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PERFORMANCE EVALUATION OF BREAD WHEAT (*TRITICUM AESTIVUM* L.) VARIETIES IN THE HIGHLANDS OF SOUTHWESTERN PART OF ETHIOPIA

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ABSTRACT

Twelve bread wheat varieties were evaluated across three environments during two main cropping seasons (2021 and 2022) at the highlands of Southwestern part of Ethiopia. The objectives of the study were to estimate the magnitude and nature of GEI for grain yield and to determine yield stability of wheat varieties in the highland areas of southwestern part of Ethiopia. The study was conducted using a randomized complete block design with three replications. The result of the combined ANOVA for grain yield revealed highly significant ($P \leq 0.001$) difference among environment (E) genotype (G) and GEI. Environment explained 77.6% of the total variation, whereas G and GEI explained 3.87% and 10.57% of the total variation, respectively. The magnitude of the environment was many times greater than the genotype, implying that most of the variation in grain yield was due to the environment. Based on the combined ANOVA over locations, the mean grain yield of environments ranged from 2tha^{-1} at Gechi 2021 to 5.8t ha^{-1} at Dedo2022. The highest yield was harvested from variety Danda'a (4.6t ha^{-1}), while the lowest was from Ogolocho (3.5t ha^{-1}) and the average grain yield of varieties was 3.8t ha^{-1}. Based on the GGE biplot analysis different wheat growing environments were grouped into three mega-environments. The first mega environment includes Gechi 2022, the second mega environment includes Dedo 2022, Gechi 2021 and Yem 2021 and third mega environment includes Yem 2022 and Dedo 2021 with the winner varieties of Ogolocho, Daka and Danda'a respectively. Even though, the wheat variety ETBW9089 not winner variety in the mega-environmnet, but showed consistent performance across locations. Variety Danda'a and ETBW9089 can be recommended for wider cultivation due to better grain yield and stability performance across the test environments in the highlands of southwestern areas of Ethiopia.

Key words: Bread wheat, Genotype by environment, Grain yield, Southwestern, stability analysis

1. BACKGROUND AND JUSTIFICATION

Wheat is the most important food security crop at the global level. It is currently grown on 215.44 million hectares annually and produced more than 730.9 million metric tons of grain in 2018/19, the second highest cereal production after maize (1,395.8 million metric tons). Wheat is also one of a food security crop in Africa. It is grown more than 7.94 million hectares and produced more than 24.23 million metric tons annually. The top three wheat producing African countries are Egypt (8.45 million metric tons), Morocco (7.34 million metric tons) and Ethiopia (4.50 million metric tons) [1].

Bread wheat (*Triticum aestivum* L.) and durum wheat (*T. Turgidum spp, durum* L.) are the two major species of wheat cultivated in Ethiopia. Ethiopia is the first largest wheat producer in Sub-Saharan Africa followed by South Africa [1].The crop ranked fourth after, maize, tef and sorghum both in terms of area coverage (1,696,082.59 ha) and quantity of production (45,378,523.39 quintals) in 2016/17 cropping season [2]. In Ethiopia, wheat has been one of the major cereals of choice, dominating the food habit and dietary practices next to tef '*injera*' and known to be a major source of energy and protein for the highland population [3].

In Ethiopia, wheat grows under diverse environmental conditions ranging in an altitude from 1500 to 3200 m.a.s.l. [4] which makes possible for the existence of different wheat growing area in Ethiopia. Though the crop has so many important merits, its production per unit areas is very low due to the lack of stable and high yielding cultivar. Therefore, improving yield and yield stability is the main objectives of national wheat breeding program in the Ethiopia.

Southwestern highland part of the country: Yem special district, Jimma and Buno Bedele zones, are among major wheat producing areas that cover 2823.3,29,257 and 1751 ha and with the productivity of 29.2, 31.4 and 28.5qt/ha respectively [5].The production and productivity of wheat at Southwestern part of Ethiopia was below from national productivity which 31qt/ha mainly due to lack of high yielding and adaptable varieties, diseases, soil acidity and other biotic and abiotic factors.

Yield is a complex character where it is highly influenced by both genes as well as environment. The existence of genotype-environment interaction (GEI) complicates the identification of superior genotypes for a range of environments and calls for the evaluation of genotypes in many environments to determine their true genetic potential [6].To identify wheat genotypes with wider or specific adaptation to different environments, multi-location yield trial are grown each year. Several stability statistics used to partition GEI include regression analysis, multivariate analysis, cluster analysis, genotype main effect plus genotype × environment (GGE) bi-plot [7] and additive main effect and multiplicative interaction (AMMI). However, both GGE and AMMI analysis are the most frequently used in analyzing GEI pattern of multi-environment data set.

GGE bi-plot analysis is effective for identifying the best performing cultivar in a given environment and the most suitable environment for each cultivar, comparing any pair of cultivars in individual environments, identifying the best cultivars for each environment and mega-environment differentiation, the yield and stability of the genotypes, and the discriminating ability and representativeness of the environments [8,9,10]. Therefore the objectives of the experiment were identifying stable and high-yielding bread wheat cultivars with specific or broad adaptation in the highlands of southwestern part of Ethiopia, validating the existing mega-environments; and identifying core testing sites within each mega environment for cultivar evaluation, release and marketing across southwestern part of Ethiopia.

