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GGE Biplot Analysis of Genotype by Environment Interaction and Grain Yield Stability of Bread Wheat Genotypes in South East Ethiopia

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Abstract: The significant G x E interaction has been a challenge to bread wheat breeders as this interaction limits accuracy of yield estimate, identification of stable genotypes and further complicate selection of genotypes. The objective of the present study was to study their adaptability and stability in six diverse environments of South Eastern Ethiopia. Twenty bread wheat genotypes and two checks were evaluated at six test locations of South Eastern Ethiopia during 2012/2013 growing season in a randomized complete block design (RCBD) with four replications. Genotype; environment and genotype by environment interaction had significant effects on grain yield. The environment accounted for 51.97%, while the genotype by environment interaction for 20.68% of the variation in grain yields. Based on the polygon view of the GGE biplot, two mega environments were detected with different winning genotypes G8 (ETBW6734), G10 (ETBW6736), G17 (ETBW6743), G13 (ETBW6739) and G16 (ETBW6742), which are therefore to be regarded as specifically adapted. Considering simultaneously mean yield and stability, the best genotypes were G2 (ETBW6728), G6 (ETBW6732), G9 (ETBW6735) and G11 (ETBW6737), which therefore can be regarded as adapted to a wide range of environments.

Key words: GGE · Genotype · Environment · Genotype by environment interaction

INTRODUCTION

Wheat is one of the major cereal crops in the Ethiopian highlands (between 6° and 16° N and 35° and 42° E, at altitudes ranging from 1500 to 3200 m a.s.l.; [1] particularly in the southeastern, central and northwestern regions of the country. The most common wheat species cultivated there are bread wheat (*Triticum aestivum* L.) and durum wheat (*Triticum durum* Desf.) [2].

Throughout 18 years, wheat production area in Ethiopia showed a 121% increase, increasing from 0.769 million ha in 1995 [3] to 1.7 million ha in 2013 [4]. At the same time, grain yield showed only a modest increase of 18%. A possible reason is poor wheat productivity in Ethiopia, with an average yield of 2.3 t ha^{-1}, that is 24% and 48% below the African and world averages, respectively.

In Ethiopia, wheat ranks 4th after teff, maize and sorghum in cropped area; 4th after maize, teff and sorghum in total grain production; and 2nd after maize in yield, accounting for more than 15% of total cereal production [4]. However, the national mean wheat yield (2.3 t ha^{-1}) is far below the average yield obtained in experimental plots in the country (>4 t ha^{-1}). This gap (over 2.7 t ha^{-1}), i.e., the difference between research plot yield and farmer's field yield, could be due to genotype by environment interaction, which makes most cultivars achieve high yields only in good environmental conditions. Hence, the genotype-by environment interaction is probably the main cause of why traditional plant breeding failed to support resource-poor farmers, especially in marginal and fragile environments [5].

To improve yielding in Ethiopia, improved varieties should be released. They should be, however, tested in various agro-ecological environments. This study aimed

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thus to assess the adaptability and yield stability of nationally released and inbreeding line of bread wheat varieties under the environmental conditions of south eastern Ethiopia. Multi-environment yield trails are essential in estimation of genotype by environment interaction (GEI) and identification of superior genotypes in the final selection cycles [6, 7].

MATERIALS AND METHODS

The experiments were conducted during the main cropping season, in six locations in 2012 and 2013. Twenty two bread wheat genotypes (Table 1) were studied in experiments arranged as a randomized complete block design (RCBD) with four replications each. Depending on weather, the genotypes were planted from mid-June to the first week of July and harvested 120-145 days after planting (Table 2). Plots were 2.5 m long and had six rows, with spacing of 0.2 m between rows and 0.5 m between plots. Distance between blocks was 1.5 m. A seed rate was 150 kg ha^{-1}. The fertilizers were applied @ 41 kg N ha^{-1} and 46 kg P_2O_5 ha^{-1} at planting and at tillering time. Grain yield was recorded from four central rows in each plot.

Different approaches are used to quantify the genotype by environment interaction and recommend the best genotypes for target environments. Examples include joint regression [8], stability variance index [9], coefficient of variation [10], additive main effect and multiplicative interaction (AMMI) analysis [11] and GGE biplot [12]. The last method is based on data visualization and proved to be helpful in: (i) detection of the genotype by environment interaction pattern, (ii) classification of mega environments, (iii) simultaneous selection of genotypes based on stability and mean yield and (iv) characterization of testing environments based on their discriminating ability and representativeness [13].

