GGE Bi Plot Analysis of Genotype X Environment Interaction and Grain Yield Stability of Bread Wheat (Triticum aestivum L.) Genotypes in Ethiopia

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Abstract

There is limitation of information on G x EI of bread wheat genotypes in Ethiopia. The study cried out with objectives to estimate Genotype x Environment interaction and stability of bread wheat genotypes in Ethiopia. Thirty Bread wheat genotypes were evaluated by Alpha lattice design using three replications at eight locations in Ethiopia. The mean grain yield of genotypes across environments was 4.53 ton ha^{-1}. Bread wheat grain yield was significantly affected by the E, G and G x E interaction. Environment, G x E interaction and genotype explained 45.59%, 25.37% and 2.59% of the total (G + E + GEI) variation respectively. Genotype ETBW71942 (3), ETBW7038 (9), ETBW8511 (1) and ETBW8512 (14) were considered specifically adapted. Considering simultaneously yield and stability, Genotype ETBW7871 (15), ETBW7058 (11), ETBW8513 (16) and ETBW7101 (25) showed the best performances.

Keywords: *genotype; environment; genotype x environment interaction; Stability.*

INTRODUCTION

Bread wheat (*Triticum aestivum* L.) belongs to the family Gramineae (Poaceae= true grasses) and to the genus *Triticum* and species *aestivum*. A very likely place of origin is the area known in early historical times as the Fertile Crescent - a region with rich soils in the upper reaches of the Tigris-Euphrates drainage basin (Junhua *et al.,* 2011). The center of its domestication is widely accepted to be somewhere in the Middle East (Anikster and Wahl 1979).

The genus *Triticum* exists as a polyploid series of diploid (2n=14), tetraploid (2n=28), and hexaploid (2n=6x=42) species complexes (Provan *et al.,* 2004). Of special cultural and economic importance are the tetraploid durum wheat *T. turgidum* L. and the hexaploid bread wheat (common wheat) *T. aestivum* L. (Baum *et al.,* 2009). Wheat is one of the most important cereal crops of the world and it is a staple food for about one third of the world's population (Hussain and Shah, 2002).

Wheat is one of the most important cereal crops of the world and it is a staple food for about one third of the world's population (Hussain and Shah, 2002). It is a major cereal crop in Ethiopia, which is largely grown in the highlands. At the national level, wheat is cultivated on 1.63 million ha of land with a total grain production of 3.43 million tons (CSA, 2013). In the country wheat is the third important crop after tef and maize and the country continues to remain as the largest producer of wheat in Sub Saharan Africa (Dagiwoine and Alamerew, 2013). In Ethiopia, more than 87 improved bread wheat varieties were released from 1974 to 2011; 30 varieties from 1974 to 1997 and from 1998 to 2011 fifty-seven varieties were released and some of them are in production in different agro-ecological zone of the country (Degewione and Alamerew, 2013). However, one challenge faced in wheat production in the country is low productivity per unit area of land. The national average yield of the crop is estimated at 2.11 tones ha-1 (CSA, 2013), which is very low compared to the world's average yield of 3.09 tones ha-1 (FAOSTAT, 2012).

Wheat is mainly grown in the highlands of Ethiopia, which lie between 6 and 16°N and 35 and 42°E, at altitudes ranging from 1500 to 2800 meters above sea level and with mean minimum temperatures of 6^{O}C to 11^{O}C (Hailu, 1991; MOA, 2012).There are two varieties of wheat grown in Ethiopia: bread wheat, accounting for 60 percent of production, and durum wheat, accounting for the remaining 40 percent (Bergh *et al.,* 2012). Bread wheat is preferred to durum wheat by farmers in Ethiopia owing to its high yield potential, ease of mechanization, relatively higher economic returns, and good bread making quality relative to the other food crops (Tanner *et al.*, 1993).

The success of crop improvement activities largely genotype evaluation by eliminating unnecessary testing depends on the identification of superior genotypes for sites (Letta, 2009). G × E interactions are of major importance, because they provide information about the effect of different environments on cultivar performance and have a key role for assessment of performance stability of the breeding materials (Moldovan *et al.,* 2000). G x E interaction may offer opportunity for selection and adaptation of that should positive interaction with specific location which helps in effective utilization of specifically adapted genotypes (Ceccarelli and Grando, 2007). The different response of genotypes across the testing environment is considered as hindrance in selecting and recommending of crops and cause yield fluctuation (Kang, 1998).