2. MATERIALS AND METHODS

2.1. Experimental materials

Twelve nationally released bread wheat varieties were obtained from Kulumisa Agricultural Research Center (KARC) used for the study (Table 1).The varieties were evaluated in three environments, over two growing seasons (2021 to 2022), in the highlands of Southwestern Ethiopia. The experiments were conducted at Dedo, Yem and Gechi districts of Southwestern part of Ethiopia during the main cropping seasons (Table 2).

Table 1: Descriptions of experimental materials used in the study

#SN	Variety name	Year of Release	Breeder/ Maintainer
1.	ETBW9089	2021	KARC/ EIAR
2.	Jajabo	2017	KARC/ EIAR
3.	Liben	-	KARC/ EIAR
4.	Lemu	-	KARC/ EIAR
5.	Wane	-	KARC/ EIAR
6.	Huluka	2012	KARC/ EIAR
7.	Alidoro	2007	KARC/ EIAR
8.	Hidasse	2012	KARC/ EIAR
9.	Ogolcho	2012	KARC/ EIAR
10.	Daka	-	KARC/ EIAR
11.	Danda'a	2010	KARC/ EIAR
12.	Boru	-	KARC/ EIAR

Where; *EIAR; Ethiopian Agricultural Research Institute KARC: Kulumisa Agricultural Research Center*

2.2. Testing Environments

Table 2: Description of the Study Sites

Stations	Zones/Regions	Altitude (m.a.s.l.)	Temp (^{0}C)	Rainfall (mm)	Soil type
Dedo	Jimma	2284	22	1850	Nitosol
Yem special dist.	SNNPR	2470	22.5	1550	Nitosol
Gechi	Buno bedele	2087	20.7	1800	Nitosol

***NB**: SNNPR=Southern Nation, Nationalities and peoples region*

2.3. Experimental Design and Trial Management

The experiment was laid out in randomized complete block design (RCBD) with three replications. The experimental plot for each variety consisted of six rows of 2.5m length and rows were spaced 20cm apart. Spacing between rows, plots and replications 25cm, 30cm and 1m respectively. The seed rate was 125kg/ha.Fertilizer was applied at rate of 100kg NPS and 150kg of urea was applied in spilt: half at the time of planting and the remaining half at the tillering stage. In addition, other relevant field trial management practices were carried out uniformly for all experimental units according to the recommendation.

2.3. Data Collection

All the data were recorded based on the wheat descriptor list [11]. Data were collected from the four middle rows of each plot on the plant and plot basis. For the data collected on a plant basis, five plants per plot were randomly selected for each of the traits; that is, number of tillers per plant, number of kernels per spike, plant height (cm), and spike length (cm) and data for number of days to heading (75%), number of days to maturity (90%), grain filling period, thousand kernel weight (gm), aboveground biomass (t/ha) and grain yield (t/ha were collected on a plot basis.

2.4. Data Analysis

The agro-morphological data parameters of the three locations were subjected to the variance analysis using GenStat 16th edition statistical software package (VSN International Ltd., London, UK) following the standard procedures described by Gomez and Gomez [12] to evaluate the performance of genotypes for each trait and location and calculate the error variances for each of the environments. For combined analysis of variance (ANOVA) over locations, the homogeneity of error variance was tested using Bartlett's test for homogeneity of variances using the same software. Difference between treatment means was compared using the least significant difference (LSD) test at 5% level of significance when the ANOVA showed a significant difference among genotypes.

3. RESULT AND DISCUSSION

3.1. Mean performances of bread wheat varieties across locations

The result of analysis of variance (ANOVA) for twelve wheat varieties across six locations was presented in Table 3. Among the testing environments, grain yields were highest at Dedo2022 as compared to the other five environments with a mean grain yield of 5.8t/ha followed by Yem2022 (4.6t/ha) and Dedo2021 (3.5t/ha).The lowest grain yield was obtained at Gechi 2021 with a mean yield of 2t/ha. The superior performance of genotypes at Dedo2022 and Yem2022 can be attributed to the uniform distribution of rainfall throughout the cropping season. The tested genotypes showed inconsistent yield advantage across environments. The mean grain yield of genotypes over environments in table 3 indicated that Danda'a (4.6t/ha, Huluka (4.5t/ha) and ETBW9089 (4.4t/ha) were the highest yielding varieties whereas variety Ogolcho (3.5t/ha) and Hidassie (3.7t/ha) with mean of 3.8t/ha (Table 3).

