center (NBWRCC) based at Kulumsa Agricultural Research Center (KARC) for use in this study. The genotypes were evaluated in six environments, over two growing seasons, in the highlands of South-western Ethiopia. The experiments were conducted at Dedo and Gomma during the main cropping season of 2016 and at Dedo, Bedelle, Gomma and Manna during the main cropping season of 2017 generating a total of six environments in location-by-year combinations. Hence the six environments were E<sub>1</sub>, E<sub>2</sub>, E<sub>3</sub>, E<sub>4</sub>, E<sub>5</sub> and E<sub>6</sub> representing Gomma-2016, Dedo-2016,

Bedele-2017, Manna-2017, Gomma-2017 and Dedo-2017, respectively.

### Experimental design and field management

The experiments were laid out in a randomized complete block design with 3 replications at all environments. Each plot had six rows in a plot size of 3 m × 1.2 m (3.6 m<sup>2</sup>) with spacing of 20 cm between rows and 5 cm between plants. Fertilizer was applied at the rate of 150 kg Diammonium phosphate (DAP) and 200 kg urea/ha. Both urea and DAP were given through split application, half dose at planting and the remaining half at full tillering stage. At planting the portions of both DAP and urea were mixed and drilled into the rows and mixed with soil before planting. Seeds were drilled into the rows at the rate of 150 kg/ha. The remaining half doses of both fertilizers were applied at full tillering through top dressing. Weeds were controlled by 3 to 4 times hand weeding. Data were recorded on all agronomic characters and grain yield. However, only grain yield was considered for stability analysis. The central four rows were hand harvested and threshed separately to determine grain yield. The moisture content of the grain was adjusted at 12.5% and grain yield was converted to quintals/ha.

### Statistical analysis

Analyses of variance (ANOVA) were conducted separately for individual environments according to Gomez and Gomez (1984). Bartlett's test was used to assess the homogeneity of error

**Table 2.** Combined analyses of variance for grain yield and the percentage sum of square of the 25 bread wheat genotypes evaluated in six environments in the highlands of South-western Ethiopia.

Sources of variation	Df	SS	SS%	MS	F-val	Pr>F
Environment (E)	5	75837.8	73.2	15167.6	1151.5	<.0001
Replication within E	2	25.91	0.02	12.95	0.98	0.3751
Genotype (G)	24	7415.58	7.15	308.983	23.46	<.0001
G X E	120	16382.7	15.8	136.52	10.37	<.0001
Error	298	3925	3.78	13.17	-	-
Total	449	103587	100	-	-	-
Grand Mean = 29.22				CV(%)= 12.4		

variances between environments to determine the validity of the combined analysis of variance across environments. Combined analyses of variance were performed with the PROC GLM procedure in SAS (2014) versions 9.3 software. Comparison of treatment means was done using Fischer's least significant difference (LSD) test at 5% probability levels. In performing the combined analyses of variance genotypes were assumed to be fixed while environments were assumed random. The following statistical model was used for combined analysis of variance over environments:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_k(j) + \epsilon_{ijk}$$

where,  $Y_{ijk}$ , Observed value of genotype  $i$  in block  $k$  of environment (location)  $j$ ;  $\mu$ , grand mean;  $G_i$ , effect of genotype  $i$ ;  $E_j$ , environment or location effect;  $GE_{ij}$ , the interaction effect of genotype  $i$  with environment  $j$ ;  $B_k(j)$ , The effect of block  $k$  in location (environment)  $j$  and  $\epsilon_{ijk}$ , error (residual) effect of genotype  $i$  in block  $k$  of environment  $j$

The combined analysis of variance was carried out to estimate effects of environment (E), genotype (G) and GXE interaction. Levels of significance of these variables were determined by using F-test.