The G x E interaction makes it difficult to select the best performing as well as the most stable genotypes in plant improvement. Lack of high yielding varieties adapted to diverse agro-ecological conditions and limitation of information on G x EI of bread wheat genotypes in Ethiopia is the major reason of low productivity. Keeping this view in mind the study was cried out with the following objectives:

- To estimate Genotype x Environment interaction and stability of bread wheat genotypes in Ethiopia.
- To evaluate the performance of bread wheat genotypes across locations in Ethiopia.

MATERIALS AND METHODS

A total of 28 elite and 2 check (Hidasse and Danda'a) wheat genotypes were evaluated for grain yield and yield components performance across different locations of Ethiopia with in altitude range of 1750 –2780 m.a.s.l. The locations where the experiment conducted were Holetta, Kulumsa, Adet, Areka, Bekoji, Asassa, Segure and Debre Tabor each with distance of 36km, 168km, 445km, 300km, 272km, 285km,198km and 666 km from capital city of Ethiopia (Addis Ababa). The locations were different in altitude, mean annual rainfall, and soil types. These locations represent the major wheat growing agro-ecologies. Thirty Bread wheat Genotypes were planted at each location in Alpha lattice design (6x5) with three replications in the 2014 cropping season. There were 6 blocks in each replication and each block had 5 Genotypes. Each plot was consisted of 6 rows with spacing of 0.2m, 2.5m length and 1.2m width. Therefore, the area of each experimental plot was 3m^2 (1.2m x 2.5 m). Sowing dates ranged from 20 June to 3 July, 2014 depending on the onset of the growing season. The seeding rate was 150 kg/ha and the plots were equally fertilized with Urea and DAP fertilizers at the rate of 50 and 100 kg/ha, respectively. All agronomic managements were implemented equally as per the recommendation. Finally, total dry weight of grains harvested from all 4 central rows were taken as grain yield kilogram per plot and converted to ton ha^{-1} for analysis.

The combined data analysis was conducted to obtain estimates of environmental, genotype, genotype x environment interaction. 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. The GGE bi plot was built according to the formula given by Yan et al. (2000):

$$yij - \mu - {}^{\beta}j = \lambda 1 \xi 1 i\, \eta 1\, j + \lambda 2 \xi 2 i \eta 2\, j + \varepsilon i\, j$$

where yij is the mean for the i-th genotype in the j-th environment, μ is the overall mean, bj is the effect for the j-th environment, λ1 and λ2 are the singular values of the first and second principal components (PC1 and PC2), ξ1i and ξ2i are the eigenvectors for the i-th genotype forPC1 and PC2, η1j and η2j are the eigenvectors for the j-th environment for PC1 and PC2 and eij is the residual error term. The analysis was performed by using Genstat 13 (Payne 2009). The details of the experimental locations and materials are listed in Tables 1 and 2.

Table 1 Description of 8 locations used for evaluation of bread wheat genotypes

Code	Location	Geographical Position		Altitude (m.a.s.l)	Average rain fall (mm)	Temperature(^{o}C)		Soil Type
		Latitude	Longitude			min	max	
1	Holetta	09^{0}04'12''N	38^{0}29'46''E	2400	1044	6.05	22.4	Red
2	Bekoji	07^{0}31'22''N	39^{0}14'46''E	2780	1010	7.9	166	Nithosols
4	Kulumsa	08^{0}01'00''N	39^{0}09'32'' E	2200	820	10.5	22.6	Luvisol
5	Asassa	07^{0}06'12''N	39^{0}11'32'' E	2340	620	5.8	28.6	Clay loam
6	Adet	11^{0}15'41''N	37^{0}2917''E	2240	860	9.27	25.7	Nitosol
3	Sagure	7^0 00'00''N	38^{0}45'00''E					Nithosols
7	Debere Tabor	11°89´N	39°9´E	2630	1106.22	9.71	21.82	Luvisol
8	Areka			1751	633	15	30	Sandy loamy soil

Source: Kulumsa Agricultural Research Center

Table 2 Description of 30 bread wheat genotypes tested at eight locations in 2014/2015

