



Research Article

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

Berhanu Sime and Shimellis Tesfaye

*Kulumsa Agricultural Research Center, Assela, P.O. Box 489, Ethiopia

*Corresponding author: birhanume2006@gmail.com

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ABSTRACT

GGE biplot is an effective method based on principal component analysis to fully explore mega-environments trials data. The study conducted was to identify the best performing, high yielding stable advanced bread wheat genotype for selection environments, the identification of mega-environments and analysis of the ideal genotype and environment by GGE biplot method. Twenty-five bread wheat genotypes were evaluated using Alpha Lattice design with three replications at six locations in Oromia, Ethiopia. The results of combined analysis of variance for grain yield of 25 bread wheat genotypes indicated that genotype, environment and GEI were highly significant ($P < 0.01$). The factors explained showed bread wheat genotypes grain yield was affected by environment (82.44%), genotype (6.23%) and GEI (11.33%). GGE biplot was constructed by plotting the first two principal components, PC1 and PC2, derived from subjecting environment centred yield data to singular value decomposition. PC1 and PC2 accounted for 86.7% (68.84% and 17.86%) of the G + GE variation for grain yield of the genotypes evaluated at six environments. As a result, a genotype located closer to the “ideal genotype” is more desirable than the others located farther away. Hence, the GGE biplot genotype ETBW9089 as an ideal genotype, while genotypes BW174464, ETBW9102, ETBW9304 and BW174461 were desirable genotypes as they were closer to the ideal genotype. Conversely, genotypes ETBW9313, ETBW9284, BW174465 and variety WANE were the least desirable genotype as indicated by the GGE biplot. Based on yield performance advanced lines ETBW9089, ETBW9102 and BW174464 are recommended to be included in variety verification trials for further release.

Key words: Adapted, Discriminating, GGE, Grain yield, Stable.

INTRODUCTION

Bread wheat is a self-pollinating annual plant in the grass family, Gramineae. It is extensively grown as staple food source in the world (Mollasadeghi and Shahryari, 2011). Wheat is one of the most important cereal crops cultivated in Ethiopia. It ranks 4th after maize (*Zea mays* L.), tef (*Eragrostis tef*) and sorghum (*Sorghum bicolor* L.) in area coverage, and 2nd in productivity (tons/ha) next to maize (CSA, 2019). It is grown annually on 1.75 million hectares of land in Ethiopia with a total grain production of 4.84 million tons and average productivity of 2.77 tons/ha, which makes the country the second largest wheat producers in sub-Saharan Africa (CSA, 2019).

Wheat has been selected as one of the target crops in the strategic goal of attaining national food self-sufficiency, income generation, poverty alleviation and achieving socio-economic growth of Ethiopia (Mulatu,

2015). It is one of the most important small cereal crops in Ethiopia widely cultivated in wide range of altitudes. Most wheat producing areas in Ethiopia are between 6^o and 16^o N latitude and 35^o and 42^o E longitude at altitudes ranging from 1500 to 3000 m.a.s.l. But with proper irrigation, wheat has been grown successfully in the Awash and Wabe-Shebelle River Basins which lie below 1000 m.a.s.l. The most suitable agro-ecological zones, however, fall between 1900 to 2700 meters above sea level (Bekele et al., 2000). Wheat in Ethiopia is produced mainly under rain fed conditions with rainfall amounts ranging from 600 mm to 2000 mm. Grain yield is a function of genotype, environment and genotype x environment interaction (GEI) as expressed by different authors (Trethowan and Crossa, 2007; Sial et al., 2007; Hamam et al., 2009). An understanding of the effects of environment, genotype and GEI is important at all stages of crop improvement programs as they have crucial effects on selection and

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cultivar adaptation trials. GEI studies thus provide a basis for selection of genotypes that are suitable for wider or specific cultivation.