Table 3: Mean performance of twelve bread wheat varieties across tested locations

Bread wheat varieties	**Locations and Years**							
	Dedo 2021	**Gechi 2021**	**Yem 2021**	**Dedo 2022**	**Gechi 2022**	**Yem 2022**	**Overall mean**	**Rank**
ETBW9089	4.6	2	4.1	6.4	4.3	4.7	**4.4**	**3**
Jajabo	4.8	1.2	4.6	6.5	3.7	4.8	**4.3**	**5**
Liben	4.8	1.5	3.4	6.3	4.4	5	**4.2**	**7**
Lemu	4	1.7	4	6.1	4.8	4.9	**4.3**	**6**
Wane	5.1	1.9	3.7	6.4	3.2	4.8	**4.2**	**8**
Huluka	4.5	2	4	7.1	4.2	5.1	**4.5**	**2**
Alidoro	4.1	2.8	3.3	6.9	3.6	5.2	**4.3**	**4**
Hidasse	4.3	1.3	3.3	5.4	3.1	4.6	**3.7**	**11**
Ogolcho	1.5	1.7	3.4	5.1	4.4	4.9	**3.5**	**12**
Daka	3.4	2.5	4.4	7.1	3.2	4.5	**4.2**	**9**
Danda'a	5.3	2	4	6.4	3.8	5.8	**4.6**	**1**
Boru	4.6	1.3	3.9	5.6	3.9	5.1	**4.1**	**10**
Mean	**3.5**	**2**	**3.9**	**5.8**	**3.2**	**4.6**	**3.8**	
F test	**<.0001**	**0.0382**	**0.0016**	**0.0058**	**0.0317**	**0.0108**		
CV (%)	**4.2**	**1.8**	**3.9**	**6.3**	**3.8**	**4.9**		
LSD value	**15.6**	**29.3**	**9**	**9.6**	**15.5**	**6.7**		

3.2. Combined analysis of variance (ANOVA) for grain yield

Bartlett's test indicated homogenous error variance for the grain yield and allowed pooled analysis across environments. The combined analysis of variance (ANOVA) of grain yield (t/ha) and yield-related traits of twelve wheat varieties tested in six locations was presented in Table 4. The ANOVA revealed that wheat grain yield was significantly ($p \leq 0.001$) affected by environment, genotype, and genotype by environment interaction. In agreement with this finding, Gadissa *et al*. [13] reported significant effects of genotype, environment, and GEI on bread wheat grain yield and yield-related traits. The significance of GEI indicated that the relative performances of the genotypes were not consistent across the test environments and the environments had different effects on the yield potential of the genotypes. This, in turn, suggested the need to conduct further analysis on GEI to understand the nature of the interaction, and to identify stable genotypes.

Table 4: Combined ANOVA for yield and the percentage sum of squares of the twelve bread wheat varieties tested at three environments over a period of two years (2021 and 2022)

Source of variation	Df	SS	MS	%SS
Environment (E)	5	412.46	82.492***	77.6
Genotype (G)	12	20.56	1.72**	3.87
Interaction (GEI)	60	56.14	0.94**	10.57
R/E	12	2.08	0.174^{ns}	0.39
Error	144	39.82	0.27	
Total	**233**	**531.07**		
Mean=4.2	**CV=**12.7	**R^2=92.5**		

Where=CV=coeffiencient of variation, *, ** significant ($p < 0.05$) and highly significant ($p < 0.01$) respectively, ns =non significant R/E=replication in the environment; SS: sum square, MS: mean square;df-degrees of freedom ;CV coefficient of variation

Table 5: Mean performance of combined bread wheat varieties of different traits at tested locations

Varieties	DH	DM	GFP	PH(cm)	PL(cm)	FT	TSW(g)	KPS	BY (t)	GY(t)	SY(t)
T1	67.2	133.0	65.8	80.9	8.1	4.3	39.3	42.2	9.9	4.4	5.9
T2	69.5	131.2	61.8	83.3	8.6	4.9	38.6	45.2	10.8	4.3	6.5
T3	70.3	132.7	62.4	80.5	8.1	5.0	34.0	40.3	9.7	4.2	5.5
T4	72.2	134.1	61.9	82.6	8.1	4.6	35.7	39.9	10.1	4.2	5.8
T5	69.7	132.6	62.9	77.9	7.5	4.6	37.6	43.4	10.3	4.2	6.1
T6	66.9	133.2	66.3	79.1	8.1	4.5	36.9	43.7	10.3	4.5	5.8
T7	69.1	131.1	61.9	87.1	8.8	4.5	37.4	44.7	11.0	4.3	6.6
T8	65.2	130.8	65.7	78.6	7.9	4.8	37.6	42.8	9.0	3.7	5.3
T9	65.6	130.1	64.5	80.9	8.2	4.2	35.7	43.3	8.3	3.5	4.8
T10	67.4	133.7	66.2	83.5	8.1	4.8	36.8	44.6	10.6	4.2	6.4
T11	70.3	134.2	63.9	83.3	8.3	4.3	37.4	42.4	10.4	4.5	5.9
T12	66.8	132.9	66.2	76.5	8.0	4.3	40.0	42.7	9.5	4.1	5.4
Mean	**68.2**	**132.7**	**64.4**	**81.7**	**8.2**	**4.5**	**37.1**	**43.1**	**10.0**	**4.1**	**5.9**
F test	***	***	***	***	**	**ns**	**	**ns**	***	***	***
LSD at 5%	**2.1**	**1.7**	**2.7**	**4.2**	**0.6**	**0.6**	**2.6**	**3.6**	**0.9**	**0.3**	**0.8**
CV (%)	**4.8**	**2.0**	**6.4**	**7.8**	**10.3**	**19.5**	**10.7**	**12.7**	**12.9**	**12.7**	**20.0**