Table 1: Bread wheat genotypes evaluated in the six environments

Entry	Genotype	Pedigree
1	Danda'a	Breeder Seed (Check)
2	ETBW 6728	ROELFS F2007
3	ETBW 6729	TRCH/SRTU/5/KAUZ//ALTAR84/AOS/3/MIAN/KAZ/4/HUITES
4	ETBW 6730	WAXWING*2/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
5	ETBW 6731	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/PARUS/6/FRET2*2/KUKUNA
6	ETBW 6732	PBW343*2/KUKUNA*2//YANAC
7	ETBW 6733	FRET2/KUKUNA//FRET2/3/PARUS/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
8	ETBW 6734	ROLF07*2/KIRITATI
9	ETBW 6735	ROLF07/YANAC//TACUPETO F2001/BRAMBLING
10	ETBW 6736	WBLL1/KUKUNA//TACUPETO F2001/5/WAXWING/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ
11	ETBW 6737	WAXWING/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TRAP#1
12	ETBW 6738	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ*2/6/PVN//CAR422/ANA/5/BOW/CROW//BUC/PVN/3/YR/4/TAP#1
13	ETBW 6739	SERI.1B//KAUZ/HEVO/3/AMAD*2/4/KIRITATI
14	ETBW 6740	PBW343*2/KHVAKI//PARUS/3/PBW343/PASTOR
15	ETBW 6741	FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ/5/PFAU/WEAVER//BRAMBLING
16	ETBW 6742	WBLL1//UP2338*2/VIVITSI
17	ETBW 6743	WAXWING/WHEAR//WAXWING/KIRITATI
18	ETBW 6744	FRET2/KUKUNA//FRET2/3/YANAC/4/FRET2/KIRITATI
19	ETBW 6745	TRCH//PRINIA/PASTOR
20	ETBW 6746	BAV92//IRENA/KAUZ/3/HUITES/4/DOLL
21	ETBW 6747	PBW343*2/KUKUNA//PARUS/3/PBW343*2/KUKUNA
22	Digelu	Breeder Seed (Check)

Source: KARC, Kulumsa Agricultural Research Center.

Table 2: Environments used in the study and their main characteristics.

Code	Locations	Annual Rainfall (mm)	Altitude (m.a.s.l.)	Latitude	Longitude	Temperature (°C)	Soil type
E1	Holeta	872	2400	09 04 N□	38 29 E□	10.1-36.4	Red
E2	Sinana	834	2600	07°4□60□□N	40°12 □ 0□□E	10-22	clay
E3	Areka	633	1751	07° 4□ 0.0□□N	37^0 42° 0.0□□E	15-30	Sandyloam
E4	Kulumsa	832	2200	08° 01□ 10□□N	39^0 09□ 11□□E	10.5-22.8	Luvisol
E5	Asassa	620	2340	07 07 N□	39 11 56 E□	5.8-23.6	Clay loam
E6	Bokoji	1020	2809	08° 31□ 60□□N	39^0 15□ 0□□E	7.9-18.6	Nithosols

We were thus using this method to analyze the data. First, the combined analysis of variance (ANOVA) was performed, with all effects fixed. The GGE biplot was built according to the following formula given by [13]:

$$Yij-\mu-\beta j=\lambda_1\xi i_1\eta_1 j+\lambda_2\xi i_2\eta_2 j+\varepsilon ij$$

where yij is the mean for the *i*-th genotype in the *j*-th environment, μ is the overall mean, b*j* 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), ξ1*i* and ξ2*i* are the eigenvectors for the *i*-th genotype for PC1 and PC2, η1*j* and η2*j* are the eigenvectors for the *j*-th environment for PC1 and PC2 and e*ij* is the residual error term. The analysis was performed by using Genstat 13 [14].

RESULTS AND DISCUSSION

Combined Analysis for Individual Environments: The combined analysis of variance revealed significant differences (P<0.01) for testing locations and genotype for grain yield (Table 3). This indicated that there was a large difference between the testing location causing different genotypes to perform differently across the testing environments. The variation of the testing environment might be attributed due to the un even distribution of rainfall across the testing location in cropping season. The result was in agreement with findings of [15] who found bread wheat grain yield was significantly affected by environment. The bread wheat genotypes also had a wider genetic variability for the entire traits. The genotype x environment interaction was significant (P<0.01) for grain yield in tested locations (Table 3). This indicated that due to the presence of the higher magnitude of genotype by environment interaction cause unstable performance of genotype across the different testing locations and complicates selection and recommendation of genotype in a specified environment [16].

