



GGE Biplot Analysis of Genotype x Environment Interaction on Bread Wheat (*Triticum aestivum* L.) Genotypes in Southern Oromia

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Abstract: Today, wheat is among the most important crops grown in Ethiopia, both as a source of food for consumers and as a source of income for farmers. Since Ethiopia is known for its diverse agro-ecology the performance of genotypes differs within and across environments and cultivars or genotypes respond differently to diverse environments. Therefore, studies on Genotype by Environment (GxE) interaction may help to determine whether or not a genotype is stable in performance over a range of environments. Therefore, this study was conducted to identify the best performing stable bread wheat genotype for selected areas and analysis of the environment by GGE biplot. In this experiment, 20 bread wheat genotypes were evaluated using RCBD with three replications at five different locations in southern Oromia. The combined analysis of variance revealed that, there were highly significant differences among environments and among genotypes ($p < 0.001$) for grain yield and yield components and for growth parameters except for days to emergence which was non-significant, indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. The GxE interaction was highly significant ($p < 0.001$) for all traits except spike length reflecting the differential response of genotypes in various environments. Environments explained 59.1%, genotypes 19.1% and GxE 14.8% of the variability in grain yield. Bore (E1) was the most discriminating environment while Adola (E3) and Liben (E4) were the least discriminating environments. GGE-II explained 89.62% of G+GEI and the angle between pair of all locations was lower than 90° ; performance of genotypes at all environments was almost similar, but Bore (E1) was separated from the remaining four environments. The bi-plot had six vertex genotypes, viz. Wane (G2), PBW-343 (G20), Galama (G13), Kakaba (G10), Hawi (G3) and ETBW8420 (G18). Hidase (G7) and Tuse (G8) gave relatively high grain yield and found to be stable, so can be recommended for wide adaptation. Wane (G2) and PBW-343 (G20) were unstable but were predicted to give the highest grain yield at all environments. Dashen (G6) and ETBW8420 (G18) can be recommended for all environments except for the high land environment, Bore (E1), while Lemu (G1) can be recommended for only Bore (E1). Lole Farm (E5) was the ideal environment while Wane (G2) was the ideal genotype. Advanced line ETBW420 (G18) is recommended to be included in variety verification trials for release as new varieties or to be included crossing program.

Keywords: GEI, Stable, Grain Yield, Adapted, Bread Wheat, Southern Ethiopia

1. Introduction

Today, wheat is among the most important crops grown in Ethiopia, both as a source of food for consumers and as a

source of income for farmers. It is an important and most widely cultivated food crop in the world and quantity produced is more than that of any other crop, feeding about 40% of the world population.

Wheat and wheat products represent 14% of the total

caloric intake in Ethiopia [1]. This makes wheat is the second-most important food, next to maize (19%) and ahead of teff, sorghum, and enset (10-12% each) [7].

Ethiopia is known for its diverse/heterogeneous agro-ecology. As a result the performance of genotypes differs within and across environments. When environmental differences are large like in Ethiopia, it may be expected that the interaction of genotypes with the environment will also be higher. This interaction may result in one cultivar having the highest yield in some environments while a second cultivar excels in others. Studies on GxE interaction may help determine whether or not a genotype is stable in performance over a range of environments. Genotype x Environmental Interaction (GEI) is useful to breeders as it can help determine if there is a need to develop cultivars for all environments or specific cultivars for specific target environments [4]. GEI is said to occur when different cultivars or genotypes respond differently to diverse environments.

Significant $G \times E$ interaction component reduces correlations between genotypic and phenotypic values [11] and affects genetic improvement of quantitative traits. $G \times E$ interaction is one of the main complications in the selection of genotypes for broad adaptation. Numerous studies have shown that a proper understanding of the environmental and genetic factors causing the interaction as well as an assessment of their importance in the relevant $G \times E$ system could have a large impact on plant breeding [15]. $G \times E$ interaction occurs universally when genotypes are evaluated in several different environments [3, 12, 13].

Different statistical model were used to describe GEI and facilitate genotype recommendations in MET such as stability

variance [20], coefficient of variability [8] and AMMI [10] have been commonly used to analyze MET data to reveal patterns of GEI. Yan et al. [22] proposed another methodology known as GGE biplot for graphical display of GEI pattern of MET data with many advantages. GGE biplot analysis considers both genotype and GEI effects and graphically displays GEI in a two way table [22]. GGE biplot is an effective method based on principal component analysis to fully explore MET data. It allows visual examination of the relationships among the test environments, genotypes and the GEI. The main objectives of the present study are to identify the best performing high yielding stable bread wheat genotype for selected environments and analysis of the ideal genotype and environment by GGE biplot method.

2. Materials and Methods

Twenty genotypes (15 released and 5 advanced lines) of bread wheat genotype were evaluated across five locations in 2018/2019 main cropping seasons. Description of test locations and wheat genotype is provided in Table 1 and Table 2, respectively.