T1=ETBW9089, T2=Jajabo, T3=Liben, T4=Lemu, T5=Wane, T6=Huluka, T7=Alidoro, T8=Hidasse, T9=Ogolcho, T10=Daka, T11=Danda'a and T12=Boru, *, ** ,ns, significant ($p < 0.05$) and highly significant ($p < 0.01$) and non significant respectively,

3.3. Stability Analysis

3.3.1. Genotype Main Effect and Genotype by Environment (GGE) Bi-plot Analysis of Genotype and Environment

3.3.1.1. Which won where/what view of GGE bi-plot Analysis

In the present study, the GGE bi-plot graphic analysis of twelve bread wheat varieties revealed that the first two principal components explained 74.51% of the total GEI variance (Figure 1). A polygon view of the GGE bi-plot was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. T9, T10, T11 and T12 were vertex genotypes and they are best in the environment lying within their respective sector in the polygon view of the GGE bi-plot [14]; thus these genotypes performed either the best or the poorest in one or more locations since they had the longest distance from the origin of the bi-plot. According to [9] and [15] genotypes within the polygon and nearer to the origin of the axes have wider adaptation and less response for environmental variation. [16] reported that responsive genotypes were those having either best or the poorest performance in one or all environments. T11 was identified as the highest yielding bread wheat variety whereas T9, T10 and T12 were considered as the lowest yielding genotype among vertex genotypes. In addition, no environment fell inside the sectors of the vertex genotypes T12, which indicated that those vertex genotypes were not the best in any of the test environments.

Another interesting feature of the GGE bi-plot is the identification of mega-environments as well as their winning genotypes. The present investigation suggested the existence of three wheat growing mega-environments (ME1, ME2, and ME3) in southwestern part of Ethiopia as shown in Figure 1. Among the testing environment, the environment Gechi2022, fell inside mega-environment one (ME1), Dedo2022, Gechi2021 and Yem2021 fell inside mega-environment two (ME2) whereas Yem2022 and Dedo2021 fell inside mega-environment three (ME3). Environments within the same sector share the same winning genotypes, and environments in different sectors have different winning genotypes. Accordingly, genotypes T9, T10, and T11 are suggested as the winner and highest yielding genotypes in mega-environment one, two, and three, respectively. [17] reported that the polygon view of GGE bi-plot is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments.