Polygon View of the GGE Biplot: The polygon view of the GGE-biplot analysis helps one detect cross-over and non-crossover genotype by environment interaction and possible mega environments in multilocation yield trials [17]. G8 (ETBW6734), G10 (ETBW6736), G17 (ETBW6743), G13 (ETBW6739) and G16 (ETBW6742) were vertex genotypes (Fig. 1). They are best in the environment lying within their respective sector in the polygon view of the GGE-biplot [18]. Thus these genotypes are considered specifically adapted. Genotypes close to the origin of axes have wider adaptation [19].

Table 3: Yield response of 22 genotypes across 6 environments

Genotype	Are	Asa	Bok	Hol	Kul	Sin
Danda'a	28.75	42.49	59.42	47.62	49.56	38.44
ETBW6728	32.75	45.6	58.15	54.4	46.66	40.09
ETBW6729	32.25	41.3	53.77	42.67	44.47	37.04
ETBW6730	33.63	45.01	55.92	40.86	48.12	41.37
ETBW6731	40.25	46.07	55.54	33.47	43.19	37.93
ETBW6732	34.24	38.97	54.56	48.11	43.18	37.98
ETBW6733	32.51	45.64	52.64	52.56	44.65	37.56
ETBW6734	34.24	49.04	56.33	53.53	45.47	38.96
ETBW6735	37.89	47.44	55.97	33.57	43.89	38.52
ETBW6736	27.68	45.16	54.46	48.04	48.02	38.28
ETBW6737	34.77	40.05	49.41	52.58	44.42	37.32
ETBW6738	33.63	42.65	56.32	42.62	48.34	40.43
ETBW6739	40.25	39.64	53.26	33.51	47.66	40.01
ETBW6740	33.79	45.42	58.13	36.16	44.35	41.98
ETBW6741	34.82	49.15	51.24	40.55	45.84	37.48
ETBW6742	46.04	49.17	56.05	36.31	47.75	37.01
ETBW6743	33.02	38.21	49.24	42.09	49.86	45.57
ETBW6744	44.63	45.92	55.53	37.51	48.46	42.64
ETBW6745	35.59	46.07	56.05	39.79	45.27	38.95
ETBW6746	45.44	45.81	55.38	44.41	43.81	40.63
ETBW6747	32.51	49.15	48.37	42.81	43.14	36.84
Digelu	32.25	47.62	54.08	43.44	52.17	38.39
Grand mean	35.5	44.8	54.54	43.03	46.29	39.25
LSD	3.78	4.34	4.30	4.49	4.25	1.77
CV	10.6	12	11.8	12.2	11.8	2.9

Enviroments are abbreviated as Are=Areka, Asa=Asassa, Bok=Bokoji, Hol=Holeta, Kul=Kulumsa and Sin=Sinana

Table 4: Combined analysis of variance for 22 bread wheat genotypes across six environments

Source	Df	SS	MS	%SS
Genotypes	21	897	42.7**	8.97
Environments	5	18718	3743.7**	51.97
GxE Interactions	105	7448	70.9**	20.68
Block within Environment	18	419	23.3**	
Error	378	8535	22.6	

** Significant at p<0.05 and 0.01 respectively

The environments fall into three quadrants while the genotypes into four quadrants (Fig. 1). G16 (ETBW6742) performed well in E3 (Areka) and E5 (Asassa) and was moderately adapted to E6 (Bokoji). G21 (ETBW6747) performed well in environments with relatively low rainfall, but also in environments with higher rainfall and more uniform distribution. Vertex genotype G13 (ETBW6739) performed well in E2 (Sinana) and E1 (Holeta), thus being adapted to high rainfall. Genotype G20 (ETBW6746) was best adapted to E5 (Asassa). Two vertex genotypes, G8 (ETBW6734) and G10 (ETBW6736), had the highest yield in none of the environments (Fig. 1).