The field experiment was laid out in RCBD with three replications. The experimental field plot was 6 rows of 2.5 m long with a 0.2 m inter-row spacing. Each plot was planted at a rate of 125 kg ha⁻¹. The fertilizer application and other crop management practices were done as per recommendations of each test locations. Weeding was conducted based on its appearance, twice for some locations and more for others, three times for Bore and Annasorra.

Table 1. Description of the locations used to evaluate bread wheat genotypes in 2018.

location	Altitude (masl)	Lat/long.	Average annual rainfall (ml)	Average annual Temperature (°C)	Soil type
Bore	2775	5°57'N/38°25'E	>1227	15	Nitosols
AnnaSora	2675	5°52'N/38°29'E	1000	20	OrthicAcrosol
Adola	1754	5°44'N/38°45'E	665	25	Chromic, orthic
Liben	1575	5°20'N39°35'E	655	25	Nitosols
Lole Farm	2450	33°29'N37°E	702.2	13.5	Silty Clay & Sandy Loam

Table 2. Lists of bread wheat genotypes included in the study.

S. N.	Genotype	Pedigree	Code	Year of release
1	Lemu	WAXWING*2/HEILO	ETBW 6861	2016
2	Wane	SOKOLL/EXCALIBUR	ETBW 6130	2016
3	Hawi	CHIL/PRL	HAR 2501	2000
4	Shorima	UTQUE96/3/PYN/BAU//MILAN	ETBW 5483	2011
5	Honqolo		ETBW5879	2014
6	Dashen	VEE #17, KVZ/BUHO"S"/KAL/BB	HAR 404	1984
7	Hidase	YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE. SQUAROSA (224)//OPATTA	ETBW 5795	2012
8	Tuse	COOK/VEE"S"/DOVE"S"/SERI	HAR 1407	2004
9	Danda'a	KIRITATI//2*PBW65/2*SERI. 1B	Danphe#	2010
10	Kakaba	KIRITATI//SERI/RAYON	Picaflore	2010
11	Kubsa	ATTILA	HAR 1685	1994
12	Alidoro	HK-14-R251	HK-14-R251	2007
13	Galama	4777 (2)//FKN/GB/3/PVN"S"	HAR 604	1995
14	Digalu	SHA7/KAUZ	HAR 3116	2005
15	Ogolcho	WORRAKATTA/2*PASTOR	ETBW 5520	2012
16	ETBW8407			Advaced breeding line
17	ETBW8415			Advaced breeding line
18	ETBW8420			Advaced breeding line
19	ETBW8369			Advaced breeding line
20	PBW-343			Advaced breeding line

2.1. Collected Data

Data was collected from the following traits; days to heading, days to maturity, grain filling period, number of grains per spike, number of spikelet per spike, plant height, number of tiller per plant, spike length, biomass yield, harvest index, TKW, HLW and grain yield per plot.

2.2. Statistical Analysis

The grain yield data for fifteen bread wheat in five environments were used to combined analysis of variance (ANOVA) to determine the effects of environment, genotype and GEI. Before combine the data Bartlett's test was used to determine the homogeneity of variances between environments to determine the validity of the combined ANOVA on the data and the data collected was homogenous.

GGE bi-plot was determined using GenStat software version 17. The GGE biplot is a biplot that displays the GGE part of MET data. GGE biplot was built according to formula given by Yan *et al.* [23]:

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

where Y_{ij} is the mean for the i^{th} genotype in the j^{th} environment, μ is the grand mean β_j is the main effect of environment j , λ_1 and λ_2 are the singular values of the 1st and

2nd principal components (PC1 and PC2), ξ_{i1} and ξ_{i2} are the PC1 and PC2 scores, respectively, for genotype i^{th} , η_{j1} and η_{j2} are the eigenvectors for the j^{th} environment for PC1 and PC2 and ϵ_{ij} is the residual error term.

3. Result and Discussion

Combined ANOVA depicted very highly significant differences among environments, genotypes and their interactions for grain yield (Table 3). This result is in line with the finding of Kifle *et al.* [14] who reported that the combined analysis of variance over two locations showed highly significant variations among the genotypes in all studied traits.

This indicated that grain yield of bread wheat was highly influenced by environmental factors. These results were in agreement with the works of Desalegn [6] and Demelsah *et al.* [5]. Mohamed [16] and Melkamu *et al.* [15] reported that bread wheat grain yield was significantly affected by environment. This result also showed the presence of high genetic variability among the tested genotypes and the inconsistency of their performance over the five locations.

Similarly Melkamu *et al.* [15] reported that the bread wheat genotypes they studied had wider genetic variability for all traits investigated.

Table 3. Combined analysis of variance of grain yield for 20 bread wheat genotypes evaluated at five environments.