#### Genotype main effect and genotype by environment interaction effect (GGE) biplot analysis

The GGE biplot analysis was conducted by using Genstat version 18th software. GGE biplot methodology which is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000) were used to visually analyze the wheat varieties. This methodology uses a biplot to show the factors (G and G X E) that are important in genotype evaluation and that are also the sources of variation in G X E interaction analysis of MLPET data (Yan, 2001). The general model for GGE Biplot is as follow:

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

where,  $Y_{ij}$ , the performance of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment;  $\mu$ , The grand mean;  $\beta_j$ , the main effect of the environment  $j$ ;  $\lambda_1$  and  $\lambda_2$ , singular value for IPCA1 and IPCA2, respectively;  $\epsilon_{i1}$  and  $\epsilon_{i2}$ , eigen vectors of genotype  $i$  IPCA1 and IPCA2, respectively;  $\eta_{j1}$  and  $\eta_{j2}$ , eigen vectors of environment  $j$  for IPCA1 and IPCA2, respectively and  $\epsilon_{ij}$  = Residual associated with genotype  $i$  and environment  $j$ .

## RESULTS AND DISCUSSION

Combined analyses of variance for grain yield revealed

highly significant ( $P < 0.0001$ ) mean squares due to genotypes, environments and GXE interaction. Environment, genotype and GXE interaction explained 73.2, 7.15 and 15.8% of the total sum of squares, respectively (Table 2). This agrees very well with a previous study which reported that environment accounted for 80% of the total variation while genotype and G X E interaction accounted for the remaining 20% of the total variation in MLPET of bread wheat (Kaya et al., 2006).

High percentage of sum of squares attached to environment indicated that environment played a dominant role in influencing yield performance of the bread wheat genotypes. The GXE interaction was highly significant ( $p < 0.001$ ) and accounted for 15.80% of the sum of squares implying the need for investigating the nature of variable responses of the genotypes to environments. Presence of the GXE interaction indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment. In other words, when significant GXE interactions are present, the effects of genotypes and environments are statistically non-additive (or the differences between genotypes depend on the environment). The presence of a significant GXE interaction complicates interpretation of the results. That means, it is difficult to identify superior genotypes across environments when GXE interaction is highly significant.

In general, from the combined analyses of variance (Table 2) superiority of genotypes across environments could not be identified by considering their mean grain yield performance because GXE interaction was highly significant. It was earlier suggested that in situations where GXE interactions minimize the usefulness of genotypes, yield levels, adaptation and stability are taken into account in MLPETs (Kang and Pham, 1991). Crossa et al., (1990) elaborated the relevance of qualitative or crossover interactions in agriculture and appropriate statistical analyses are required for quantifying them. Furthermore, the traditional analysis of variance determines the values of each variance source and the significance of the contribution of each component, but it does not partition the interaction into several components and thus other types of analyses should be performed.

Hence, such multi-environment trial data along with a highly significant GXE interaction requires measures of stability analysis techniques that will help to get more information on the GXE interaction as well as to assess the adaptation regions of the genotypes according to their favorable interaction. However, the findings of these study are in accordance with other researchers (Fentaw, 2011; Mehari et al., 2015; Misganaw and Fisseha, 2016) who reported that variety of environmental factors are important in selecting wheat genotypes under Ethiopian conditions.

The lowest and the highest mean grain yields were 6.43 Qt/ha obtained in G8 (Hulluka) at E5 (Gomma-2017) and 68.78 Qt/ha obtained in G6 (Ogolcho) at E3 (Bedelle-2017), respectively. E3 (Bedelle-2017) was the highest yielding environment with mean grain yield of 48.2 Qt/ha and E4 (Manna-2017) was the least yielding environment with mean grain yield of 12.6 Qt/ha, which was far below the grand mean (29.2 Qt/ha) (Table 3). Better soil condition and distribution of rainfall at E3 (Bedele-2017) helped better yield performance while poor fertility status of the soil and terminal moisture stress caused low yield performance at E4 (Manna-2017). The genotypes ranked differently from one environment to another environment in their grain yield performance showing deferential responses to environments and possibly a cross-over type of genotype X environment interaction. Among the genotypes G20 (Tay) (38.03 Qt/ha), G14 (Ga`ambo) (34.34 Qt/ha) and G15 (Kakaba) (33.94 Qt/ha) were the first three best yielders in terms of grain yield data pooled across environments.