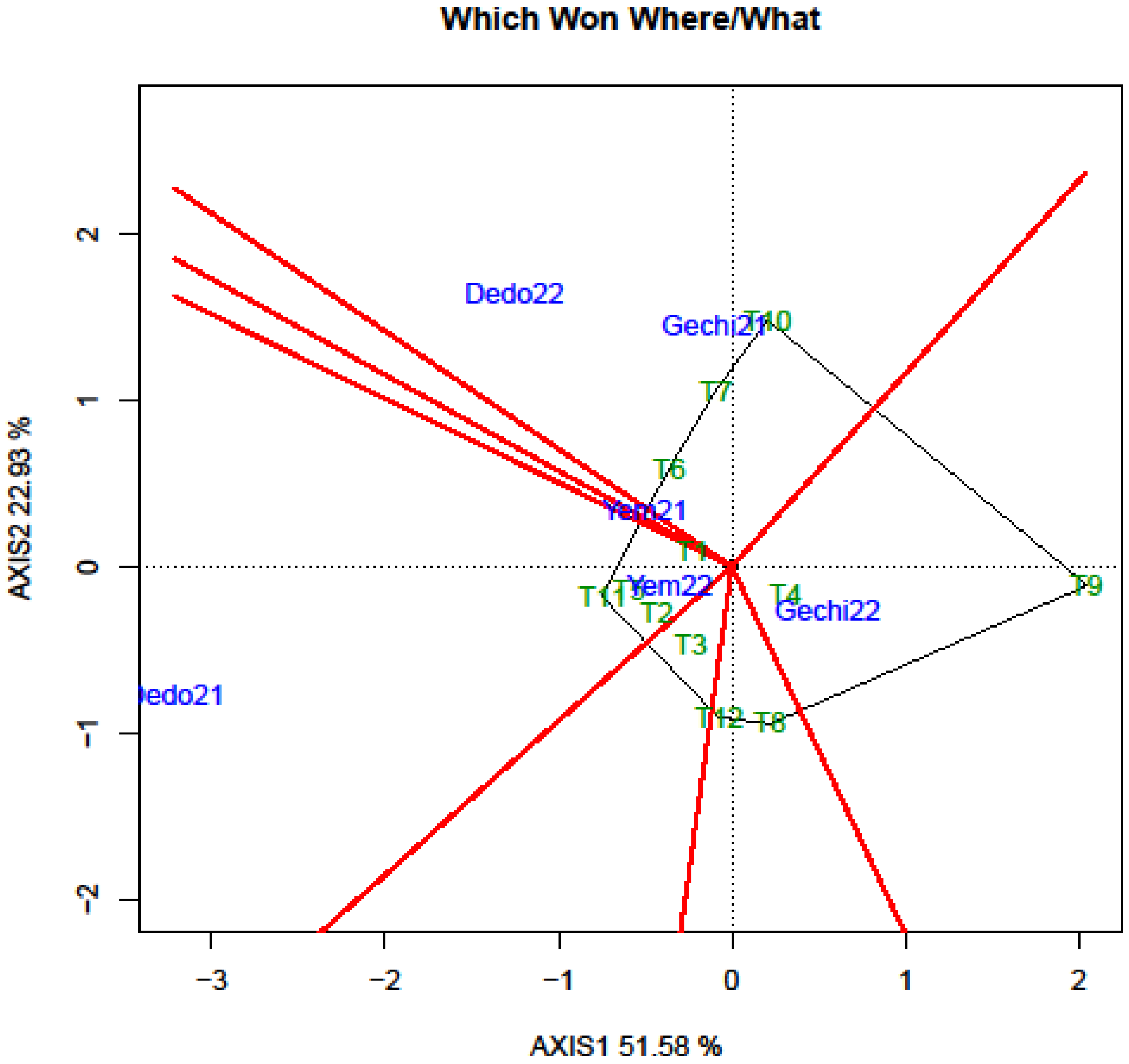

***Figure 1**: The polygon view of GGE bi-plot to the identification of winning genotypes and their related Mega environments:* T1=ETBW9089, T2=Jajabo, T3=Liben, T4=Lemu, T5=Wane, T6=Huluka, T7=Alidoro, T8=Hidasse, T9=Ogolcho, T10=Daka, T11=Danda'a and T12=Boru

3.3.1.2. Mean performances and Stability of Genotypes

The graphical method for mean performance and stability analysis of genotypes is presented in figure 2. It was based on row metric preserving where the singular values were entirely partitioned into genotype scores. For this procedure, single arrowed line that passes through the bi-plot origin and points to higher mean yield across environments was drawn. This line is called the Average Environment coordination (AEC) abscissa and labeled as AEA. The arrow directs towards higher average yield. Single arrowed line that is perpendicular to AEC abscissa was also drawn and this line is called the AEC ordinate and is labeled as Perpendicular Line (PL). This line points towards greater variability in either direction and hence genotype that has longer vector along this line is highly unstable [18]).The shorter the genotype vector is the more stable than others. Thus, among the tested genotypes T1, T11,T2 and T6 were identified as high yielder and stable genotypes while T10,T7,T9,T12 and T8 were found to have lower mean grain yield with longer vector length and identified as the most unstable genotypes across the test environments, which is in agreement with the previous findings of [19] in sorghum,[20] in quality protein maize hybrids; [21] and [13] in bread wheat and [22] on sesame.

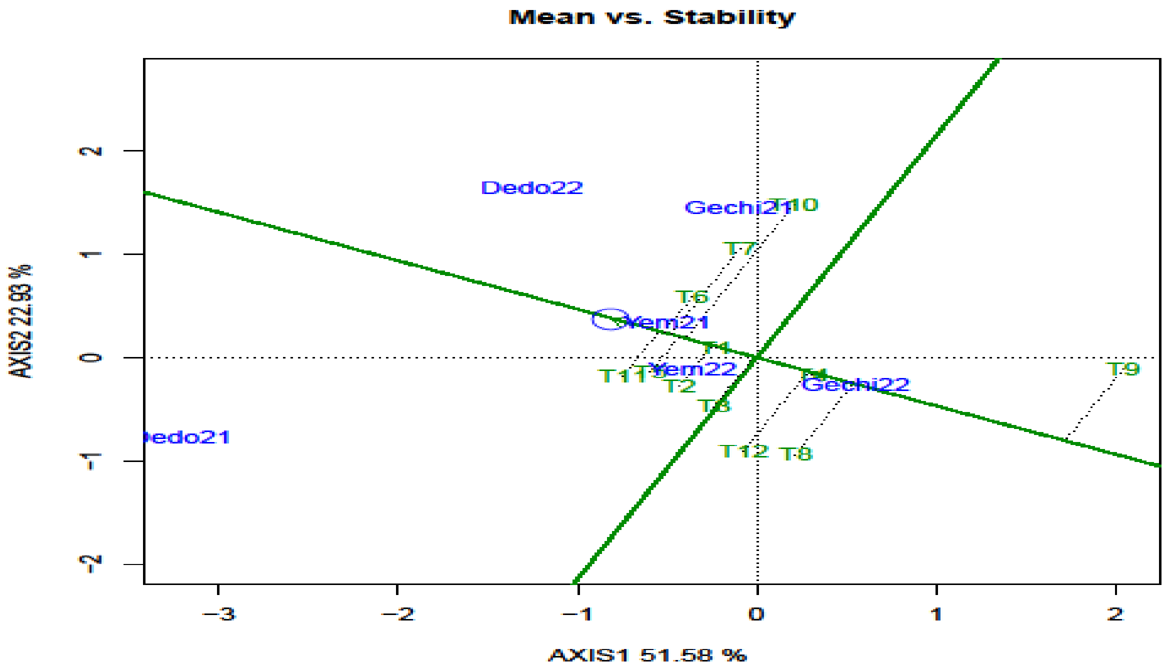

Figure 2: *GGE biplot visualization of the genotypes ranking for both yield and stability performance over environments;* T1=ETBW9089, T2=Jajabo, T3=Liben, T4=Lemu, T5=Wane, T6=Huluka, T7=Alidoro, T8=Hidasse, T9=Ogolcho, T10=Daka, T11=Danda’a and T12=Boru,