Source	D. F	S. S	M. S	Total variation Explained (%)	GXE Explained (%)	Cumulative (%)
Total	299	799.4	2.67			
Genotypes	19	152.7	8.04**	19.10		
Environments	4	472.2	118.04**	59.06		
Rep (Env)	10	7.3	0.73			
Interactions	76	118.2	1.56**	14.78		
IPCA 1	22	75.4	3.43**		63.80	63.79
IPCA 2	20	28.8	1.44**		24.36	88.16
IPCA 3	18	12.9	0.72**		10.92	99.08
Residuals	16	1.1	0.07			
Error	190	49.0	0.26			

**p<0.001; IPCA=Interaction Principal Component Axis, DF=degree of freedom, SS=sum of squares, M. S=mean squares.

Note that the biplot captured 88.16% of the interaction Sum of Squares. Because the GxE component of the AMMI model is based on the product of interaction PCA scores, it follows that genotypes or environments with small interactions (smaller scores) will appear close to the center of the axes. Genotypes Hidase (G7), Tuse (G8), Alidoro (G12), ETBW8407 (G16) and ETBW8369 (G19) exhibit this trait, and therefore are relatively more stable (Figure 1).

All five locations exhibited larger interactions (i.e they are relatively far from the origin) and were discriminating environments, although Lole farm (E5) was relatively less discriminating as compared to other environments. The position of the genotypes relative the position of the environments also contain important information on the interaction. As an example, genotype Kubsa (G11), Galema (G13), Hawi (G3), Digalu (G14) ETBW8415 (G17) and Kakaba (G10) are nearer to Adola (E3) and Liben (E4) and

interacted positively with these environments but are placed opposite to Environments E1 (Bore), E2 (Annasorra) and E5 (Lole Farm) and interacted negatively with these environments (Figure 1). Adola (E3) (1754 m.a.s.l) and Liben (E4) (1575 m.a.s.l) are at lower elevation and obtain relatively low average annual rainfall (665 and 655 mm).

These two environments were low yielding environments. Annasore (E2) and lole Farm (E5) which were closer together on the biplot are at relatively higher altitude (2675 and 2450 m.a.s.l) and obtain relatively higher annual rainfall (1000 and 702 mm). Bore (E1) which was separated from all other environments is a typical highland (2775 m.a.s.l) and obtains high annual rainfall (1227 mm) and characterized by cool wether (Table 1). However below average yield was obtained at this environment. Genotypes Wane (G2), PBW-343 (G20), Shorima (G4), Honqolo (G5) Danda'a (G9) and Ogocho (G15) interacted positively with Bore (E1) and

AnnaSora (E2) but negatively with Adola (E3) and Liben (E4). Thus, the biplot can give information on relative

stability, as well as suggesting trends of similar or dissimilar genotypes and environments (Figure 1).

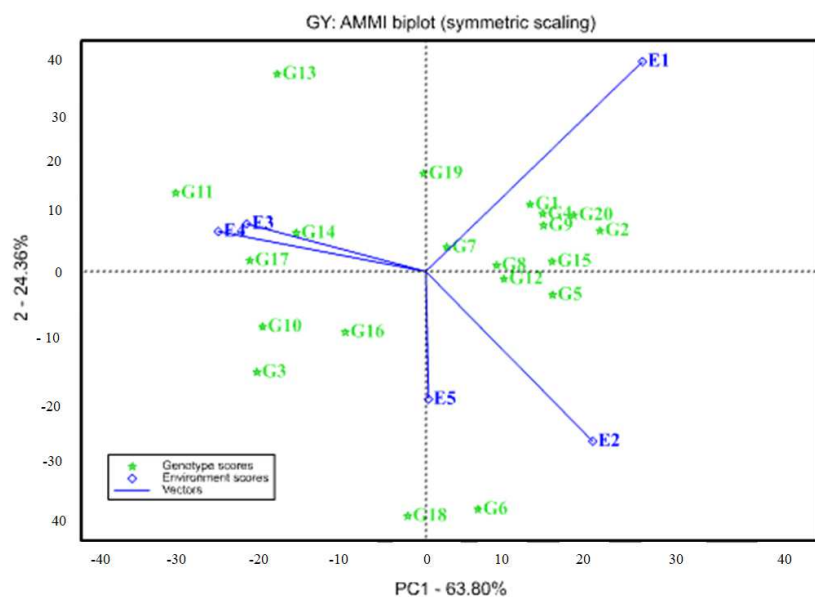


Figure 1. Biplot of interaction principal components analysis (PCA) axis 1 versus axis 2 for grain yield (kg/ha) for 20 bread wheat genotypes grown in 5 environment.

Where; G1=Lemu, G2=Wane, G3=Hawi, G4=Shorima, G5=Honqollo, G6=Dashen, G7=Hidase, G8=Tuse, G9=Danda'a, G10=Kakaba, G11=Kubsa, G12=Alidoro, G13=Galama, G14=Digalu, G15=Ogolcho, G16=ETBW8407, G17=ETBW8415, G18=ETBW8420, G19=ETBW8369, G20=PBW-343.

The second biplot is of interaction PCA axis 1 versus mean yield of both genotypes and environments (Figure 2). The vertical line represents the grand mean of yield while the horizontal line is the grand mean of IPCA1 which is zero. Seven genotypes (35%) gave below average yield while the remaining 13 genotypes (65%) gave above-average grain yield.