### Genotype main effect and genotype-by-environment interaction (GGE) biplot analysis

The GGE (genotype main effect (G) and genotype-by-environment interaction (GE)) concept is based on the understanding that genotype main effect (G) and genotype-by-environment interaction (GEI) are the two sources of variation that are relevant to genotype evaluation and that they must be considered simultaneously for appropriate genotype evaluation (Yan, 2001). The graphical method was employed to investigate environmental variation and interpret GXE interaction. The partitioning of GXE interaction through GGE biplot analysis showed that IPCA 1 and IPCA 2 accounted for 63.88% and 15.71% of sum of squares, respectively, with a total of 79.59% variation for grain yield.

### The Polygon View of the GGE Biplot (The “which-won-where” patterns)

The polygon view of the GGE biplot points out the best genotype in each environment. It graphically addresses important concepts such as crossover interaction, mega

environment differentiation, particular adaptation, etc. (Yan and Tinker, 2005). The term mega environment analysis defines the partitioning of a crop growing region into different target zones (Gauch and Zobel, 1997). Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments is given below in Figure 1.

The GGE bi-plot showed six vertex genotypes, G8 (Hulluka), G7 (Hoggana), G14 (Ga'ambo), G10 (Mekelle-4), G6 (Ogolcho) and G16 (Danda'a). There were six rays, which divided the biplot into six sections. The environments fell into only two sections but the genotypes were distributed throughout all the six sections. The vertex genotype of each sector is the one that gave the highest grain yield in the environments which fell within that sector (Figure 1).

The GGE biplot identified two wheat growing mega-environments. The first mega environment consisted of environments E1 (Gomma-2016), E2 (Dedo-2016), E3 (Bedele-2017), E4 (Manna-2017) and E5 (Gomma-2017) with a vertex genotype G6 (Ogolcho). Hence, G6 (Ogolcho) was the winning genotype in most of the environments. E6 (Dedo-2017) was the only environment that was found in the second mega environment with G8 (Hulluka), as its vertex genotype. It was also noted that no mega-environments fell into sectors where genotype G10 (Mekelle-4), G7 (Hoggana), G16 (Danda`a) and G14 (Ga`ambo) were the vertex genotypes, indicating that these genotypes were not suitable to any of the test environments.

### Ranking of varieties based on mean grain yield and stability performance

In GGE biplot methodology, the estimation of grain yield and stability of genotypes was done using the average environment (tester) coordinate (AEC) methods (Yan and Hunt, 2002). The line passing through the biplot origin is called the average environment (tester) coordinate (AEC), which is defined by the average PC1 and PC2 scores for all environments. The AEC ordinate separates genotypes with below average means from those with above average means. So genotypes with mean grain yield exceeding grand mean grain yield were G15 (Kakaba), G5 (Hidasse), G25 (King bird), G1 (ETBW 5879), G16 (Danda'a), G14 (Ga'ambo), G17 (Gassay), G20 (Tay), G11 (Shorima), G18 (Alidoro) and G4 (Millan) (Figure 2). The line, which passes through the origin and is perpendicular to the AEC, represents the stability of genotypes. Either direction away from the biplot origin, on the axis, indicates greater GXE interaction and reduced stability. For selection, the ideal genotypes are those with both high mean grain yield and high stability. In the biplot, they are close to the origin and have the shortest vector from the AEC. A longer projection to the AEC, regardless of direction, represents a greater tendency of the GXE

**Table 3.** Mean grain yield (Qt/ha) of 25 bread wheat varieties, evaluated in the highland environments of South-western Ethiopia.