3.3.1.3. Ranking genotypes relative to the ideal genotype

GGE bi-plot based on ranking of genotypes relative to the ideal genotype for grain yield was presented (center of the concentric circle) in Figure 3. According to this ranking procedure, the genotypes closer to the ideal genotype are stable, while genotypes far from the ideal genotypes were the unstable. T1 followed by T5 were the “ideal” genotype with high mean grain yield and closer to the small circle being located on the AEC abscissa and with an arrow pointing to it (Fig. 2).Genotype is more desirable if it is located closer to the ideal genotype. Therefore, T11, T12 and T6 were plotted closer or near to the ideal genotype and considered as the most desirable and stable genotypes, while T10, T7 and T9 were high yielding genotypes associated with genotypic instability. Similar results were reported by various authors [19; 24; 23; 22].

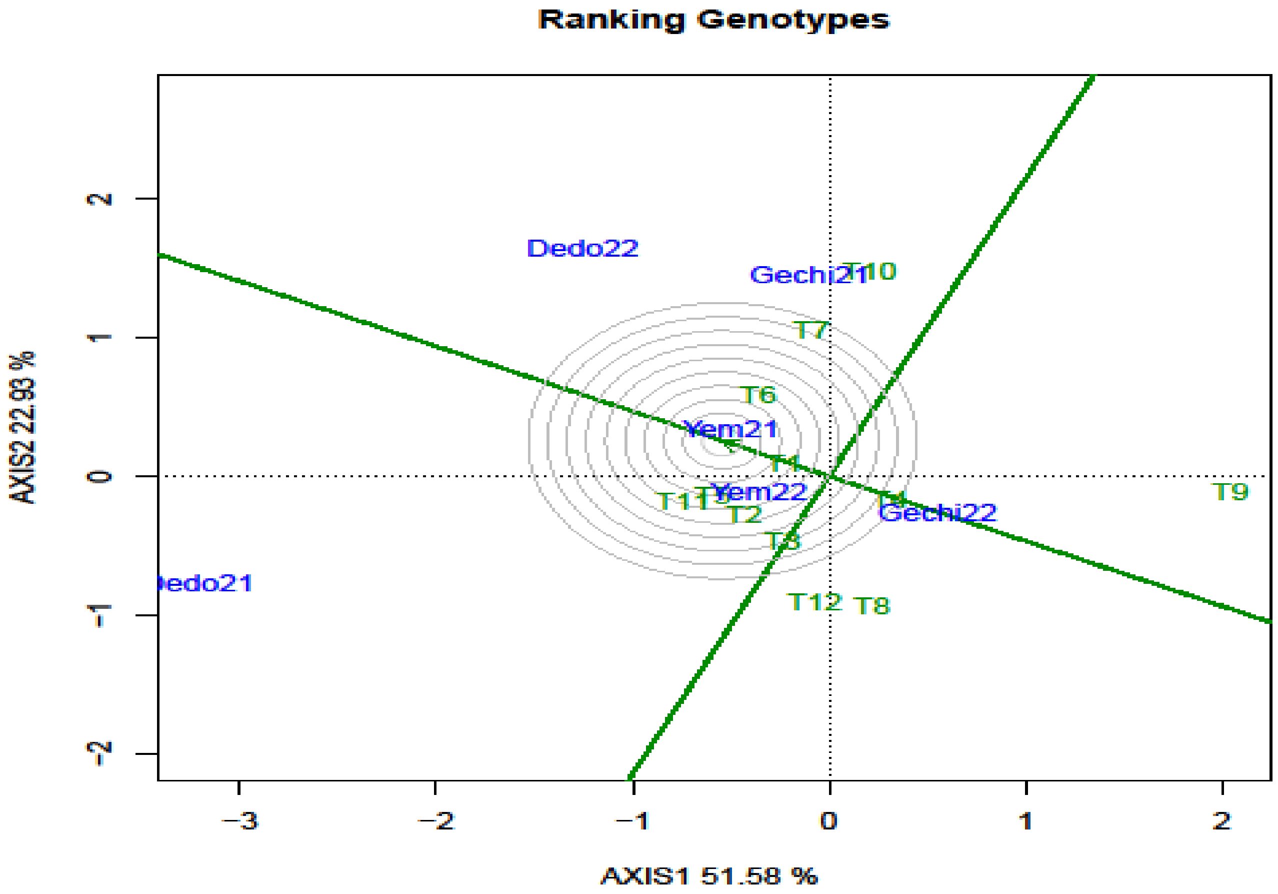

Figure 3: *GGE biplot of ideal genotypes and comparison of the genotypes with respect to the ideal genotype:* where,T1=ETBW9089, T2=Jajabo, T3=Liben, T4=Lemu, T5=Wane, T6=Huluka, T7=Alidoro, T8=Hidasse, T9=Ogolcho, T10=Daka, T11=Danda'a and T12=Boru,

3.3.1.4. Ranking of Environments Relative to the Ideal Environment

Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment focused bi-plot as shown figure 4. Desirable environments are close to the ideal environment. Accordingly, nearest to the first concentric circle, the environment Dedo2022 followed by Dedo2021 was the ideal environments to select widely adapted wheat genotypes, whereas, Gechi 2021 and Gechi 2022 were not an ideal environment.

