

## Genotype by environment interactions and grain yield stability: Analysis in bead wheat genotypes at Western Oromia, Ethiopia

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### Abstract

Bread wheat is the most important cereal crop occupying a prominent position among major food crops in the world in terms of acreage and production and is an important cereal crop that receives the most attention from specialists in plant breeding and production worldwide. The interaction between genotypes/varieties and environment is important for effective selection of the variety/ies. This study aimed to observe the genotypic stability of fifteen bread wheat genotypes across four locations for three years and to select genotypes combining a high level of grain yield and yield stability. The combined ANOVA analysis for grain yield of fifteen bread wheat genotypes at 10 environments showed that bread wheat grain yield was significantly affected by environment, which explained a high percentage of the total treatment variation, whereas the G and GEI were significant and accounted for a lower percentage. The additive main effects and multiplicative interactions (AMMI) analysis indicated that two principal component analyses (PCA) were significant.

**Keywords:** AMMI; Bread wheat; Genotype; PCA; stability.

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## 1. Introduction

Worldwide, wheat (*Triticum aestivum* L.) is an important cereal crop that receives the most attention from specialists in plant breeding and production. Yet, its production is limited by adverse environmental conditions. Meanwhile, genotype by environment interaction (GEI) refers to the differential responses of different genotypes across a range of environments (Kang MS, 2004). This is a universal issue relating to all living organisms, even from bacteria to plants to humans (Kang MS, 1998), and it is important in agricultural, genetic, evolutionary, and statistical research. In breeding programs, genotype X environment interaction (G x E) cause many difficulties, while environmental factors such as temperature affect the performance of genotypes.

Genotype + environment (GE) interaction reduces the genetic progress in plant breeding programs by minimizing the association between phenotypic and genotypic values (Comstock and Moll, 1963). So multi-environment yield trials are essential in the estimation of genotype by environment interaction (GEI) and identification of superior genotypes in the final selection cycles (Kaya et al., 2006; Mitrovic et al., 2012). Phenotypes are a mixture of genotypes (G) and environment (E) components and interactions (G x E) between them. G x E interactions complicate the process of selecting genotypes with superior performance. Consequently, Multi-environment trials (METs) are widely used by plant breeders to evaluate the relative performance of genotypes for target environments (Delacy et al., 1996).

Various methods have been developed to show the patterns of genotype by environmental interaction, such as joint regression (Perkins and Jinks, 1968), Sum of squared deviations from regression (Eberhart and Russell, 1966), stability variance (Shukla, 1972), coefficient of determination (Pinthus, 1973), and coefficient of variability (Francis and Kannenberg, 1978).

These methods are commonly used to analyze MET data to reveal patterns of GE interaction. On the other hand, the additive main effects and multiplicative interaction (AMMI) model have led to more understanding of the complicated patterns of genotypic responses to the environment (Gauch, 2006). These patterns have been successfully related to biotic and abiotic factors. (Yan et al., 2000), proposed another methodology known as GGE-biplot for the graphical display of GE interaction pattern of MET data with many advantages. GGE biplot is an effective method based on principal component analysis (PCA) which fully explores MET data. It allows visual examination of the relationships among the test environments, genotypes, and GE interactions. The first two principal components (PC1 and 2) are used to produce a two-dimensional graphical display of genotype by environment interaction (GGE-biplot). If a large portion of the variation is explained by these components, a rank-two matrix, represented by a GGE-biplot, is appropriate (Yan and Kang, 2003). Using a mixed model analysis may offer superior results when the regression of genotype by environment interaction on environment effect does not explain all the interactions (Yan and Rajcan, 2002).

### 1.1. Purpose of study

Therefore, the objectives of this study were: to observe genotypic stability (concerning grain yield) of fifteen bread wheat genotypes across four locations for three years and to select genotypes combining a high level of grain yield and yield stability.