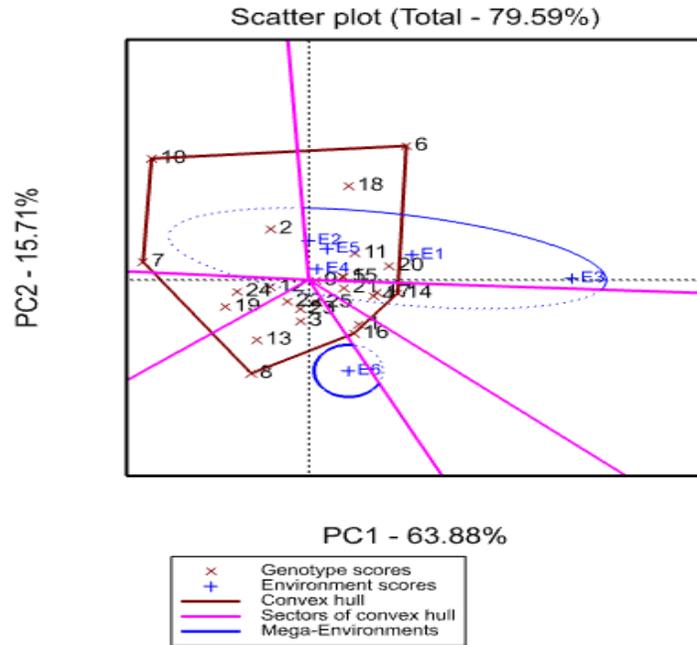
No.	Entry Code	Genotypes	Test environments (Location X year combinations)					Mean	Overall rank	
			Gomma-2016 (E1)	Dedo-2016 (E2)	Bedele-2017(E3)	Manna-2017(E4)	Gomma-2017(E5)			Dedo-2017(E6)
1	G1	ETBW 5879	33.7	18.7	58.4	10.4	15.86	47.67	30.79	10
2	G2	ETBW 6095	38	16.8	39.7	10.8	11.38	30.94	24.60	21
3	G3	Worrakatta	27.2	12.4	47.9	11.97	21.26	44.49	27.54	19
4	G4	Millan	39.1	20.6	60.26	10.7	13.16	44.55	31.40	9
5	G5	Hidasse	35.1	19.8	56.2	9.3	10.31	38.85	28.26	16
6	G6	Ogolcho	41.1	27.1	68.78	13.1	21.51	27.13	33.12	5
7	G7	Hoggana	18.2	22	17.58	10.1	19.22	35.31	20.40	25
8	G8	Hulluka	24.1	23.5	37.9	12.2	6.43	51.6	25.96	20
9	G9	Mekelle-3	36.6	15.5	48.9	13.3	13.16	39.31	27.80	18
10	G10	Mekelle-4	25.4	35.1	17.59	16.1	20.21	27.37	23.63	22
11	G11	Shorima	35.4	26.8	57.58	14.7	17.07	41.1	32.11	7
12	G12	Mekelle-1	28.7	23.52	40.77	13.5	18.69	43.4	28.10	17
13	G13	Mekelle-2	29.9	25.99	36.47	14.7	12.93	51.3	28.55	14
14	G14	Ga'ambo	38.3	24.23	65.1	13.5	17.55	47.33	34.34	2
15	G15	Kakaba	35.9	24.8	52.95	15.8	26.7	47.51	33.94	3
16	G16	Danda'a	32.9	15.5	57.89	11.5	13.39	46.78	29.66	11
17	G17	Gassay	38.5	26.4	60.5	13.8	15.52	47.49	33.70	4
18	G18	Alidoro	36.3	29.3	56.73	14.3	21.66	33.18	31.91	8
19	G19	Digelu	25.7	15.9	32.7	14.1	12.79	40.42	23.60	23
20	G20	Tay	41.5	28.5	60.69	20.6	27.16	49.75	38.03	1
21	G21	Sofumar	33.2	15.4	55.86	10.5	19.72	41.6	29.38	13
22	G22	MadaWolabu	30.7	22.1	43.75	10.2	18.22	45.16	28.36	15
23	G23	Pavon-76	31	24	46.2	10.7	17.64	47.2	29.46	12
24	G24	Geferson	23.8	16.9	36.4	8.1	16.11	38.38	23.28	24
25	G25	King Bird	31.7	31.4	48.9	11.3	21.69	51.01	32.67	6
Mean			32.5	22.49	48.2	12.6	17.17	42.3	29.21	-
CV(%)			8.14	10.82	6.47	7.48	8.5	17.3	-	-
F-test			**	**	**	**	**	*	-	-