The measured yield of each cultivar in each test environment is a function of genotype main effect (G), environment main effect (E) and genotype x environment (G x E) interaction (Yan and Kang, 2003). Though, environment mostly accounts for the major portion of the total yield variation, only genotype and genotype x environment interaction are relevant to cultivar evaluation and mega environment classification (Yan et al., 2000; Yan, 2002; Yan and Rajcan 2002; Rao et al., 2005 and Kaya et al., 2006). Additive Main-effect and Multiplicative Interaction (AMMI) and Genotype main effect and Genotype x Environment interaction (GGE) models are singular value decomposition (SVD) based statistical methods and they have been applied to yield trial studies for visualizing the data. The methods help in understanding complex genotype x environment interactions (GEI) and determining which genotype has been in which environments and also helping in grouping environments with the same winner (or similar winners) into mega-environments. Evaluating genotypes over diverse environments is a universal practice to ensure the stability of performance of genotypes. It provides breeder with better strategy for selecting high yielding and consistently performing varieties over diverse environmental conditions. According to Asnake et al. (2013), GEI in multi-environment trials shows differential responses of wheat genotypes across ranges of environments. 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 advanced bread wheat genotype for selection environments, the identification of mega-environments and analysis of the ideal genotype and environment by GGE biplot.

MATERIALS AND METHODS

The experiment was conducted during the 2019/20 main cropping season across six locations. The locations were Kulumsa, Bekoji, Assasa, Arsi-Robe, Debre-Zeit and Holeta. The description of the testing locations is presented in Table 1. These locations represent different agro-ecologies of the major wheat growing areas in Oromia, Ethiopia.

Experimental Materials

Totally 25 bread wheat genotypes, (23 selected from national variety trials and 2 nationally released varieties), were included in this study as shown in Table 2 below. The two released check bread wheat varieties were selected based on their per se performance and disease resistance and the remaining are considered advanced materials. They were obtained from Kulumsa Agricultural Research Centre.

Experimental Design and Field Management

The trials were conducted at six locations using 5 x 5 Alpha Lattice design replicated three times during the 2019/20 cropping season. Each treatment was planted on six rows of 2.5m length with 20cm distance between any

two rows. The sowing dates were at the onset of the main rainy season as usual. Seed rate of 150 kg/ha was used. Fertilizer was applied at the rate of 100 kg/ha of NPS and 100 kg/ha Urea at each location. Recommended rate of NPS was applied at planting, while urea was applied in two splits, half at planting and the remaining half at tillering stage. In addition, other relevant field trial management practices were carried out across all locations as per the recommendations.

Data collection

Data was collected on the following traits: days to heading, days to maturity, grain filling period, number of grains per spike, number of spikelets per spike, plant height, number of tillers per plant, spike length, Number of spikelets per spike, thousand kernel weights and grain yield per plot.

Statistical Analysis

The grain yield data for twenty-five bread wheat in six environments were used to combine analysis of variance (ANOVA) to determine the effects of environment, genotype and GEI. ANOVA was used to partition genotype deviations from the grand mean, environment deviations from the grand mean, and GE deviations from the grand mean. Subsequently, AMMI analysis was used to partition GE deviations into different interaction PC axes. 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 biplot is a biplot that displays the GGE part of MET data The GGE biplot was built according to the formula given by Yan et al. (2000):

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

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.

RESULTS AND DISCUSSION

According to the results of combined analysis of variance (Table 3) for grain yield genotype, environment and GEI were highly significant ($P < 0.01$) for grain yield. Mohamed and Ahmed (2013) and Melkamu et al. (2015) reported that bread wheat grain yield was significantly affected by the environment. The highly significant GEI effects suggest that genotypes may be selected for adaptation to specific environments, which is in line with the findings of Alemu et al. (2019) in GGE biplot analysis for yield stability in multi-environment trials of promising bread wheat. The factors explained showed that bread wheat genotype grain yield was affected by environment (82.44%), genotype (6.23%) and GEI (11.33%).