## 2. Materials and Methods

### 2.1. Materials

Fifteen genetically diverse wheat genotypes (Table 1) were evaluated against the standard check at Hawa Galan sub-site (altitude 1905 masl, 08° 38' N, 034° 50'E), Mata (2016 masl, 08° 34' N, 034° 44'E), Badesso (2054 masl, 08° 40' N, 034° 47'E) and at Tajo (2269 masl), in western Oromia, Ethiopia, during the 2016-2018 main cropping season at Haro sebu agricultural research center. The design was randomized complete block design (RCBD) and replicated three times. Six rows per plot of 0.2 m spacing between rows and 3 m row length and harvestable plot size were 2.4 m<sup>2</sup> (four harvestable

rows per plot). A seed rate of 125 kg/ha and fertilizer rate of 100 kg/ha NPS and 150 kg/ha Urea were used. Urea was applied in split form. Data were recorded for grain yield per plot and converted plot grain yield to tons per hectare.

## 2.2. Statistical analysis

Analysis of variance is calculated using the model:

$$Y_{ij} = \mu + G_i + E_j + GE_{ij}$$

Where  $Y_{ij}$  is the corresponding variable of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $\mu$  is the total mean,  $G_i$  is the main effect of the  $i^{\text{th}}$  genotype, and  $E_j$  is the main effect of  $j^{\text{th}}$  environment,  $GE_{ij}$  is the effect of genotype x environment interaction.

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^N \lambda_k Y_{ik} \delta_{jk} + \varepsilon_{ij}$$

The AMMI model used was:

Where  $Y_{ij}$  is the grain yield of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment,  $\mu$  is the grand mean,  $g_i$  and  $e_j$  are the genotypes and environment deviation from the grand mean, respectively,  $\lambda_k$  is the eigenvalue of the principal component analysis (PCA) axis  $k$ ,  $Y_{ik}$  and  $\delta_{jk}$  are the genotypes and environment principal component scores for axis  $k$ ,  $N$  is the number of principal components retained in the model, and  $\varepsilon_{ij}$  is the residual term.

**Table1**

*List of bread wheat genotypes evaluated*

No	Codes	Genotypes	Sources
1	G1	Local check	farmer
2	G2	ETBW7056	KARC
3	G3	ETBW7104	KARC
4	G4	king bird	KARC
5	G5	ETBW7068	KARC
6	G6	ETBW7076	KARC
7	G7	ETBW7077	KARC
8	G8	ETBW7072	KARC
9	G9	Liban	KARC
10	G10	ETBW7075	KARC
11	G11	ETBW7092	KARC
12	G12	ETBW7069	KARC
13	G13	ETBW7052	KARC
14	G14	ETBW7088	KARC
15	G15	ETBW7071	KARC

*Note: G-genotype, KARC-Kulumsa Agricultural Research center*

GGE-biplot methodology, which is composed of two concepts, the biplot concept (Gabriel, 1971) and the GGE concept (Yan et al., 2000) was used to visually analyze the METs data. This methodology uses a biplot to show the factors (G and GE) that are important in genotype evaluation and that are also the source of variation in GEI analysis of METs data (Yan,2001). The GGE-biplot shows the first two principal components derived from subjecting environment-centered yield data (yield variation due to GGE) to singular value decomposition (Yan et al., 2000)

AMMI Stability Value (ASV): ASV is the distance from the coordinate point to the origin in a two-dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997). Because the IPCA1 score contributes more to the GXE interaction sum of squares, a weighted value is needed.

This weighted value was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2 to the interaction sum of squares as follows.

$$ASV = \sqrt{[(SS_{IPCA1} \div SS_{IPCA2})(IPCA1score)]^2 + (IPCA2score)^2}$$

Where  $SS_{IPCA1}/SS_{IPCA2}$  is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. The larger the ASV value, either negative or positive, the more specifically adapted a genotype is to certain environments. Smaller ASV values indicate more stable genotypes across environments (Purchase, 1997). Genotype Selection Index (GSI): Stability is not the only parameter for selection as most stable genotypes would not necessarily give the best yield performance. Therefore, based on the rank of mean grain yield of genotypes (RYi) across environments and the rank of AMMI stability value RASVi, the genotype selection index (GSI) was calculated for each genotype as:

$$GSli = RASVi + RYi$$

A genotype with the least GSI is considered the most stable (Farshadfar, 2008). Analysis of variance was carried out using statistical analysis system (SAS) version 9.2 software (SAS, 2008). Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE bi-plot analysis were performed using the Gen Stat 15th edition statistical package (VSN, 2012).