From the biplot, environments are distributed from lower yielding environments in quadrants II (top left) and III (bottom left) to the high yielding environments in quadrants I (top right) and IV (bottom right) (Figure 2). The high

yielding environments classified according to the AMMI 1 model were AnnaSorra (E2) and Lole Farm (E5). The lower yielding environments were Liben (E4) and Adola (E3). Bore (E1) gave near average yield.

It is further noted that Lole Farm (E5) was the most favorable environment and Adola (E3) and Liben (E4) were the least favorable environment among the five environments, this situation is clearly indicated in figure 2 where the three environments variations are plotted far apart from the mean.

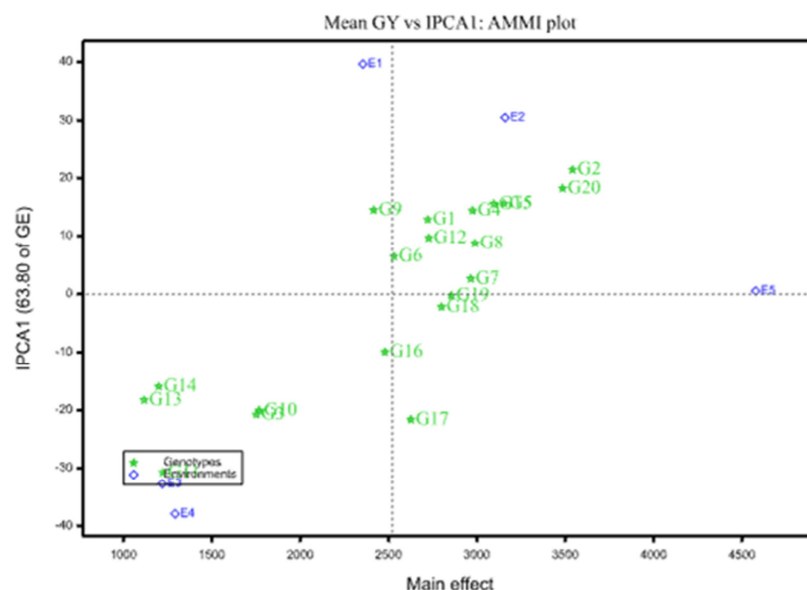


Figure 2. Biplot of interaction principal components analysis (PCA) axis 1 mean yield (kg/ha) for 20 bread wheat genotypes grown in 5 environments.

In summary, interaction patterns revealed by AMMI model biplot analysis indicate that genotypes ETBW8420 (G18), ETBW8369 (G19), Dashen (G6), Alidoro (G12) and Hidase (G7) exhibit smaller interactions with environments and are therefore more stable as observed across both interaction axes (Figures 1 and 2). They are the most desirable genotypes among the 20 genotypes tested and can be recommended for wider adaptation.

3.1. AMMI Stability Value (ASV)

AMMI stability value (ASV) is a stability parameter developed by Purchase to quantify and rank the genotypes on the basis of their yield stability. Genotypes with least ASV scores are the most stable; on the other hand, genotypes with high ASV score are unstable [19]. According to this model, Hidase (#7), ETBW8369 (G19), Tuse (#8), Alidor (#12) and ETBW8407 (#16), were the most stable, whereas Kakaba (#10), Galama (#13), and Hawi (#3) were unstable (Table 5). Out of the five stable genotypes only ETBW8407 (#16) gave below-average grain yield while the remaining four genotypes gave above- average grain yield.

3.2. Yield Stability Index (YSI)

Stability is not the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance [17], hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability: rank-sum, modified rank-sum and the statistics

yield stability [8, 2]. In this regard, ASV takes into account both IPCA1 and IPCA2 and justifies most of the variation in the GEI. The least YSI is considered as the most stable with high yield mean.

Based on YSI, Hidase (#7), Tuse (#8), ETBW8369 (#19) and Honqolo (#5) were the most stable. Conversely, Galama (#13), Hawi (#3) and Kubsa (#11) were the most unstable (Table 5). Similar results were reported by Olayiwola *et al* [18] in okra.

3.3. GGE Bi-plot for Evaluation of Environments and Genotypes

3.3.1. Evaluation of Genotypes Relative to Ideal Genotypes

Wane (G2) is the nearest to the arrow and is considered to be the “ideal” genotype and the highest yielding genotype. A genotype is more desirable (higher yielding) if it is located closer to the ideal genotype along PCA1 and undesirable (lower yielding) if it is located far from the ideal genotype. Genotypes above PCA1=0 give above-average yield while those below PCA1=0 give below-average yield. PBW-343 (G20) considered the most high yielding genotype as it closer to ideal genotype (Figure 3). Kubsa (G11) and Galema (G13) from low yielding, and ETBW8420 (G18) and Dashe (G6) from high yielding were most unstable genotypes as they are far from ideal genotype and PCA2=0 relatively. PBW-343 (G20), Honqolo (G5), Ogocho (G15), Tuse (G8), Shorima (G4) and Hidase (G7) were plotted to the ideal genotype and close to PCA2=0 are considered as desirable (high yielding and stable) genotypes relatively (Figure 3).