Code	Name	Pedigree
1	Hidasse	
2	ETBW6861	WAXWING*2/HEILO
3	ETBW8506	AGUILAL/FLAG-3
4	ETBW8507	DURRA-4
5	ETBW7120	QAFZAH-23/SOMAMA-3
6	ETBW8508	REYNA-8
7	ETBW7213	CHAM-4/SHUHA'S'/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB
8	ETBW8509	REYNA-29
9	ETBW7038	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA….
10	ETBW8510	HIJLEEJ-1
11	ETBW7058	ROLF07//TAM200/TUI/6/WBLL1/4/HD2281/TRAP#1/3/KAUZ*2/TRAP..
12	ETBW8511	BOW #1/FENGKANG 15/3/HYS//DRC*2/7C
13	ETBW7147	CROC-1/AE.SQUARROSA(224)// OPATA/3/QAFZAH-21/4/SOMAMA-3
14	ETBW8512	BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1
15	ETBW7871	PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING
16	ETBW8513	MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING
17	ETBW6940	UTIQUE 96/FLAG-1
18	ETBW8514	TUKURU//BAV92/RAYON/3/WBLL1*2/BRAMBLING/4/WBLL1*2
19	ETBW7368	D. 56455
20	ETBW8515	BECARD/3/PASTOR//MUNIA/ALTAR 84
21	ETBW7364	ACSAD1115
22	ETBW8516	KACHU/KIRITATI
23	ETBW7194	VAN'S'/3/CNDR'S'/ANA//CNDR'S'/MUS'S'/4/TEVEE-5
24	ETBW8517	FRNCLN*2/TECUE #1
25	ETBW7101	KAMB2/PANDION
26	ETBW8518	SUP152/AKURI//SUP152
27	ETBW7872	QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
28	ETBW8519	ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE
29	ETBW6937	AGUILAL/FLAG-3
30	Danda'a	

Source: Kulumsa Agricultural Research Center
ETBW= Ethiopian bread wheat

RESULT AND DISCUSSIONS

COMBINED ANALYSIS FOR INDIVIDUAL ENVIRONMENTS

Mean grain yield performance of genotypes: The mean grain yield of the genotypes across eight locations were 4.53 ton ha^{-1} with grain yield range of 3.85 ton ha^{-1} for genotype ETBW8507 (4) to 5.54 ton ha^{-1} for genotype ETBW7038 (9) (Table 3). This shows that there was broad diversity in genetic yield potential between tested genotypes. The observed environmental mean grain yield ranged from 3.05 to 5.82 ton ha^{-1} from Holetta and Asassa respectively. This may be due to prolonged rain fall during harvesting time at Holetta. At Asassa all genotypes perform highest yield than the grand mean except ETBW8511(12) and ETBW7147(13) which were less grain yield than grand mean and at Holetta all genotypes grain yield were less than grand mean except ETBW6940 (17), ETBW7101(25) and ETBW7038 (9) genotypes.

The combined ANOVA showed that bread wheat grain yield was significantly affected by the environment, Genotype and G x E interaction because of significant variance at 1% level (Table 4). Environment explained 45.56% of the total (G + E + GEI) variation, while G x E interaction captured 25.37% of the total sum of squares and Genotype variation accounted about 2.59% of the total sum square. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing variation in the bread wheat grain yields. This was with agreement of Gauch and Zobel (1996, 1997); Kaya *et al.* (2006) in bread wheat; Farshadfar *et al.* (2012) in wheat-barley; Mohamed (2013) in bread wheat; Roostaei *et al.* (2014) in winter wheat.

Table 3 Mean grain yield of 30 bread wheat genotypes tested across 8 locations in 2014/2015.