The advanced genotype ETBW9089 ranked first in terms of combined mean grain yield over the six locations and ranked 1st at four locations viz. Kulumsa, Bekoji, Debre-Zeit and Holeta, and also ranked 2nd and 3rd at Arsi-Robe and Assasa, respectively. The advanced genotype ETBW9102 ranked 2nd for mean grain yield over the six

Table 1: Location descriptions and weather conditions of experimental sites.

Location	Geographic position		Altitude	Soil type	Temperature (°C)		Rainfall (mm)
	Latitude	Longitude			Min	Max	
Kulumsa	08°02'N	39°10'E	2200	Luvisol	10.5	22.8	820
Bekoji	07°32'N	39°15'E	2780	Nitosol	7.9	18.6	1020
Assasa	07°07'N	39°11'E	2340	Gleysol	6.6	21.9	642
Arsi-Robe	07°53'N	39°37'E	2420	Vertisol	6.0	21.1	890
Debre-Zeit	08°44'N	38°58'E	1900	Vertisol	8.9	28.3	851
Holeta	09°00'N	38°30'E	2400	Nitosol	6.2	22.1	1044

Table 2: Entry code, Genotype code and pedigree of genotypes evaluated.

Entry Code	Genotype code	Pedigree
G1	WANE	Check (SOKOLL/EXCALIBUR)
G2	ETBW9185	KISKADEE#1/5/KAUZ*2/MNV//KAUZ/3/MILAN/4/BAV92/6/WHEAR//2*PRL/2*PASTOR
G3	ETBW9193	CHWINK/GRACKLE #1//FRNCLN
G4	ETBW9086	MINO/898.97/4/2*PFAU/SERI.1B//AMAD/3/KRONSTAD F2004
G5	ETBW9087	ATTILA/3/URES/PRL//BAV92/4/WBLL1/5/CHYAK1/6/NAVJ07
G6	ETBW9089	BABAX/LR42//BABAX/3/ER2000/4/BAVIS
G7	ETBW9109	PFAU/MILAN/3/BABAX/LR42//BABAX/8/JUP/ZP//COC/3/PVN/4/TNMO/5/TNMO/6/SITE/7/TNMO
G8	ETBW9284	PRL/2*PASTOR//WAXWING*2/KRONSTADF2004/4/PBW343*2/KUKUNA//KRONSTAD F2004/3/PBW343*2/KUKUNA
G9	ETBW9299	WHEAR/SOKOLL/4/WBLL1/KUKUNA//TACUPETOF2001/3/UP2338*2/VIVITSI
G10	ETBW9304	CROC_1/AE.SQUARROSA(205)//BORL95/3/PRL/SARA//TSI/VEE#5/4/FRET2*2/5/WHEAR/SOKOLL
G11	ETBW9313	ROLF07/YANAC//TACUPETOF2001/BRAMBLING*2/3/WHEAR//2*PRL/2*PASTOR
G12	ETBW9094	THELIN/3/BABAX/LR42//BABAX/4/BABAX/LR42//BABAX*2/5/KIRITATI/2*TRCH
G13	ETBW9066	PRL/2*PASTOR/4/CHOIX/STAR/3/HE1/3*CNO79//2*SERI/5/KIRITATI/2*TRCH
G14	ETBW9102	CETA/AE.SQUARROSA (174)//2*MUU
G15	ETBW9315	BABAX/LR42//BABAX/3/ER2000/11/CROC_1/AE.SQUARROSA(213)//PGO/10/ATTILA*2/9/KT/BAGE//F N/U/3/BZA/4/TRM/5/ALDAN/6/SERI/7/VEE#10/8/OPATA/12/BAVIS
G16	BW174459	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B
G17	BW174460	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/SAFI-1//NS732/HER/3/SAADA,
G18	BW174461	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/SAFI-1//NS732/HER/3/SAADA,,
G19	BW174462	PASTOR//HXL7573/2*BAU/3/SOKOLL/WBLL1/4/SAFI-1//NS732/HER/3/SAADA
G20	BW174463	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESWYT99#18/ARRIHANE/5/SITTA/BUCHIN//CHIL/BOMB
G21	BW174464	PFAU/MILAN//FUNG MAI 24/3/ATTILA*2/CROW
G22	BW174465	FLOKWA-2/85 Z 1284//ETBW 4920/3/LOULOU-18
G23	BW174466	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5
G24	BW174467	CHEN/AEGILOPSSQUARROSA(TAUS)//BCN/3/VEE#7/BOW/4/PASTOR/5/HUBARA-1
G25	LEMMU	Check (WAXWING*2/HEILO)

G= Genotype; G1, G2 ... G25, represent codes for genotypes.