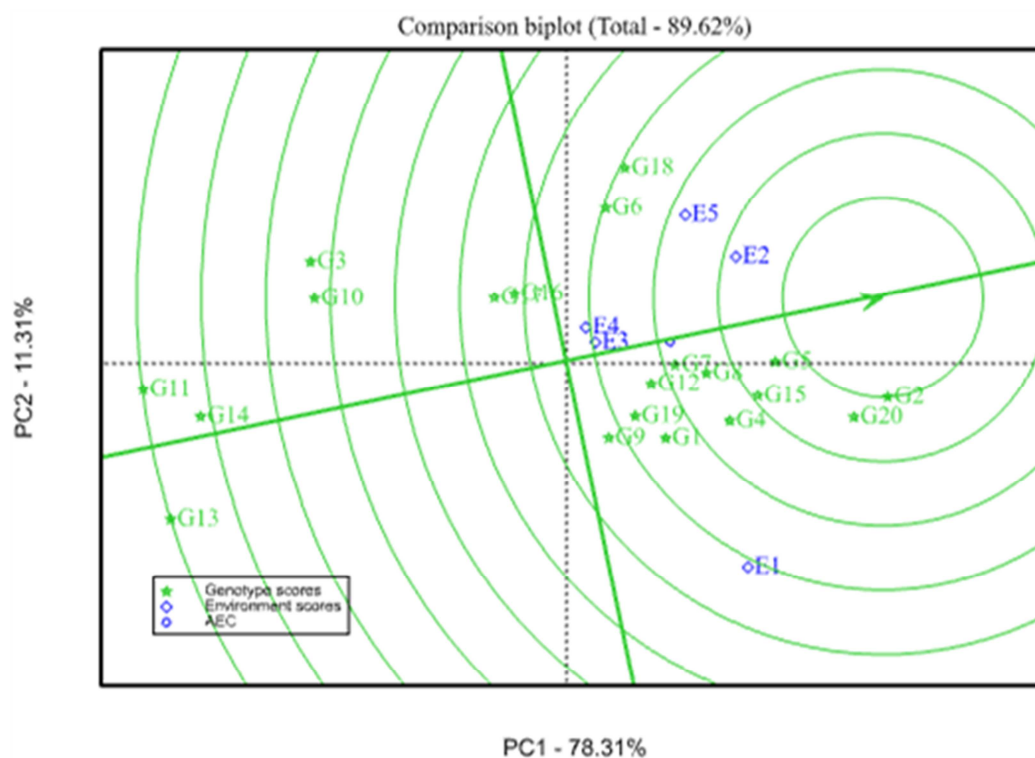


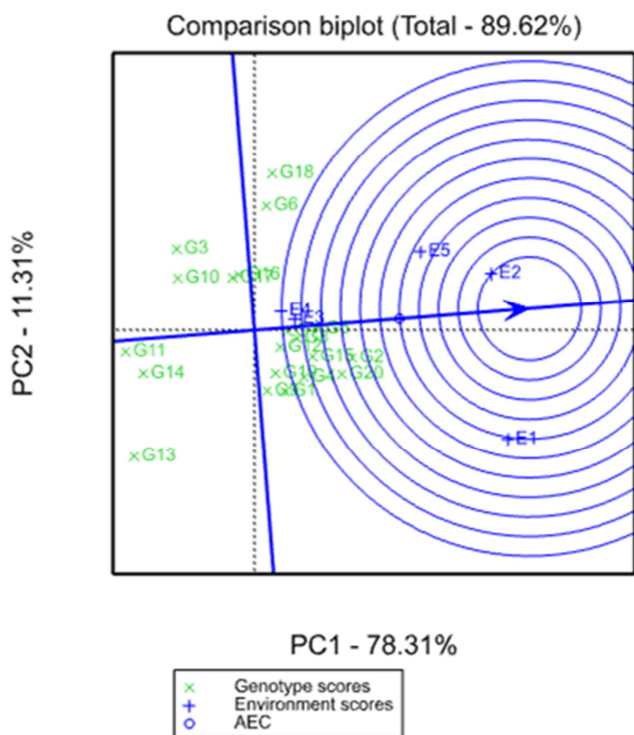
Figure 3. GGE-bi-plot showing the “ideal” genotype.

3.3.2. Evaluation of Environments Relative to the Ideal Environments

Genotypes closer to the ideal genotype and at the same time closer to zero by PCA2 of the GGE biplot are considered to be the most stable ones, while genotypes far from the ideal genotype and far from PCA2=0 in both directions are considered to be unstable.

E2 (Anna Sorra) had the longest vector with small PCA2, and fell into the center of the concentric circles and is considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes (Figure 4).

From figure 4, it show that, E5 (Lole farm) followed by E1 were closer to the ideal environment and are considered as suitable to select widely adapted genotypes respectively. E4 (Liben) and E3 (Adola) were far from the ideal environment and are considered to be unsuitable environments to select desirable genotypes (Figure 4). This result is in line with the findings of Yan *et al.* [21, 23] and Fiseha *et al.* [9].