### 3. Results

#### 3.1. Additive Main Effects and Multiple Interaction (AMMI) models

The combined ANOVA and AMMI analysis for grain yield at 10 environments exhibited bread wheat grain yield was significantly affected by environments, which explained 69.66% of the total treatment (G+E+GEI) variation, while the G and GEI were significant and accounted for 9.23 and 8.56%, respectively (Table 2). Similar findings have been reported in previous studies (Farshadfar et al., 2012; Kaya et al., 2006). A study by Gauch and Zobel, 1997, reported in standard multi-environment trials (METs), the environment effect contributes 80% of the total sum of treatments and 10% effect of genotype and interaction. In additive variance, the partitioning of the GEs data matrix by using AMMI analysis indicated two PCAs were significant ( $P < 0.01$ ). PCA 1 and 2 accounted for 3.98% and 1.61% of the GE interaction, respectively representing a total of 5.59% of the interaction variation (Table 2). Similar results have been reported in earlier studies (Mohammadi and Amri, 2009). Large yield variation explained by environments indicated environments were diverse, with large differences between environmental means contributing to maximum variation in grain yield (Table 3). Grain yield of environments ranged from 2.29 t/ha in E10 to 5.02 t/ha in E5. Genotype mean grain yield varied from 2.95 t/ha in G1 to 4.06 t/ha in G6 with an overall mean of 3.37 t/ha (Table 3)

**Table 2**

*Analysis of variance for grain yield using additive mean effect and multiple interactions (AMMI) model.*

Source	D.F.	S.S.	M.S.	V.R.	EX. SS%	prob.
Total	449	477.9	1.064			
Treatments	149	417.8	2.804	14.79	87.42	**
Genotypes	14	44.1	3.149	16.61	9.23	**
Environments	9	332.9	36.984	105.76	69.66	**
Block	20	7	0.35	1.85	1.46	*
Interactions	126	40.9	0.324	1.71	8.56	**
IPCA 1	22	19	0.863	4.56	3.98	**
IPCA 2	20	7.7	0.384	2.02	1.61	**
IPCA 3	18	5.3	0.292	1.54	1.11	ns
Residuals	66	8.9	0.135	0.71		ns
Error	280	53.1	0.19			

Key: df = degree of freedom, SS = sum of squares, MS = mean squares, IPCA = Interaction Principal Component Axis, EX.SS%= Explained Sum of squares \*, \*\* non-Significant, Significant at the 0.5% and 0.1% level of probability respectively.

**Table 3**

*Average grain yield (tons/ha) of 15 bread wheat genotypes tested across 10 environments*

Gen/Env	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	mean
G1	2.68	3.41	2.29	2.35	4.90	2.57	3.88	2.84	2.61	2.01	2.95
G10	3.77	5.07	3.24	2.16	4.35	3.01	4.36	3.16	3.23	2.56	3.49
G11	3.96	4.41	2.54	2.74	5.15	3.11	4.35	3.27	2.85	2.32	3.47
G12	3.32	3.87	2.19	2.57	5.29	2.76	4.02	2.90	2.49	1.95	3.14
G13	3.57	4.31	2.56	2.28	4.56	2.83	4.11	3.01	2.78	2.20	3.22
G14	3.56	3.92	2.30	2.35	4.46	2.80	4.05	3.07	2.69	2.14	3.13
G15	3.43	4.21	2.41	2.16	4.53	2.68	3.97	2.84	2.60	2.02	3.09
G2	3.88	5.40	3.61	2.52	5.00	3.29	4.66	3.39	3.52	2.84	3.81
G3	3.36	4.39	2.94	2.91	5.81	3.13	4.47	3.27	3.09	2.48	3.58
G4	3.33	3.59	2.14	2.33	4.42	2.70	3.95	3.02	2.60	2.06	3.01
G5	4.53	4.89	2.52	2.44	4.48	3.12	4.32	3.24	2.80	2.29	3.46
G6	4.00	5.49	3.70	2.99	5.85	3.53	4.90	3.57	3.61	2.95	4.06
G7	3.73	4.23	2.29	2.96	5.95	3.04	4.28	3.09	2.57	2.07	3.42
G8	3.70	4.13	1.92	2.36	5.04	2.65	3.87	2.70	2.18	1.69	3.02
G9	3.59	3.85	2.74	3.23	5.59	3.35	4.61	3.69	3.25	2.71	3.66
mean	3.63	4.34	2.63	2.56	5.02	2.97	4.25	3.14	2.86	2.29	3.37