Table 3: Combined analysis of variance for grain yield of 25 bread wheat genotypes across six locations.

Source of Variation	df	SS	MS	Explained%
Environment (E)	5	1261.90	252.38**	82.44
Genotype (G)	24	95.35	3.97**	6.23
Interactions (G x E)	120	173.38	1.44**	11.33
Error	300	63.87	0.21	
Total	449	1594.5	3.55	

*, ** =Significant at 0.05 and 0.01, respectively.

locations, but ranked 1st, 2nd, 3rd, 4th, and 5th sequentially at Arsi-Robe, Bekoji, Holeta, Kulumsa and Debre-Zeit; however, it ranked 7th at Assasa. Rank changes of the same genotype over locations for the same trait are due to a highly significant genotype by environment interactions. For the top performer ETBW9089, one of the main contributors to yield most probably is TKW (Table 4). Genotype ETBW9089 showed the higher yield performance of 9.03 t/ha at the highest-yielding location of Kulumsa, and also gave higher yield of 4.00 t/ha in the lowest-yielding environment of Holeta. In general, the ranking of genotypes changed from one environment to another environment and this indicated the existence of G x E interaction due to environmental differences among the testing locations. The finding of this study is in agreement with that of Zelalem (2011) who reported that the G x E interactions further complicate the selection of superior genotypes for a target population of environments.

Remark

G stands for genotype and description of abbreviations on genotypes is presented in Table 2.

GGE biplot analysis

Which Won Where Pattern: The visualization of "which won where" pattern is important to know the existence of different mega environments within an agro-ecology. It is important because evaluations of test locations and genotypes are most useful when conducted within a mega environment (Yan et al., 2007). The perpendicular lines to the polygon sides divide the biplot into sectors, each having its own winning cultivar. The winning genotype for a sector is the vertex genotype at the intersection of the two polygon sides whose perpendicular lines form the boundary of that sector; it is positioned usually, but not necessarily, within its winning sector (Yan, 2002). GGE biplot was constructed by plotting the first two principal components,

Table 4: Mean values of Days to heading, Spike length, thousand kernel weight and Grain Yield of bread wheat genotypes tested across six locations.

Entry code	Genotype	DH	SL	TKW	GY
G1	WANE	65.06l	6.59m	35.50eg	4.88hk
G2	ETBW 9185	72.11ce	8.10fh	33.89gj	4.83ik
G3	ETBW 9193	69.11fh	7.98fk	32.78ij	4.62kl
G4	ETBW 9086	68.78gi	8.26cg	34.56fi	5.08gi
G5	ETBW 9087	68.11hj	8.58b	35.39eg	4.92hj
G6	ETBW 9089	65.94kl	8.19dg	42.89a	6.29a
G7	ETBW 9109	72.50cd	7.66l	34.67fh	4.86hk
G8	ETBW 9284	67.28ik	8.51bc	32.94hj	4.54l
G9	ETBW 9299	70.67ef	9.13a	35.44eg	4.91hk
G10	ETBW 9304	65.67kl	8.08fi	36.83ce	5.58cd
G11	ETBW 9313	71.28ed	8.15eg	33.78gj	4.25m
G12	ETBW 9094	65.06l	7.67l	36.50ce	5.41df
G13	ETBW 9066	76.00a	7.84hj	34.00gj	4.74jl
G14	ETBW 9102	66.67jl	8.29bf	37.33cd	5.87b
G15	ETBW 9315	67.39hk	7.74jl	36.94ce	5.14fh
G16	BW174459	74.61ab	8.46bd	35.94df	4.92hj
G17	BW174460	69.00fi	7.83hl	38.11bc	5.27eg
G18	BW174461	68.33hj	7.96gl	37.94c	5.54ce
G19	BW174462	70.44eg	7.82hl	37.50cd	5.14fh
G20	BW174463	68.39hj	7.96gl	32.67j	5.11gi
G21	BW174464	65.22l	7.68kl	36.11df	5.76bc
G22	BW174465	73.72bc	7.78il	30.11k	4.51lm
G23	BW174466	65.06l	8.43be	35.50eg	5.33dg
G24	BW174467	68.67gi	8.42be	39.83b	5.43de
G25	LEMMU	71.17de	8.01fj	34.00gj	4.75jl
	Mean	69.05	8.05	35.65	5.11
	Minimum	65.06	6.59	30.11	4.25
	Maximum	76.00	9.13	42.89	6.29
	LSD (0.05)	1.80	0.31	1.80	0.91