Keys: E1=Bore, E2=Anna Sorra, E3=Adola, E4=Liben, E5=Lole farm

Figure 4. GGE-biplot based on the ranking of environments relative to an ideal environment.

3.4. 'Which-Won-Where' Pattern and Mega-environment Identification

The polygon view of GGE biplot is the best way for the identification of winning genotypes with visualizing the interaction patterns between genotypes and environments in MET data analysis [23], which is helpful in estimating the possible existence of different mega environments. The polygon view of a GGE biplot indicates the presence or absence of crossover or non-crossover GE interactions

involving the most responsive genotypes, and is suggestive of the existence or absence of different mega-environments among the test environments [21]. In this biplot, a polygon is formed by connecting the vertex genotypes with straight lines so that the rest of the genotypes are placed within the polygon. GGE biplot is constructed by plotting the first two principal components, PC1 and PC2, derived from subjecting environment centered yield data to singular value decomposition. These genotypes are the best or worst in some or all environments because they are farthest from the origin of the biplot [23] and are more responsive to environmental change and are considered as specifically adapted genotypes. They are best in the environments lying within their respective sector in the polygon view of the GGE-biplot [23].

The polygon view of the GGE biplot was constructed to show which genotypes performed best in which environment (Figure 5). PC1 and PC2 accounted for 89.62% (78.31 and 11.31%) of the G + GE variation for grain yield of the genotypes evaluated at five environments. The vertices of the polygon were the genotype markers located farthest away from the biplot origin in various directions, such that all genotype markers were contained within the resulting polygon. Based on this, six genotypes were identified as the markers farthest away from the biplot origin and the remaining fourteen genotypes lied within this polygon. The vertex genotypes were ETBW8420 (G18), Wane (G2), PBW-343 (G20), Galama (G13), Kubsa (G11) and Hawi (G3). The vertex genotype ETBW8075 (G3), Kubsa (G11) and Galama (G13) were the poorest genotypes in almost all of the test environments since they had the longest distance from the origin of the biplot on the opposite side of the environments. Additionally Digalu (G14), Kakaba (G10), ETBW8407 (G16), ETBW8415 (G17), Danda'a (G9) and ETBW8369 (G19) were also on the opposite side of all five environments and gave below-average yield at all environments. The highest rank for these genotypes was 9th for G19 at E1. Lemu (G1) was also the lowest yielding genotype at all locations except at E1 where it stood 6th.

All environments were in the same quadrant although Bore (E1) is far from other four environments. Wane (G2) and PBW-343 (G20) were the winning genotypes in this sector and were the highest and second highest yielding genotypes, respectively, at each of the five environments. Genotypes G4 (Shorima), G5 (Honqolo) and G15 (Digalu) were also among the highest yielding genotypes at all five locations. The angle between the farthest environments, Bore (E1) and Liben (E4), was less than 90° and performance at all locations was correlated. The correlation between E1 and E4 was ($r=0.79^{***}$) and all other correlations between pairs of environments were between $r=0.86^{***}$ and 1.00^{***} . Genotypes had very similar performance in E2, E3, E4 and E5.

Adola (E3) and Liben (E4) had very short vectors and were the lowest yielding and the least discriminating environments (mean yields of 1.53 and 1.62 vs 5.72 t ha⁻¹ at Lole farm (E5)). They are among moisture stress areas in

Guji Zone of Southern Oromia and lie at altitude of 1754 and 1575 masl and obtain annual rainfall of 655 and 655 mm, respectively. These two locations had the shortest growing season (days to flowering of 63 and 64 days, respectively, vs 83 days at Bore (E1) and days to maturity of 103 and 104 days, respectively, versus 153 days at Bore (E1). Although Lole farm (E5) gave the highest mean yield, Bore (E1) was the most discriminating environments with mean yield of genotyping from 1.127 to 0.06 and range of 1.071 t ha⁻¹. This

range was from 1.56 to 0.58, a range of 0.99 t ha⁻¹ at Lole farm (E5), which was the third most discriminating environment. E2 (AnnaSora) was the second most discriminating environment with mean grain yield ranging from 1.18 to 0.14 a range of 1.04 t ha⁻¹. Bore (E1) and AnnaSora (E2) gave moderately high grain yield (2.94 and 3.95 t ha⁻¹, respectively). They are in the highland agro ecology (2775 and 2675 masl) and have high mean annual rainfall (1227 and 1000 mm).