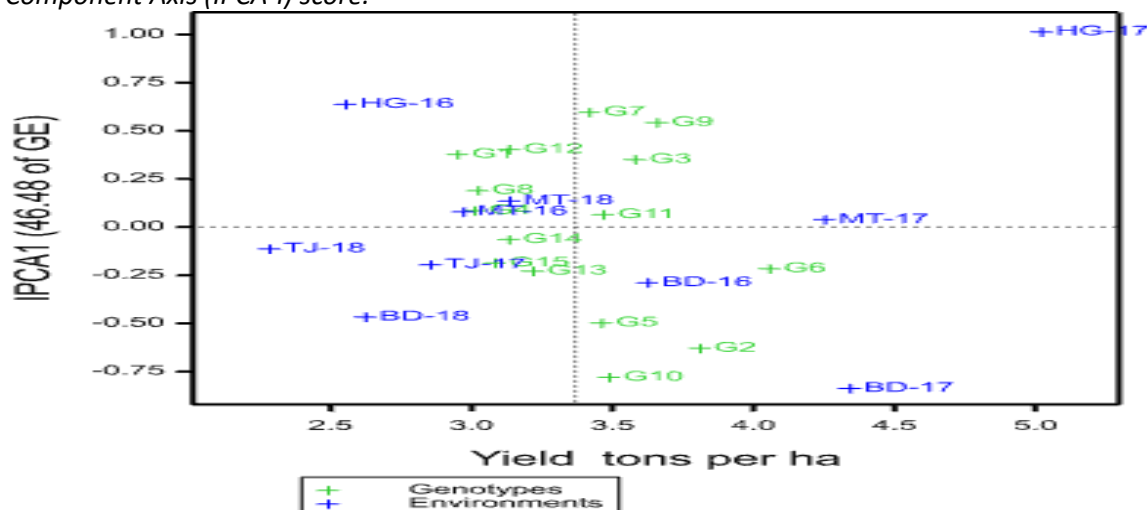
Source: Gen., genotype; Env., environment

A GGE-biplot based on genotype-focused scaling was depicted to detect the locations of genotypes, where the genotypes that had PC1 scores > 0 were identified as higher-yielding, while the genotypes that had PC1 scores < 0 were identified as lower-yielding (Figure 1). On the other hand, PC2 which was related to genotypic stability or instability, divided genotypes of importance into four sets based on their scores. The first set included three stable genotypes (G6, G3, and G11) that were high yielding because near-zero PC2 scores exhibited genotypic stability. Set 2 included two unstable genotypes (G2 and G9), but were higher-yielding, as absolute larger PC2 scores were associated with genotypic stability, whereas setting 3 (G4, and G14) were low yielding and stable genotypes, and Set 4 contain two genotypes (G1 and G8).that were low yielding and genotypic instability (Figure 2).

By projecting the genotypes on the AEA axis, the genotypes are ranked by yield, where the yield increases in the direction of the arrow. In this cause, the highest yield had genotypes G6, G9, G2, and G3 but, the lowers had G1, G4, and G15 (Figures 1 and 2). The stability of the genotypes depends on their distance from the AE abscissa. Genotypes closer to or around the center of the concentric circle indicated these genotypes are more stable than others. Therefore, the greatest stability in the high-yielding group had genotypes G6, G11, and G3, whereas the most stable of all was G6 (Figure 2).