Code	Geotype	Holetta	Bekoji	Segure	Kulumsa	Asassa	Adet	D Tabor	Areka	Mean
1	Hidasse	4.32	5.09	4.94	4.53	5.89	4.61	5.14	4.86	4.92
2	ETBW6861	3.12	6.43	5.41	4.90	5.99	4.95	4.66	3.64	4.88
3	ETBW8506	3.81	6.19	5.38	5.46	6.15	3.63	6.19	3.58	5.05
4	ETBW8507	1.92	3.10	4.53	3.44	5.06	4.81	4.12	3.81	3.85
5	ETBW7120	3.98	5.39	5.34	4.79	5.78	4.53	5.83	2.94	4.82
6	ETBW8508	1.85	4.18	4.38	3.42	5.05	4.35	6.08	2.65	3.99
7	ETBW7213	2.49	4.71	4.73	3.11	5.14	4.96	6.57	3.96	4.46
8	ETBW8509	3.05	4.71	4.69	2.46	5.78	4.40	6.98	4.54	4.58
9	ETBW7038	4.73	6.72	6.62	5.90	6.26	5.37	4.14	4.56	5.54
10	ETBW8510	2.73	2.94	4.57	3.20	5.65	4.97	6.62	4.7	4.42
11	ETBW7058	3.07	5.34	6.45	3.93	6.57	4.79	4.3	3.76	4.78
12	ETBW8511	3.78	4.83	4.08	1.88	2.94	4.31	6.19	3.63	3.95
13	ETBW7147	3.65	5.21	4.58	2.39	4.39	4.48	4.96	2.72	4.05
14	ETBW8512	1.94	3.64	4.80	2.65	5.37	5.58	5.15	2.78	3.99
15	ETBW7871	3.28	4.98	5.42	3.14	5.46	3.22	4.91	3.89	4.29
16	ETBW8513	3.69	5.37	5.95	3.92	6.66	4.88	4.15	3.39	4.75
17	ETBW6940	5.21	6.82	5.10	5.08	5.81	4.41	6.04	4.2	5.33
18	ETBW8514	1.98	3.09	4.88	4.05	6.10	5.36	6.38	3.57	4.42
19	TBW7368	2.15	4.25	4.74	4.00	6.23	5.05	5.37	3.8	4.45
20	ETBW8515	2.36	4.90	5.93	3.01	6.11	4.25	5.82	4.4	4.59
21	ETBW7364	3.24	4.61	4.27	3.62	6.10	4.60	4.96	3.68	4.38
22	TBW8516	2.07	5.58	5.70	3.73	5.69	3.30	5.02	3.93	4.38
23	ETBW7194	2.40	4.08	3.94	2.67	8.11	4.54	5.81	3.36	5.28
24	ETBW8517	2.20	4.45	5.28	4.10	6.56	4.63	4.72	2.72	4.33
25	ETBW7101	4.52	4.57	5.61	4.54	6.55	3.87	4.97	2.81	4.68
26	ETBW8518	2.67	4.11	5.83	3.51	6.26	4.80	3.4	2.98	4.19
27	ETBW7872	1.89	3.30	5.69	2.48	6.11	4.88	4.71	3.65	4.08
28	ETBW8519	3.43	6.06	5.76	4.10	5.63	5.85	5.81	3.89	5.06
29	ETBW6937	3.76	5.77	5.08	4.75	5.80	5.86	5.61	3.41	5.01
30	Danda'a	2.23	3.88	5.27	2.16	5.44	6.10	4.3	3.46	4.12
Mean		3.05	4.81	5.17	3.70	5.82	4.71	5.30	3.64	4.53

Table 2 Combined analysis of variance for grain yield (ton/ha.) and % explained of bread wheat tested in eight environments in 2014/15 cropping seasons.

Source.	df	SS	MS	F-value	P r > F	% Explained
Total	719	1090.813				
Environment	7	508.199	72.600	41.20	0.0001**	46.56%
Reps within environment	16	28.192	1.762			
Genotype	29	28.192	5.292	3.88	0 001**	2.59%
G x E interaction	203	276.733	1. 36	3 5.09	0.0001**	25.37%
Residual	464	124.221	0. 268			
Grand mean = 4.559	R-squared = 0.8861		C.V. = 11.35%			

*, ** Significant at 0.05 and 0.01 respectively

N.B. Abbrevation: G x E=genotype environment interaction; Reps=replication; df=degree freedom; SS= sums quare, MS=mean square

POLYGON VIEW OF THE GGE BIPLOT

The polygon view of the GGE-bi plot analysis helps one detect cross-over and non-crossover

Genotype x environment interaction and possible mega environments in multi location yield trials (Yan *et al*. 2007). Genotype ETBW71942 (3), ETBW7038 (9), ETBW8511 (1) and ETBW8512 (14) were vertex genotypes (Figure 1). They are best in the environment lying within their respective sector in the polygon view of the GGE-bi plot (Yan and Tinker 2006); thus these genotypes are considered specifically adapted. Genotypes close to the origin of axes have wider adaptation (Abay and Bjornstand 2009). The environments fall into three quadrants while the genotypes into four quadrants (Figure 1). Vertex Genotype ETBW7038 (9) performed well in location Adet (6), Debretabor (7) and Kulumsa (4) and was moderately adapted to location Areka (8) and Bekoji (2).