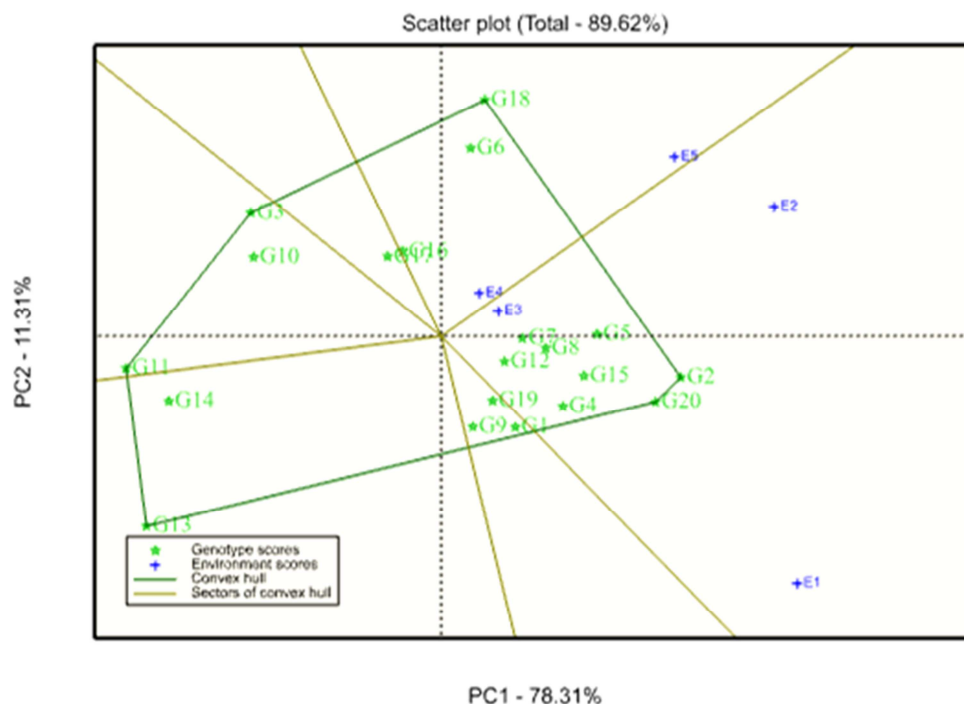


Figure 5. Which-Won-Where View of GGE bi-plot genotypes and environments of yield.

The vertex genotype ETBW8420 (G18) and Dashen (G6) were among the highest yielding genotypes at Annasorra (E2), Adola (E3), Liben (E4) and Bore (E5), but ranked 13th and 12th at Bore (E1), respectively. Genotypes nearer to the center of the biplot Hidase (G7), Tuse (G8) and Alidoro (G12) had smaller in absolute value PC1 and PC2 scores and are relatively stable over the five environments. However Alidoro (G12) gave low average yield (ranked 10th) at all locations, while Hidase (G7) and Tuse (G8) gave above average grain yield and can be recommended for wide adaptation.

4. Summery and Conclusion

Wheat and wheat products represent 14% of the total caloric intake in Ethiopia [1]. However, the productivity and production is low due to environmental factors, genotypes and GEI. Therefore, the experiment was carried out to evaluate GEI for grain yield and to identify stable high yielding genotypes and assess their performance across locations. In this study, twenty bread wheat genotypes were tested at five environments in southern Oromia during 2018 main cropping seasons.

From the combined analysis of variance, the effects environment, genotype and environment x environment were highly significant for grain yield and accounted for 59.064%, 19.10% and 14.789% of the total sum of squares. The high percentage of the environment is an indication that the major factor that influence yield performance of bread wheat in Ethiopia is the environment. In particular, the GEI is highly significant ($p < 0.001$) accounting for 14.789% of the total sum of squares implying the need for investigating the nature of differential response of the genotypes to environments. The presence of the GEI indicates that the phenotypic expression of one genotype is superior to another genotype in one environment but inferior in a different environment. In other words, presence of GEI does not permit to define an overall ranking of varieties across environments. All of the variance components were highly significant ($p < 0.001$), and indicates that factors such as soil fertility, rainfall, temperature, and disease incidence can result in conditions unique to each location combination and that the genotypes respond differently to these conditions.

The selection process of good performing and stable genotypes is mainly complicated by the phenomenon of genotype by environment (GXE) interaction. GXE interaction

is a differential genotypic expression across environments or generally the inconsistency of relative performance of genotypes over environments. The large occurrence of GXE interactions causes the relative rankings of genotypes to change from location to location. Hence, it is imperative to have a proper understanding of the effects of GXE interactions on variety evaluation, which will help to apply appropriate analytical methods and wise application of resources.

Various stability models were used in measurement of genotype stability. AMMI model were used to identify potential and poor environments, evaluation of genotype performance and identification of genotype and environment stability and identification of genotype interaction. GGE biplot were used to identify mega environments, genotype and environment evaluation, stability of genotypes and identification of ideal genotype and environments.

The classification of wheat growing areas in to homogenous

groups requires the repetition of similar experiments over years due to the year-to-year variation in factors such as rainfall and temperature of the growing season.

Based on the results of this research the following recommendations are made.

All advanced genotypes gave above average mean grain yield and genotype PBW-343 (#20) was the highest yielding while ETBW8407 (#16) was a stable genotype. These two genotypes should be crossed and high yielding and stable genotypes selected in their segregating progenies.

Genotypes such as Tuse (#8), Honqollo (#5), Ogolcho (#15) and Hidase (#7) are widely adapted across tested environments relative to the remaining genotypes, and hence are recommended to be grown across wheat growing areas of southern Oromia.