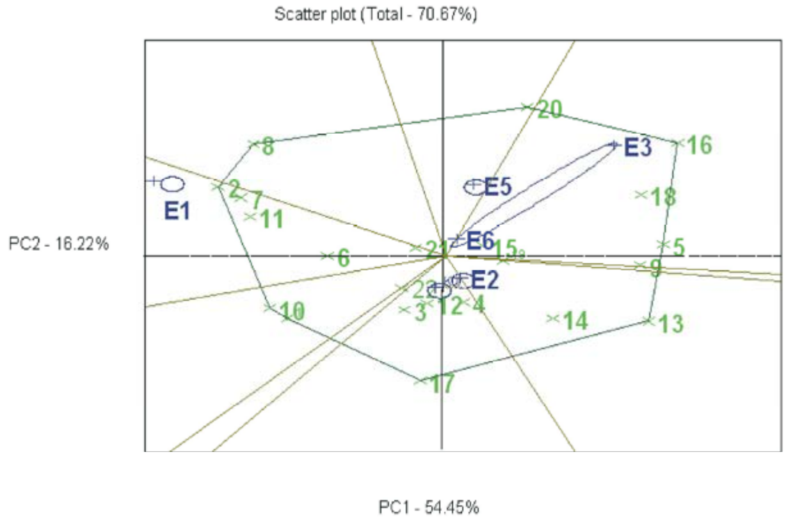

Fig. 1: Polygon view of the GGE biplot using symmetrical scaling of 22 bread wheat genotypes across six environments. The genotypes are abbreviated as G1, G2… G22 and the environments as E1, E2… E6 (Tables 2 and 3)

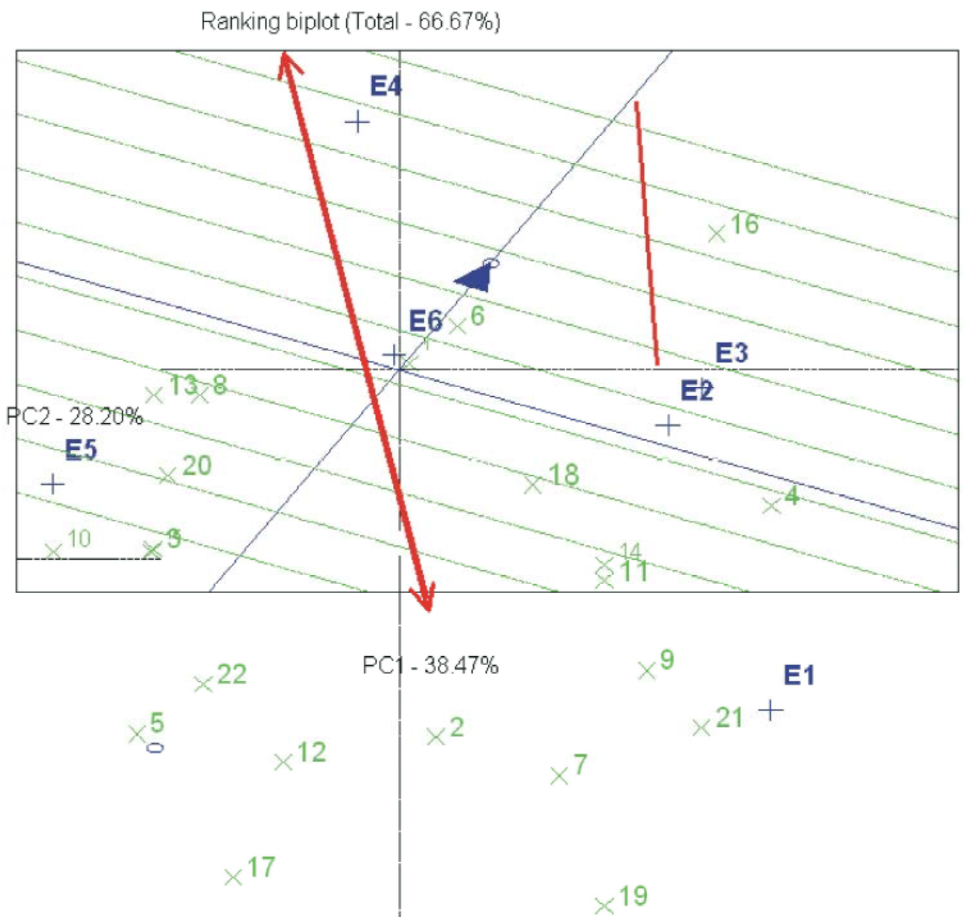

Fig. 2: GGE biplot with scaling focused on genotypes, for mean grain yield and stability of 22 bread wheat genotypes tested across six environments. The genotypes are abbreviated as G1, G2…, G22 and environments as E1, E2…E6 (Tables 2 and 3)