\*and \*\* represent statistically significant differences at 0.05 and 0.01 probability levels, respectively.

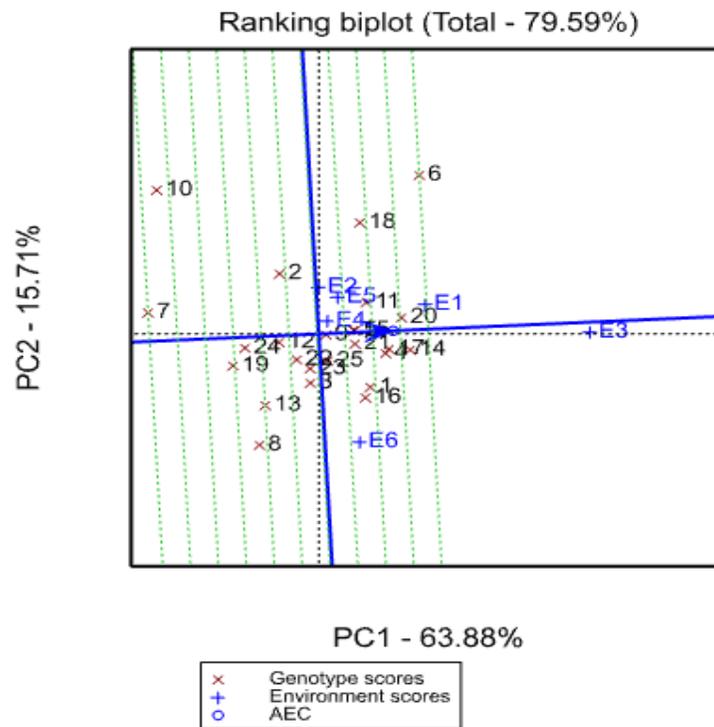
interaction of a genotype that means less stability across environments. Thus, G15 (Kakaba), G21 (Sofumar), G11 (Shorima), G20 (Tay), G14

(Ga'ambo), G17 (Gassay) and G4 (Millan) were the most stable genotypes with mean grain yield exceeding grand mean grain yield. On the other