**Figure 1**

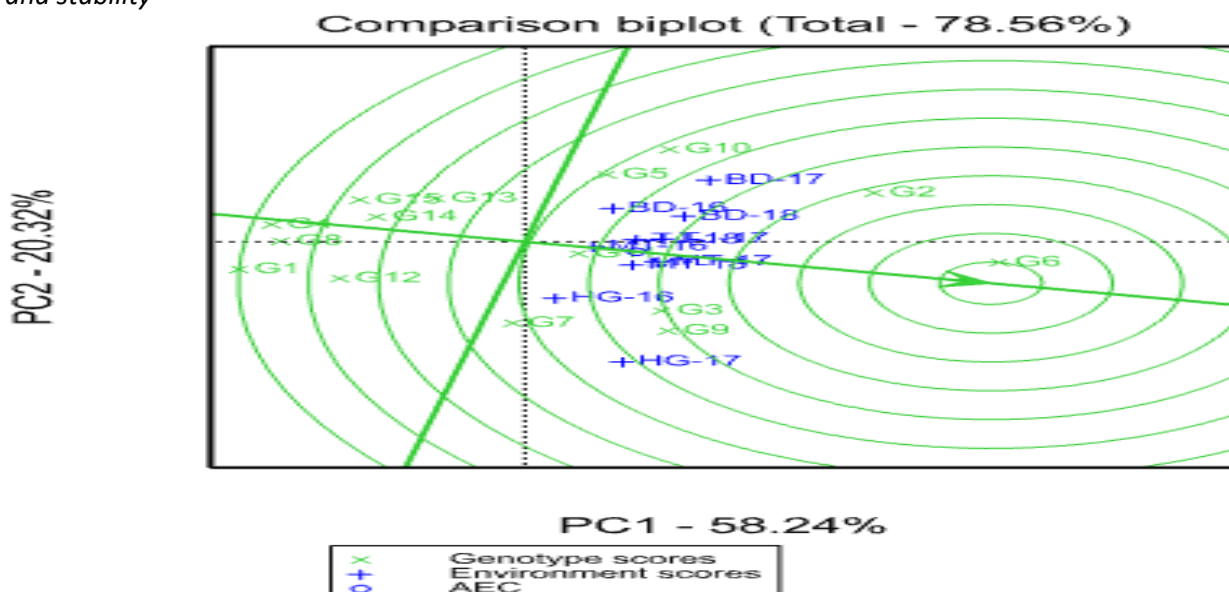
Matrix plot of environment and genotypes mean grain yield (tons ha<sup>-1</sup>) versus Interaction Principal Component Axis (IPCA-I) score.



Note: The reference line on the x-axis is the average grain yield and on the y-axis is the IPCA-I value indicating genotype stability.

**Figure 2**

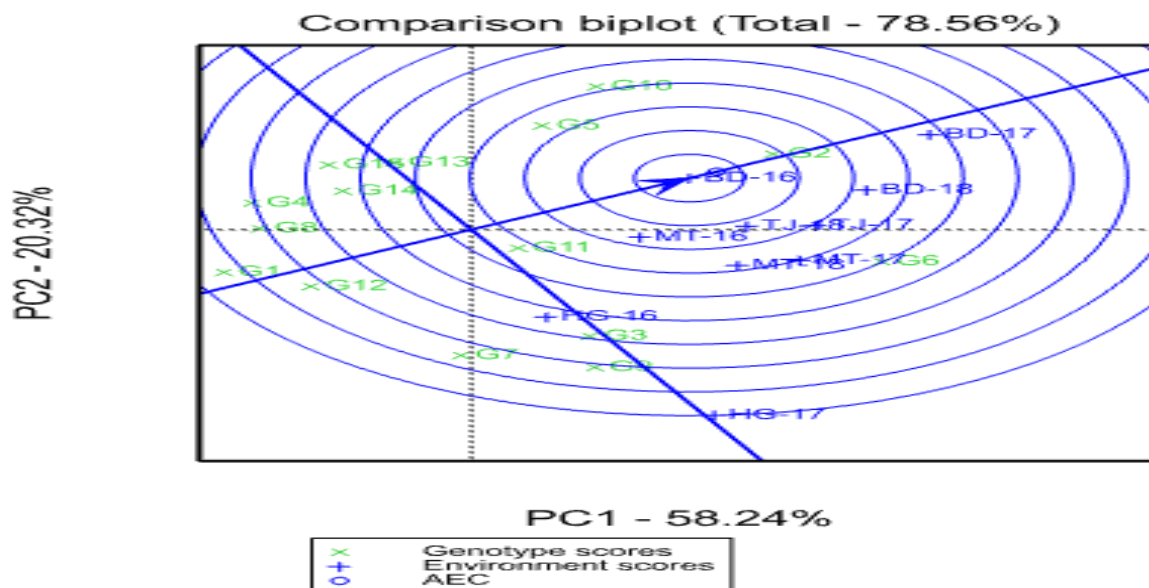
GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability



The genotype ranking is shown on the graph of genotype so-called “ideal” genotype (Figure2). Accordingly, E1 (BD16=Badesso) which fell into the center of concentric circles, was an ideal test environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. Favorable environments were E6 (MT-16=Mata) and E10 (TJ-18=Tajo) while the unfavorable were E4 (HG-16 = Hawa Galan) and E5 (HG-17 = Hawa Galan) (Figure 3).

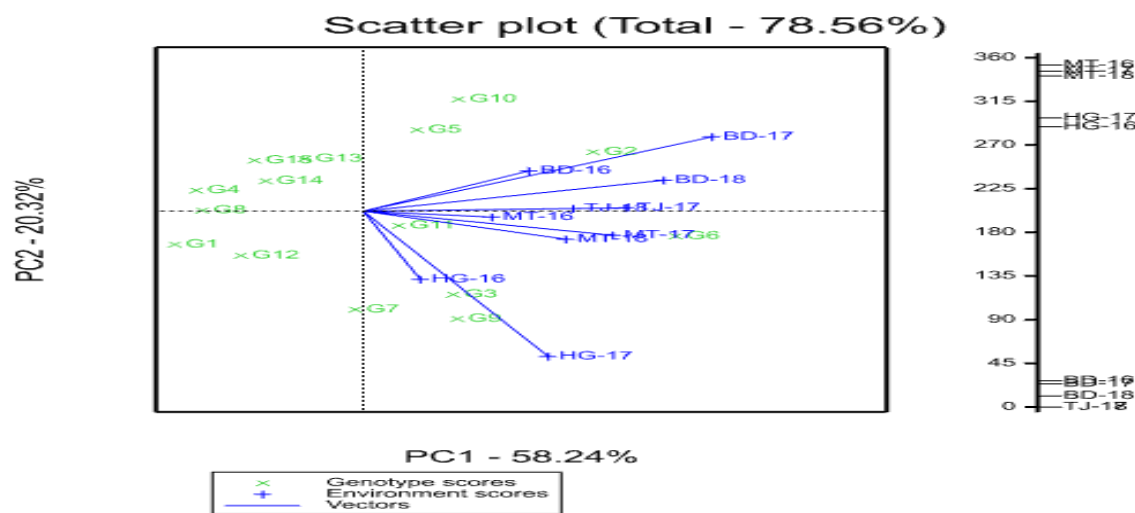
**Figure 3**

*GGE bi-plot based on tested environments-focused comparison for their relationships*



**Figure 4**

*GGE bi-plot based on tested environments-focused comparison for their relationships*



Key: HG-16 = Hawa Galan (E4), HG-17 = Hawa Galan (E5), BD-16=Badesso(E1), BD-17=Badesso(E2), BD-18=Badesso(E3), MT-16=Mata (E6), MT-17=Mata (E7), MT-18=Mata (E8), TJ-17=Tajo (E9), TJ-18=Tajo (E10). The number following each location indicates the year (16= 2016, 17 = 2017, 18 = 2018), E=environment.