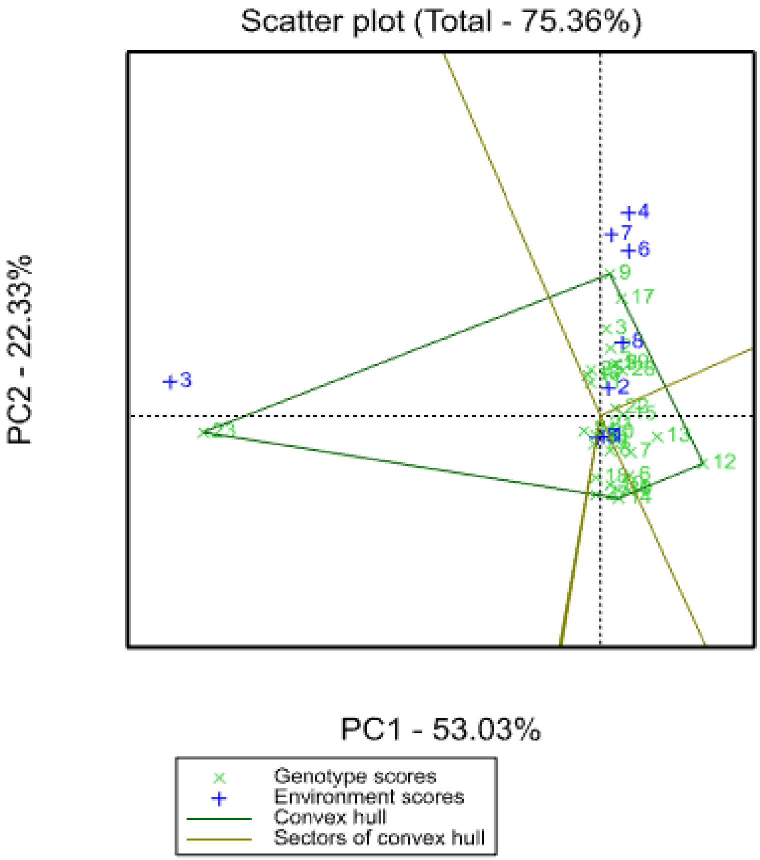

Figure 1 Polygon view of the GGE bi plot using symmetrical scaling of 30 bread wheat genotypes across eight environments. The genotypes are represented as 1, 2, …, 30 and the environments as 1, 2, …, 8 (See Tables 2 and 3).

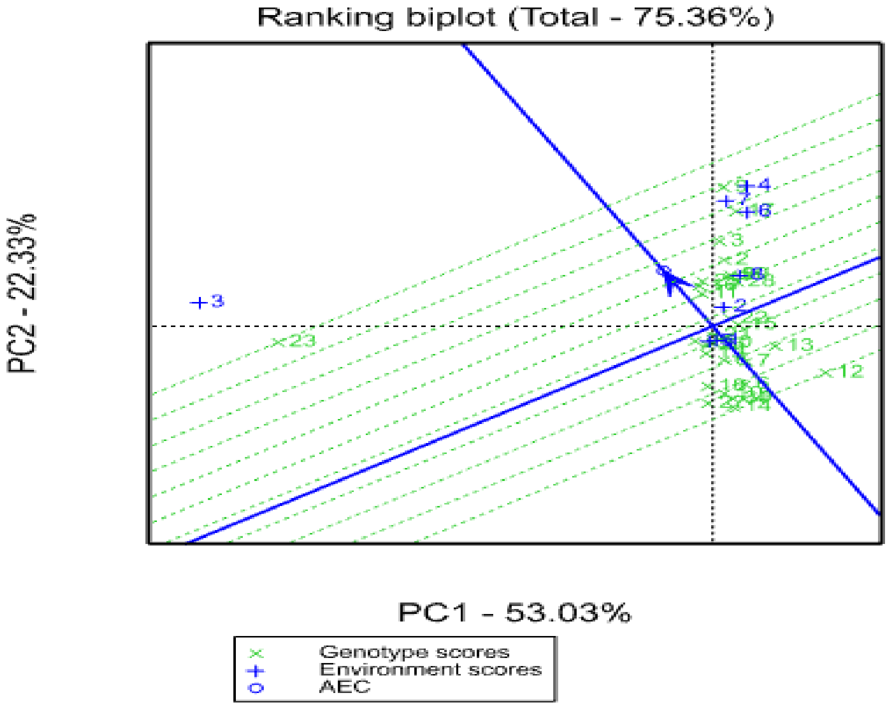

Figure 2 GGE bi plot with scaling focused on genotypes, for mean grain yield and stability of 30 bread wheat genotypes tested across eight environments. The genotypes are represented as 1, 2, …, 30 and the environments as 1, 2, …, 8 (See Tables 2 and 3).

MEAN GRAIN YIELD AND ITS STABILITY

The best genotype can be defined as the one with the highest yield and stability across environments. In the GGE bi plot, genotypes with high PC1 scores have high mean yield, and those with low PC2 scores have stable yield across environments (Yan and Tinker, 2006). The average environment abscissa is represented in Figure 2 by a single head arrow pointing towards higher yield across environments (Yan and Hunt, 2001). Genotypes ETBW8511 (12), ETBW7147 (13), ETBW8508 (6), ETBW7213 (7), ETBW8510 (10), ETBW8507 (4), ETBW8512 (14), ETBW7872 (27), ETBW7194 (23), ETBW8516 (22), ETBW8514 (18) and ETBW7368 (19) had mean grain yield lower than the grand mean. The genotypes that yielded higher than the grand mean were Genotype ETBW7038 (9), ETBW6940 (17), ETBW8506 (3), ETBW6861 (2), Hidasse (1), (29), ETBW8519 (28), ETBW7101 (25), ETBW8513 (16), ETBW7120 (5), ETBW7058 (11), ETBW7871 (15), ETBW8517 (24) and ETBW8518 (26) (Figure 2).