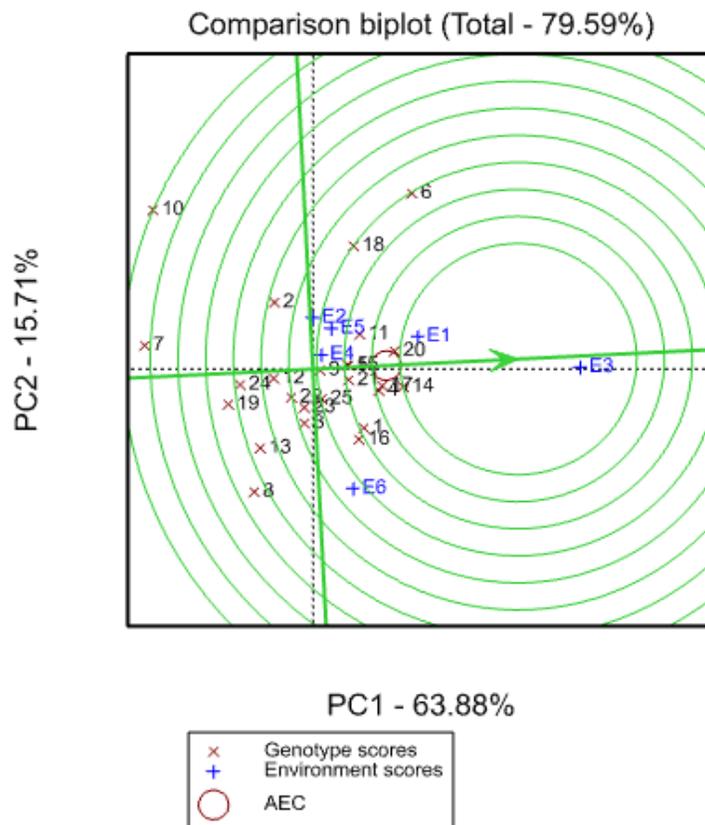
hand, G10 (Mekelle-4) and G6 (Ogolcho) were far from AEC (long vector) indicating their least stability.



**Figure 1.** Polygon view of the GGE biplot using symmetrical scaling for the which-won-where pattern of the genotypes environments. Details of environment are given in Table 2. Numbers 1 to 25 represent genotypes as indicated in Table 2.



**Figure 2.** Average environment coordination (AEC) views of the based on environment-focused scaling for the mean grain yield performance and stability of 25 bread wheat genotypes tested across six environments. Details of environment are given in Table 2. Numbers 1 to 25 represent genotypes as indicated in Table 2.



**Figure 3.** GGE biplot with scaling focused on genotypes, for the evaluation based on the ideal genotype of 25 bread wheat genotypes across six environments. Details of environment are given in Table 2. Numbers 1 to 25 represent genotypes as indicated in Table 2.

However it should be noted that the former genotype represent low yielding compared to grand mean and instable genotypes while the later exemplifies higher yielding but instable genotypes.

**Evaluation of varieties based on the ideal genotype**

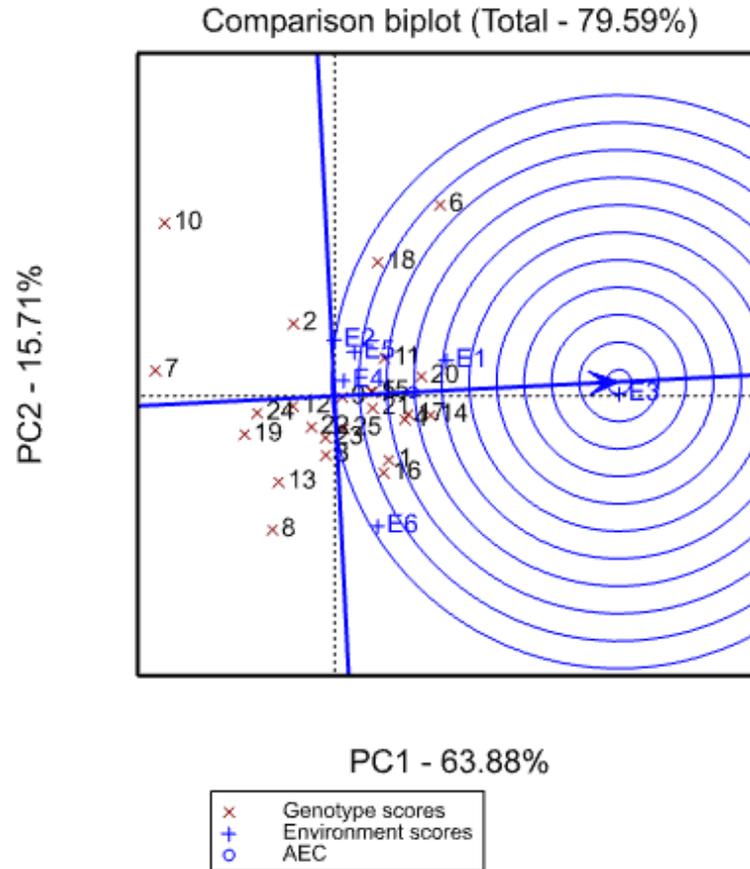
An ideal genotype is expected to have the highest mean grain yield performance and stability in performance across environments (Farshadfar et al., 2012). Though such an ideal genotype may not exist in reality, it can be regarded as a reference for genotype evaluation (Kaya et al., 2006). The ideal genotype is located in the first concentric circle in the biplot. Genotypes found closer to the ideal genotypes are desirable genotypes and those found far from the ideal genotype are considered as undesirable genotypes.