**Table 4**

*Correlation Coefficients among 10 Test Environments*

	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10
E1	1									
E2	0.729**	1								
E3	0.363*	0.832**	1							
E4	0.17	0.105	0.288*	1						



E5	0.001	0.117	0.245*	0.894**	1					
E6	0.611**	0.712**	0.799**	0.715**	0.54**	1				
E7	0.529**	0.741**	0.874**	0.674**	0.536**	0.988**	1			
E8	0.457**	0.508**	0.729**	0.716**	0.438*	0.942**	0.928**	1		
E9	0.337*	0.713**	0.964**	0.418*	0.273*	0.859**	0.916**	0.864**	1	
E10	0.393*	0.703**	0.94**	0.487*	0.311*	0.903**	0.944**	0.913**	0.994**	1

\*, \*\* Significant at the 0.05 and 0.01 probability level respectively

The correlation coefficients among the 10 test environments and the vector view of the GGE-bi-plot delivered a summary of the interrelationship between the environments and the correlation coefficients were significant (Figure4). Most environments were positively correlated since the angles among them were smaller than 90° apart from environments E4 and E5 which have negatively correlated with E1, E2, and E3 of obtuse angles between them (Figure 4).

### 3.2. Additive Main Effects and Multiple Interaction (AMMI) Stability Value (ASV)

**AMMI Stability Value (ASV):** Genotypes exhibited significant genotype by environment interaction effect and the additive and multiplicative interaction effect stability analysis (ASV) implied to split the interaction effect. Because of mean grain yield as the first criteria for evaluation, G6 was the highest mean grain yield (4.06t/ha) followed by the genotypes G2 and G9 with the mean grain yield of (3.81and 3.66 t/ha) respectively. Whereas, genotypes G1, G4, and G8 were with low mean grain yields across the testing locations (Table5). TheIPCA1 and 2 scores in the AMMI model are indicators of stability (Purchase,1997). Considering IPCA1, G6 was the most stable genotype with an IPCA1 value (-0.78) followed by G2 with an IPCA1 value of (-0.63). Likewise, in IPCA2, G1 was the most stable with an interaction principal component value (-0.46) followed by the genotype G3 with the IPCA2 value (-0.37).

The two principal components have their extremes, however calculating the AMMI stability value (ASV) is a balanced measure of stability (Purchase,1997). Genotypes with lower ASV values are considered more stable and genotypes with higher ASV are unstable. According to the ASV ranking in (Table5), G4 was the most stable with an ASV value of 1 followed by G14 with an ASV value of 2. However, G10 was the most unstable since the higher ASV value of 15. The stable genotype was followed by mean grain yield above the grand mean and this result was in agreement with (Hintsa and Abay, 2013), who have used ASV as one method of evaluating grain yield stability of bread wheat varieties in Tigray and similar reports been made by Abay and Bjørnstad (2009); Sivapalan et al. (2000) in barley in Tigray and bread wheat Using AMMI stability value. A genotype with the least Genotype Selection Index (GSI) is considered the most stable genotype (Farshadfar, 2008). Accordingly, G6 was the most stable genotype with the least of Genotype Selection Index (GSI) (Table5).

**Table 5**

*AMMI Stability Value, AMMI rank, Yield, Yield Rank and Genotype Selection Index and Principal Component Axis*

Genotype	ASV	ASV rank	YLD tons/ha	YLD rank	GSI	IPCAg1	IPCAg2
G6	0.94	6	4.06	1	7	-0.78	-0.34
G2	1.39	14	3.81	2	16	-0.63	-0.36
G9	1.25	11	3.66	3	14	0.54	-0.23
G3	1.11	9	3.58	4	13	0.35	-0.37
G10	1.47	15	3.49	5	20	-0.22	-0.22
G11	0.65	3	3.47	6	9	0.06	0.26



G5	1.38	13	3.46	7	20	-0.50	0.68
G7	1.32	12	3.42	8	20	0.60	0.28
G13	0.76	5	3.22	9	14	-0.23	0.01
G12	1.03	8	3.14	10	18	0.40	0.06
G14	0.52	2	3.13	11	13	-0.06	0.11
G15	0.70	4	3.09	12	16	-0.19	0.03
G8	1.00	7	3.02	13	20	0.19	0.53
G4	0.49	1	3.01	14	15	0.08	0.03
G1	1.18	10	2.95	15	25	0.38	-0.46

ASV=stability value, YLD= yield, GSI=genotype selection index, IPCAg=interaction principal component axis for genotype

#### 4. Discussion

The estimation of yield and stability of genotypes was done by using the average coordinates of the environment (AEC) methods (Yan, 2001; Yan and Hunt, 2001). The average environment is defined by the average values of PC1 and 2 for all environments and it is presented with a circle. The average ordinate environment (AOE) is defined by the line which is perpendicular to the AEA (average environment axis) line and passes through the origin. This line divides the genotypes into those with higher yields than average and into those with a lower yield than average.