The most stable genotypes were genotype ETBW8508 (6), ETBW7213 (7), ETBW7364 (21), ETBW8516 (22), ETBW8509 (8), ETBW8515 (20), ETBW7871 (15), ETBW7058 (11), ETBW8513 (16) and ETBW7101 (25) because they showed the shortest distance from the average environment abscissa. Genotype ETBW6940 (17), ETBW7872 (27), ETBW8514 (18), ETBW8512 (14), ETBW8507 (4), ETBW7038 (9), ETBW8510 (10), Danda'a (30) and ETBW8511 (12) had a large contribution to the genotype x environment interaction; they were unstable across environments, having the longest distance from the average environment abscissa. Considering simultaneously yield and stability, Genotype ETBW7871 (15), ETBW7058 (11), ETBW8513 (16) and ETBW7101 (25) showed the best performances (Figure 2), suggesting their adaptation to a wide range of environments (Annicchiarico 1997). Also in studies by Muez et al. (2015); Mohamed et al. (2013) and Farshadfar et al. (2012) the highest-yielding wheat genotypes were stable, a desirable situation for plant breeders.

EVALUATION OF GENOTYPES BASED ON THE IDEAL GENOTYPE

An ideal genotype has the highest mean grain yield and is stable across environments (Farshadfar et al. 2012). The ideal genotype is located in the first concentric circle in the Bi-plot. Desirable genotypes are those located close to the ideal genotype. Thus, starting from the middle concentric circle pointed with arrow concentric circles was drawn to help visualize the distance between genotypes and the ideal genotype (Yan and Tinker 2006). 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). Placed near to the first concentric circle, genotypes ETBW7038 (9), ETBW6940 (17) and ETBW8506 (3) can be thus used as benchmarks for evaluation of bread wheat genotypes. Genotype ETBW6861 (2), ETBW8519 (28), ETBW6937 (29), ETBW7120 (5), Hidasse (1), ETBW7101 (25), ETBW8513 (16) and ETBW7058 (11) were located near the ideal genotype, thus being desirable genotypes. Undesirable genotypes were those distant from the first concentric circle, namely, Genotype ETBW8511 (12), ETBW7147 (13), ETBW8512 (14), ETBW8507 (4), ETBW8510 (10), ETBW8508 (6), ETBW7194 (23), Danda'a (30), ETBW7872 (27), ETBW8514 (18), ETBW7213 (7), ETBW7364 (21), ETBW8516 (22), ETBW7038 (9), and ETBW8515 (20) (Figure 3). Our results confirm those by Sharma et al. (2010), who found outstanding genotypes near to the ideal genotype in wheat for five consecutive years, and those by Mulugeta et al. (2011), who found an ideal genotype of potato in the first concentric circle.

EVALUATION OF ENVIRONMENTS BASED ON THE IDEAL ENVIRONMENT

The ideal environment is representative and has the highest discriminating power (Yan and Tinker 2006). Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused bi plot, and desirable environments are close to the ideal environment. Nearest to the first concentric circle, Environment Kulumsa (4), Debre Tabor (7) and Adet (6) were close to the ideal environment (Figure 4); therefore, they should be regarded as the most suitable to select widely adapted genotypes.