The following table shows the specifically adapted genotypes for their respective environments.

Table 4. The four highest yielding genotypes selected by AMMI for each environment.

Locations	1 st	2 nd	3 rd	4 th
Bore	Wane	PBW-343	Shorima	Ogolcho
AnnaSorra	Wane	PBW-343	Honqollo	ETBW8420
Lole Farm	ETBW8420	Wane	PBW-343	Honqollo
Adola	ETBW8415	ETBW8369	PBW-343	Hidase
Liben	ETBW8415	ETBW8369	Hidase	PBW-343

Appendix

Table 5. Mean yield (kg/ha) and yield related agronomic traits parameters of 20 bread wheat genotypes across 5 environments in 2018 main season.

Statistic	Geno	GY	TKW	Bm	HI	HLW	ED	TPP	HD	MD	GFP	KPS	SkPS	PH	SL
	G1	2722.8	50.25	7711.8	35	81.33	6.25	2.03	75.54	130.02	53.58	42.91	15.16	67.45	7
	G2	3541.4	53.86	8895.8	40.64	81.39	6.54	2.69	64.91	121.47	53.78	43.65	14.95	69.51	5.35
	G3	1752	52.37	5592	28.41	79.68	6.2	3.35	64.86	120.45	53.45	34.36	15.05	64.05	6.02
	G4	2976	49.45	7322.8	41.16	82.48	6.73	2.69	72.49	126.01	52.99	38.71	15.54	70.11	7.13
	G5	3155	51.47	7879.8	41.04	81.18	6.77	2.8	75.13	131.25	53.95	43.12	15.75	66.33	6.46
	G6	2530.6	48.67	7085.4	32.58	79.44	6.87	2.69	75.07	132.38	54.41	47.19	15.51	69.8	7.28
	G7	2965.2	57.14	7253	42.49	80.53	6.77	3.02	66.56	122.48	53.67	40.21	13.5	68.68	5.84
	G8	2989.4	50.74	7589.4	39.52	82.28	6.68	2.37	68.2	125.42	54.17	45.88	14.42	70.35	5.99
	G9	2416	52.85	7202.8	30.92	78.55	6.39	2.69	76.36	133.02	54.15	41.41	14.76	72.55	6.81
	G10	1768	52.84	5989.4	28.61	78.81	6.49	3.35	65.03	120.23	53.49	35.62	15.7	66.08	6.16
	G11	1224	48.5	4733.2	24.9	76.68	6.25	2.69	68.61	117.4	51.77	31.65	14.26	65.79	6.09
	G12	2728	56.59	8386.8	35.21	79.69	6.73	2.69	71.14	127.46	53.8	44.15	17.4	75.99	8.34
	G13	1117.2	50.56	4383.8	26.08	79.21	6.68	2.91	75.43	129.92	53.93	32.79	14.45	66.74	6.81
	G14	1200.2	49.67	4370.6	25.96	80.01	6.63	2.37	76.25	131.95	53.84	33.57	13.84	69.97	5.42
	G15	3095.8	50.05	8485.2	36.47	80.89	6.54	3.24	69.32	125.69	53.78	43.25	15.99	71.08	6.86
	G16	2480	53.98	6600.2	38.44	81.68	6.73	2.69	69.49	122.7	52.77	39.94	15.47	66.08	6.71
	G17	2626.6	51.03	7333.4	37.63	81.05	6.39	4.99	63.92	119.65	53.47	39.11	15.61	63.92	6.34
	G18	2799.8	53.74	7008	38.65	79.17	6.87	3.35	72.61	129.17	53.98	43.33	16.08	66.68	6.91
	G19	2856	53.92	7618.6	41.98	81.45	6.54	2.37	73.31	128.74	53.73	42.29	15.58	69.7	7.18
	G20	3485.2	51.85	7802.4	44.56	81.53	6.63	2.69	69.49	125.74	53.73	40.28	15.55	72.04	6.39
Heritability		0.8	0.62	0.75	0.68	0.67	0.57	0.99	0.88	0.8	0.28	0.63	0.72	0.67	0.89
Genotype Variance		0.03	9.39	0.08	22.57	3.15	0.07	0.38	20.29	27.99	1.2	31.63	1.07	13.77	0.55
GenxLoc Variance		0.03	23.33	0.1	23.12	6.79	0.03	0	12.32	33.39	13.77	70.02	1.44	14.47	0.05
Grand Mean		2521	52	6962	35.5	80.4	6.58	2.9	70.7	126.1	53.6	40.2	15.2	68.7	6.6
LSD		0.09	3.02	0.24	6.91	1.34	0.6	0.24	1.5	1.32	1.75	2.68	0.71	4.99	0.64
CV		21.1	7.9	19.8	26.8	2.3	11.15	14.7	3.4	1.6	4.7	7.4	5	7.8	10.3
Genotype significance		***	0	0	0	0	0.02	0	0	0	0.36	0	0	0	0
GenxLoc significance		0	0	0	0	0	0.43	1	0	0	0	0	0	0	0.26

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