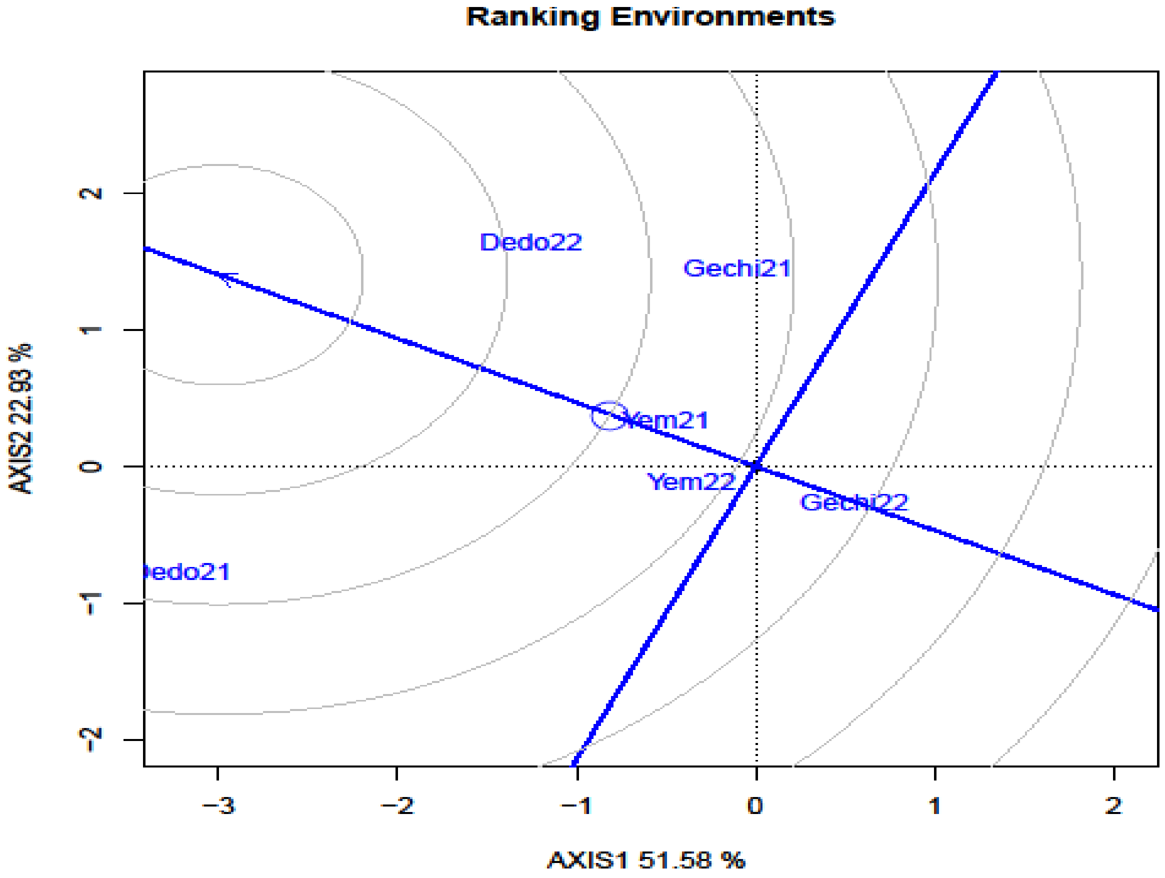

Figure 4: GGE bi-plot of ideal environments and comparison of the environments with respect to the ideal environment

3.3.1.5. Discriminating ability and representativeness of environments

According to [17], the discriminating ability and representativeness view of the GGE biplot is the important measure of test environments, which provide valuable and unbiased information about the tested genotypes. [9] also reported that environments with longer vectors had the more discriminating ability of the genotypes whereas environments with very short vectors had little or no information on the genotype difference. From this study, the test environments Dedo2022, Dedo2021 and Gechi 2021 were identified as the most discriminating environments which provided much information about differences among genotypes, while Yem2021, Yem2022 and Gechi2022 provided little information about the genotype differences figure 5.Another equally important measure of a test environment is its representativeness of the target environments. If a test environment is not representative of the target environments, it is not only useless, but also misleading since it may provide biased information about the tested genotypes [8].To know the representativeness of a test environment, understanding some important terms such as average environment (the small circle used as a benchmark for measuring the representativeness of a test environment), the average environment coordinate axis (the line that passes through the bi-plot origin and the average environment), and environmental vector (the line that connects the origin of bi-plot and a testing environment) is a very crucial task before measuring the representativeness of a test environment. Thus, based on the size of the angle between the vector of an environment and the abscissa of the average environment coordination (AEC) axis, it is possible to measure the representativeness of a testing environment.