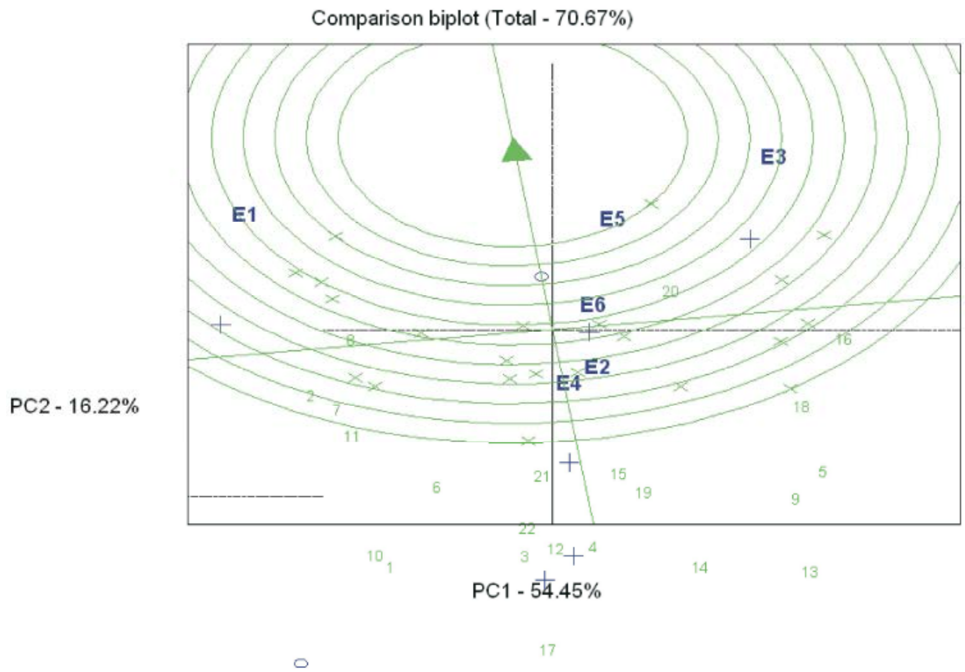

Fig. 3: GGE biplot with scaling focused on genotypes, for the evaluation based on the ideal genotype of 22 bread wheat genotypes across seven environments. The genotypes are abbreviated as G1, G2… G22 and environments as E1, E2… E6 (see Tables 2 and 3). Figure 4

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 biplot, genotypes with high PC1 scores have high mean yield and those with low PC2 scores have stable yield across environments [18]. The average environment abscissa is represented in Fig. 2 by a single head arrow pointing towards higher yield across environments. The average environment ordinate (AOE) is represented as a double-headed arrow and points towards lower stability in both directions [20]. Genotypes G3 (ETBW6729), G5 (ETBW6731), G10 (ETBW6736), G12 (ETBW6738), G17 (ETBW6743) and G22 (Digelu) had mean grain yield lower than the grand mean. The genotypes that yielded higher than the grand mean were G1 (Danda'a), G2 (ETBW6728), G7 (ETBW6733), G11 (ETBW6737), G14 (ETBW6740), G18 (ETBW6744), G19 (ETBW6745) and G21 (ETBW6747) (Fig. 2).

The most stable genotypes were G2 (ETBW6728), G3 (ETBW6729), G10 (ETBW6736) G11 (ETBW6737), G14 (ETBW6740) and G18 (ETBW6744), because they showed the shortest distance from the average environment abscissa. G5 (ETBW31), G12 (ETBW6738), G16 (ETBW6742), G17 (ETBW6743) and G22 (Digelu) had a large contribution to the genotype-by environment interaction; they were unstable across environments, having the longest distance from the average environment abscissa.

Considering simultaneously yield and stability, G2 (ETBW6728), G6 (ETBW6732), G9 (ETBW6735), G11 (ETBW6737), G14 (ETBW6740) and G18 (ETBW6744) showed the best performances (Fig. 2), suggesting their adaptation to a wide range of environments [21]. Also in studies by [15, 22] 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 [22]. The ideal genotype is located in the first concentric circle in the biplot. 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 [18].