An ideal genotype is defined as one that is the highest yielding across test environments and it is completely stable in performance (that ranks the highest in all test environments) (Farshadfar et al., 2012; Yan and Kang, 2003). Even though such an “ideal” genotype may not exist in reality, it could be used as a reference for genotype evaluation (Mitrovic et al., 2012). A genotype is more appropriate if it is located closer to the “ideal” genotype (Farshadfar et al., 2012; Kaya et al., 2006). So, the closer to the “ideal” genotype in this study was G6 (Figure 2). The ideal test environment should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments).

Such an ideal environment was represented by an arrow pointing to it (Figure 3). Actual, such an ideal environment may not exist but, it can be used as an indication for genotype selection in the METs. An environment is more desirable if it is located closer to the ideal environment. Therefore, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan and Rajcan, 2002).

Most environments were positively correlated since the angles among them were smaller than 90° apart from environments E4 and E5 which have negatively correlated with E1, E2, and E3 of obtuse angles between them (Figure 4). Similarly, Farshadfar et al. (2012), in their study reported environments ER3 and EI3 which represented rain-fed and irrigated conditions in the 2011 cropping seasons, respectively, made an obtuse angle with each other, indicating a negative correlation between the response of genotypes to rain-fed and irrigated conditions. Indirect selection could be functional in the case where the same character was measured on the same genotypes in different environments. Where there are no correlations of error effects among environments, the phenotypic correlation between environments may be used to investigate the indirect response to selection (Cooper & Delacy, 1994). Indirect selection for grain yield can be partial across the tested environments. This means, for instance, the genotypes adaptable or higher productivity in E9 may also show similar responses to E6, E7, and E8 as well.

#### 5. Conclusions

The interaction between genotypes/varieties and environment is important for effective selection of the variety/ies. The combined ANOVA analysis for grain yield of fifteen bread wheat genotypes at 10 environments showed that bread wheat grain yield was significantly affected by environment, which explained 69.66% of the total treatment (genotype + environment + genotype by environment

interactions) variation, whereas the G and GEI were significant and accounted for 9.23% and 8.56%, respectively. The additive main effects and multiplicative interactions (AMMI) analysis indicated that two principal component analyses (PCA) were significant ( $P < 0.01$ ). PCA 1 and 2 accounted for 3.98% and 1.61% of the genotype + environment (GE) interaction, respectively.

Graphical display of genotype by environment interaction (GGE-biplot) based on genotype-focused scaling was depicted to detect the locations of genotypes, whereas the bread wheat genotypes were divided into four groups based on their scores of PCA 1 and 2: Three stable and high yielding genotypes (G6, 3 and 11), two unstable high yielding genotypes (G2 and G9), two stable low yielding genotypes (G4, and G14) and two low yielding unstable genotypes (G1 and G8). The correlation coefficients among the ten test environments and the vector view of the GGE-biplot provided a summary of the interrelationship between the environments whereby 41 of the 45 correlation coefficients were significant. Most environments were positively correlated. However, environments E4 and E5 have negatively correlated with E1, E2, and E3. The G6 is stable and adaptable to a wide range of environmental conditions.

Generally, based on the two analyses of AMMI and GGE-biplot models, G6, G3, and G11 are considered by high yield and more stability, consequently, G6 is close to the ideal genotype, so this genotype is adaptable to a wide range of environmental conditions. In contrast, G1 and G8 revealed lower scores for both yield and stability. Therefore, G6 is the most appropriate in the wide-ranging environmental conditions.

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### Abbreviations and Symbols

AMMI =additive main effects and multiplicative interactions E= environment, G= genotype, GEI= genotype environment interaction, MET = Multi-environment trials, PCA =principal component analysis (axes), kg/ha= killogram per hectare=gram, t/ha= tons per hectare, NPS=nitrogen phosphourse sulpher, IPCA=interaction principal component.

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