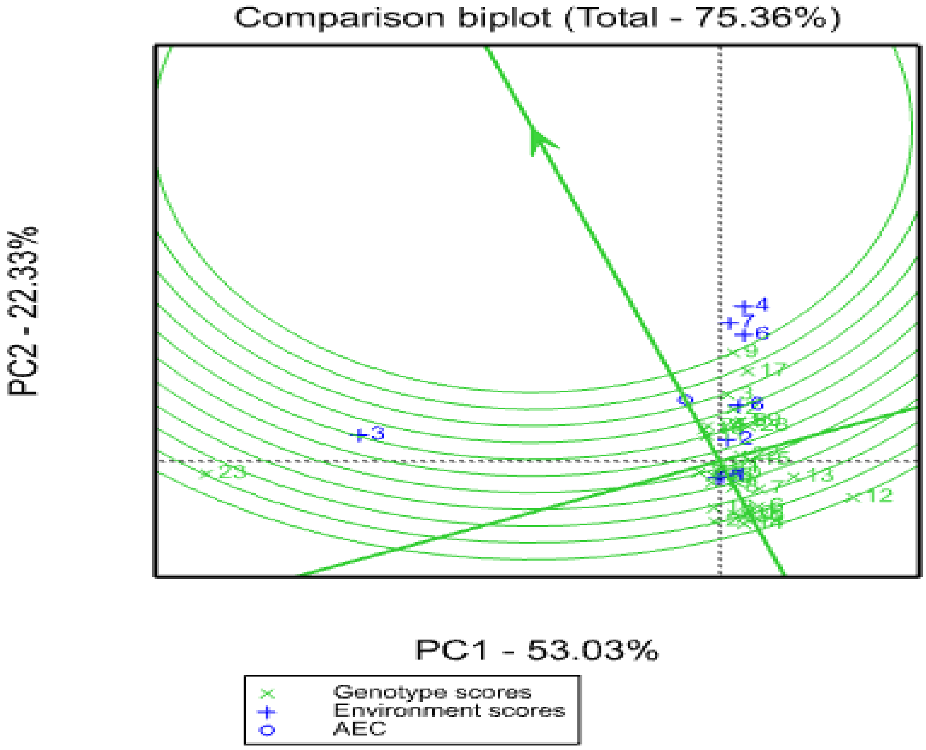

Figure 3 GGE bi plot with scaling focused on genotypes, for the evaluation based on the ideal genotype of 30 bread wheat genotypes across eight environments. The genotypes are represented as 1, 2, …, 30 and the environments as 1, 2, …, 8 (See Tables 2 and 3).

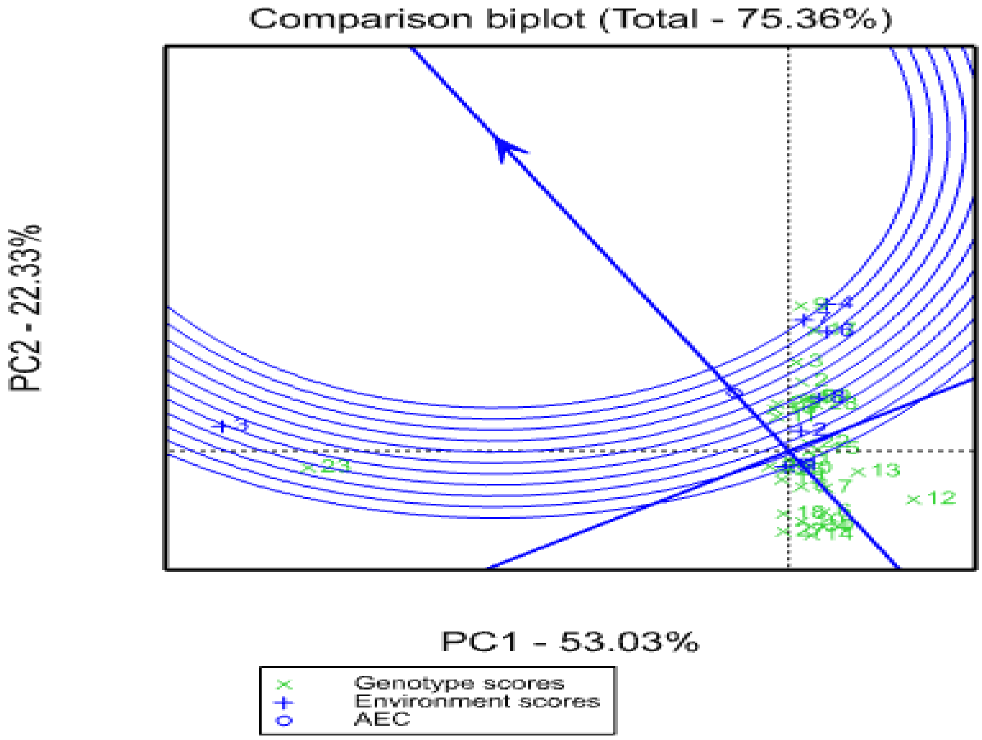

Figure 4 GGE bi plot with scaling focused on environments, for the evaluation based on the ideal environment of 30 bread wheat genotypes across eight environments. The genotypes are represented as 1, 2, …, 30 and the environments as 1, 2, …, 8 (See Tables 2 and 3).