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 [23]. Placed near to the first concentric circle,

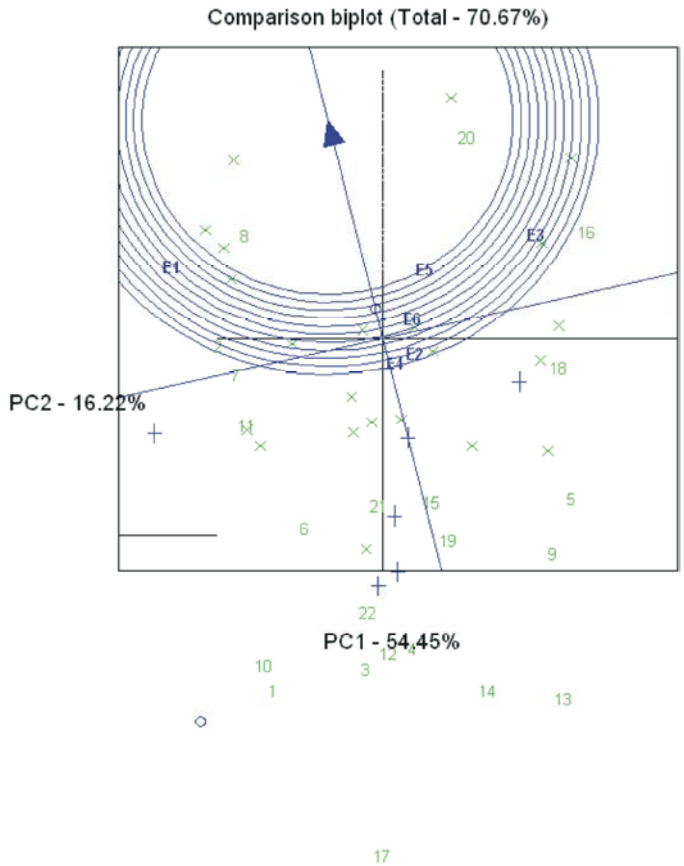

Fig. 4: GGE biplot with scaling focused on environments, for the evaluation based on the ideal environment of 22 bread wheat genotypes across six environments. Environments are abbreviated as E1, E2... E6 (Table 2)

genotypes G2 (ETBW6728), G11 (ETBW6737), G14 (ETBW6740) and G18 (ETBW6744) can be thus used as benchmarks for evaluation of bread wheat genotypes. G12 (ETBW6738), G14 (ETBW6740), G15 (ETBW6741) and G21 (ETBW6747) were located near the ideal genotype, thus being desirable genotypes. Undesirable genotypes were those distant from the first concentric circle, namely, G2 (ETBW6728), G8 (ETBW6734), G10 (ETBW6736) and G17 (ETBW6743) (Fig. 3). Our results confirm those by [24], who found outstanding genotypes near to the ideal genotype in wheat for five consecutive years and those by [25] 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 [18]. Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot and desirable environments are close to the ideal environment. Nearest to the first concentric circle, environment E6 (Bokoji) was close to the ideal environment (Fig. 4); therefore, it should be regarded as the most suitable to select widely adapted genotypes.

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-biplot. 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 [18].

With the longest vectors from the origin, environments E3 (Areka) and E1 (Holeta) were the most discriminating. E5 (Asassa) and E6 (Bokoji) were moderately discriminating while E4 (Kulumsa) was least discriminating. Considering the angles between environmental vectors, yield results in E5 (Asassa), E6 (Bokoji), E2 (Sinana) and E4 (Kulumsa) were strongly correlated.

CONCLUSIONS

The GGE biplot analysis is an important tool for selecting high yielding; stable genotype. The genotype and environment main effects and genotype by environment interaction effect were significant for bread wheat genotypes studied in South East Ethiopia. The environment contributed most to the variability in grain yield. Genotypes G2 (ETBW6728), G3 (ETBW6729), G10 (ETBW6736) G11 (ETBW6737), G14 (ETBW6740) and G18 (ETBW6744) were close to the ideal genotype and can thus be used as benchmarks for the evaluation of bread wheat genotypes in the South East Ethiopia. Considering simultaneously mean yield and stability, G2 (ETBW6728), G6 (ETBW6732), G9 (ETBW6735) and G11 (ETBW6737), were the best genotypes.

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