That is, a testing environment that makes an acute angle with AEC axis has a positive correlation with other testing environments and it is considered as a representative of the other testing environments, whereas the testing environment that makes an obtuse angle with AEC axis has a negative correlation with other testing environments and least representative [9]. From this study, Dedo2022 was identified as the most representative testing environment, which was able to provide unbiased information about the performance of the tested genotypes, whereas Dedo2021 was identified as the least representative testing environment (Figure 3).

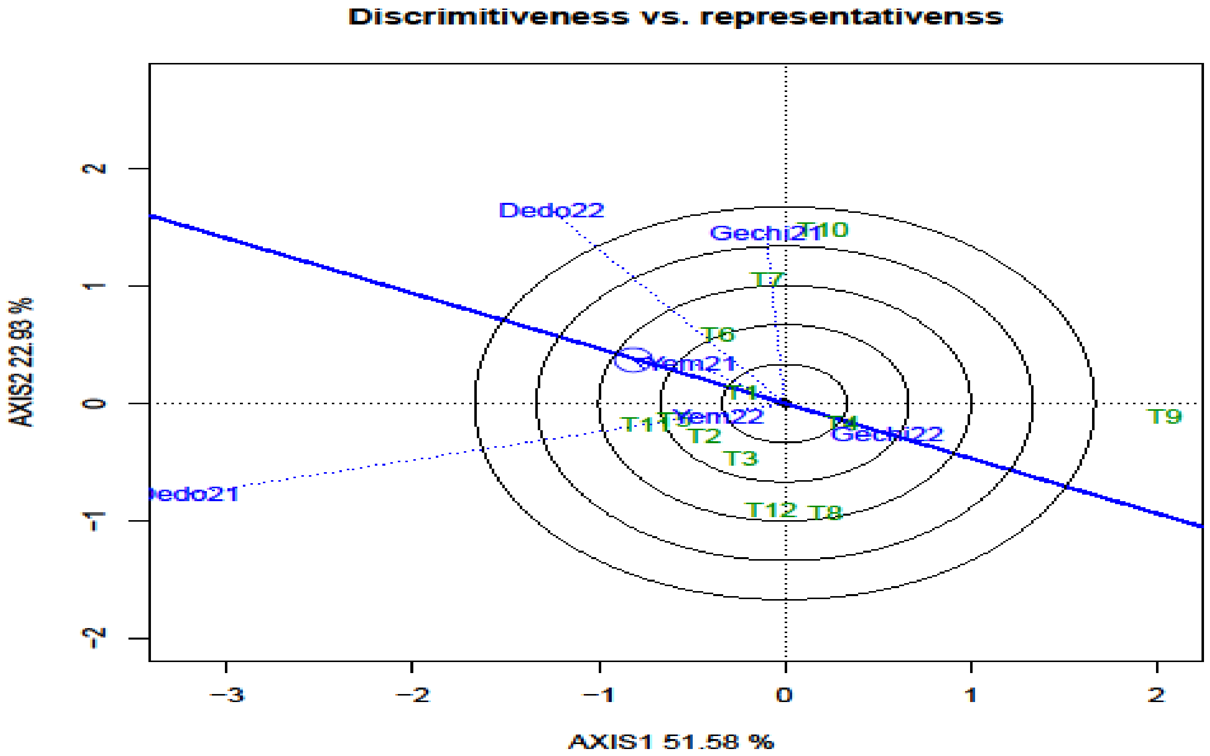

Figure 5: Discriminating power and representativeness of test environments: where,T1=ETBW9089, T2=Jajabo, T3=Liben, T4=Lemu, T5=Wane, T6=Huluka, T7=Alidoro, T8=Hidasse, T9=Ogolcho, T10=Daka, T11=Danda'a and T12=Boru

4. CONCLUSION AND RECOMMENDATION

The study revealed highly significant (P≤0.001) difference among environment (E), genotype (G) and genotype × environment interaction (GEI). Environment explained 77.6% of the total (G + E +GE) variation, whereas, G and GE explained 3.87% and 10.57% of the total variation, respectively. Based on the combined ANOVA over locations, the mean grain yield of environments ranged from 2tha^{-1} in Gechi2021 to 5.8t ha^{-1} in Dedo2022. The highest yield was obtained from Danda'a (4.6t ha^{-1}), while the lowest was from Ogolocho (3.5tha^{-1}) and the average grain yield of varieties was 3.8tha^{-1}.Based on the GGE bi-plot analysis different wheat growing environments were grouped in to three mega-environments: The first mega environment includes Gechi2022, the second mega environment includes Dedo2022, Gechi2021 and Yem2021 and third mega environment includes Yem2022 and Dedo2021 with the winner varieties of Ogolocho, Daka and Danda'a respectively. Even though, the wheat variety ETBW9089 not winner variety in the mega-environmnet, showed consistent performance across locations. Variety Danda'a and ETBW9089 can be recommended for wider cultivation due to better grain yield and stability performance across the test environments in the highlands of southwestern areas of Ethiopia.

5. Acknowledgment

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6. Conflict of interest

The author declared no conflict of interest

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