Thus, the ideal genotype can be used as a benchmark for selection. Genotypes that are far away from the ideal genotype can be rejected in early breeding cycles while genotypes that are close to it can be considered in further tests (Yan and Kang, 2003). Mean grain yield

performance and stability of 25 bread wheat genotypes tested across six environments. Details of environment are given in Table 2. Numbers 1 to 25 represent genotypes as indicated in Table 2. Accordingly, genotypes placed near to the first concentric circle, G14 (Ga'ambo) and G20 (Tay) were found to be benchmarks for evaluation of bread wheat genotypes (Figure 3). G4 (Millan), G17 (Gassay), G11 (Shorima), G16 (Danda'a) and G1 (ETBW 5879) were located near the ideal genotype, thus were desirable genotypes. Undesirable genotypes were those distantly located from the first concentric circle, namely, G10 (Mekelle-4), G7 (Hoggana), G2 (ETBW 6095), G12 (Mekelle-1), G19 (Digelu), G24 (Gefferson), G8 (Hulluka) and G13 (Mekelle-2).

**Evaluation of environments relative to ideal environments**

Discriminating ability and representativeness are important properties of a test environment. An ideal environment should be differentiating the tested



**Figure 4.** GGE biplot with scaling focused on environment, for the comparison of environments with ideal environment. Details of environment are given in Table 2. Numbers 1 to 25 represent genotypes as indicated in Table 2.

genotypes and at the same time be a representative of the target agro-ecology (Yan, 2001; Yan and Kang, 2003). Similar to ideal genotype, an ideal environment is defined and shown by the small circle. Meaning that the environment is more desirable and discriminating when located closer to the center of a circle or to an ideal environment. Yan et al. (2001) suggested that favorable test environments should have large PC1 scores (more discriminating of the genotypes) and near zero PC2 scores (more representative of an average environment). Accordingly, E3 (Bedele-2017), which had the longest vector which fell into the center of concentric circles, was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. Thus, E3 (Bedele-2017) was an ideal environment which could be used as a benchmark to evaluate the remaining environments. E1 (Gomma-2016) was closer to the ideal environment, thus, it was regarded as the most desirable environment to select widely adapted genotypes (Figure 4). Conversely environments E6 (Dedo-2017), E2 (Dedo-2016), E4 (Manna-2017) and E5 (Gomma-2017) were

located far from the ideal environment, thus were considered as less powerful to discriminate the genotypes.

## Conclusion

The results from this study indicated that bread wheat genotypes responded differentially to environments with significant genotype X environment interaction. Genotypes G15 (Kakaba), G21 (Sofumar), G11 (Shorima), G20 (Tay), G14 (Ga'ambo), G17 (Gassay) and G4 (Millan) were the most stable. Genotypes G14 (Ga'ambo) and (G20) Tay were benchmarks/ideal genotypes that could be used as checks when evaluating the performance of other genotypes and also can be recommended for wider cultivation in the highland environments of South-western Ethiopia. The study also identified two bread wheat mega environments. Therefore, bread wheat breeding research should be started to identify higher yielding genotypes for the highland environments of South-western Ethiopia with

testing sites established at Bedelle and Dedo to address the two mega environments.

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## CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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