RELATIONSHIP AMONG TEST ENVIRONMENTS

Further information about the discriminating power of environments, together with a representation of their mutual relationships, can be obtained by the environment-vector view of the GGE-bi plot. In this case, a long environmental vector reflects a high capacity to discriminate the genotypes. Furthermore, the cosine of an angle between vectors of two environments approximates the correlation between them: a wide obtuse angle indicates a strong negative correlation; an acute angle indicates a positive correlation while a close-to- 90° angle indicates lack of correlation (Yan and Tinker 2006). With the longest vectors from the origin, environments Segure (3) and Kulumsa (4) were the most discriminating. Environment Adet (6), Debere Tabor (7), Areka (8) were moderately discriminating while Environment Holetta (1) and Asassa (5) were least discriminating. Considering the angles between environmental vectors, yield results in Environment Kulumsa(4), Debre Tabor (7), Adet (6), Bekoji (2) and Areka (8) were strongly correlated, similarly to those obtained in Environment Holetta (1) and Asassa (5) were strongly correlated(Figure 5).

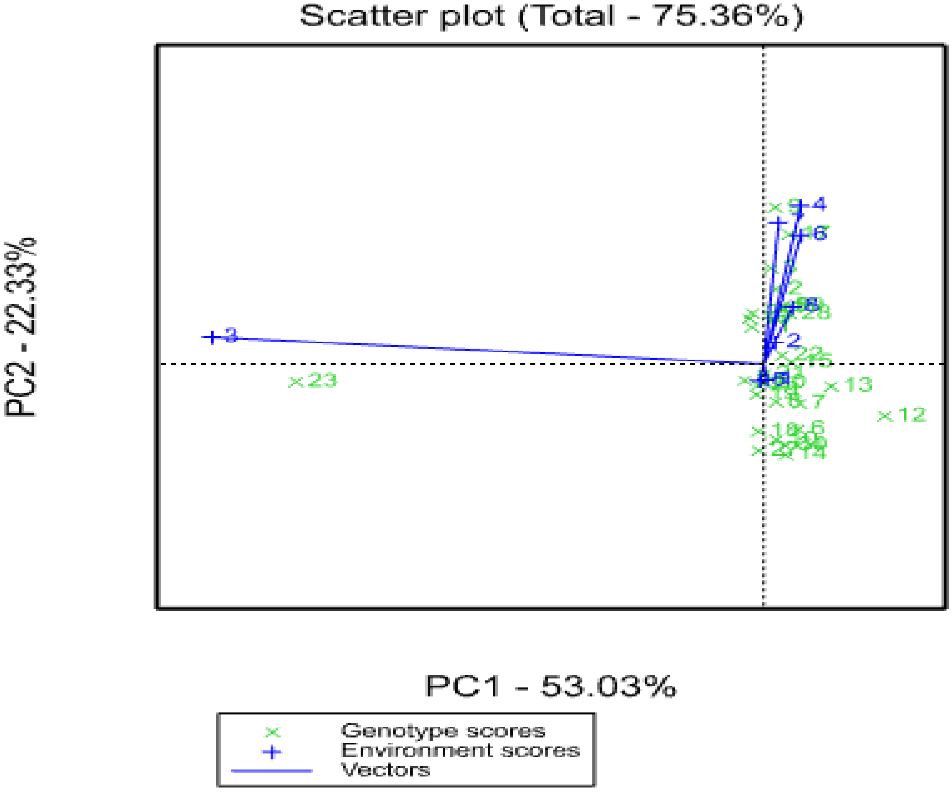

Figure 5 GGE bi plot for the evaluation of the relationships among the eight environments.
The genotypes are represented as 1, 2, …, 30 and the environments as 1, 2, …, 8 (See Tables 2 and 3).

CONCLUSIONS

The genotype and environment main effects and genotype x environment interaction effect were significant for bread wheat genotypes studied in Ethiopia. The environment contributed most to the variability in grain yield. Genotype ETBW71942 (3), ETBW7038 (9), ETBW8511 (1) and ETBW8512 (14) were vertex genotypes; thus these genotypes are considered specifically adapted. Considering simultaneously yield and stability, Genotype ETBW7871 (15), ETBW7058 (11), ETBW8513 (16) and ETBW7101 (25) showed the best performances, suggesting their adaptation to a wide range of environments. With the longest vectors from the origin, environment Segure (3) and Kulumsa (4) were the most discriminating. Environment Adet (6), Debere Tabor (7), Areka (8) were moderately discriminating while Environment Holetta (1) and Asassa (5) were least discriminating.

ACKNOWLEDGEMENTS

We would like to acknowledge Kulumsa Agricultural Research Centre (KARC) wheat breeding staff for all the assistance we obtained from them and Meko District Land and environmental protection office for financial support.

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