Within the same column, values with the same letter are not significantly different.

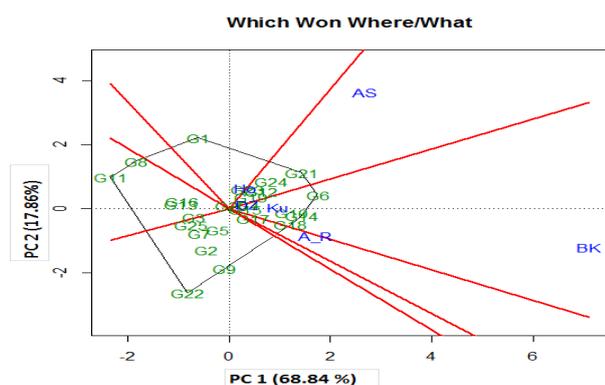


Fig. 1: Polygon views of the GGE biplot based on symmetrical scaling for the which-won-where pattern of genotypes and environments: Where, G1, G2, --- G25 sequentially represent the genotypes (description of Abbreviation of Genotypes (G) is given in Table 2): Key: A_R=Arsi-Robe; AS=Assasa; BK=Bekoji; D-Z=Debre-Zeit; HO=Holeta and KU=Kulumsa.

PC1 and PC2, derived from subjecting environment center yield data to singular value decomposition (Yan et al., 2000). PC1 and PC2 accounted for 86.7% (68.84% and 17.86%) of the G + GE variation for grain yield of the genotypes evaluated at six environments. Accordingly, the vertex genotypes were ETBW9089, BW174464, WANE, ETBW9313, ETBW9102 and genotype BW174465 as shown in Figure 1. This means that the vertex genotype for each sector was the one that gave the highest yield for that environment and found within that sector. Genotype ETBW9089 was the highest yielding genotype at Kulumsa, Bekoji, Debre-Zeit and Holeta. The other vertex genotypes

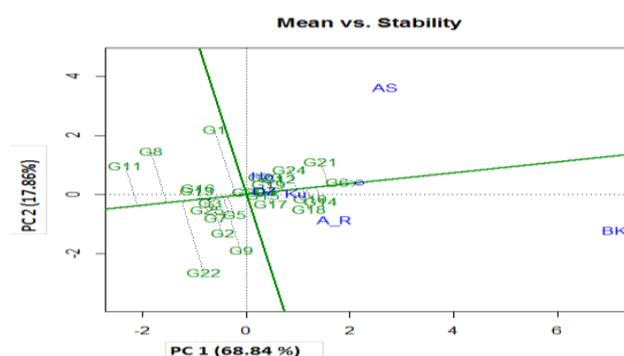


Fig. 2: Average environment coordination (AEC) views of the GGE-biplot based on environment- focused scaling for the means performance and stability of genotypes: Key: A-R= Arsi-Robe, AS = Assasa, BK = Bekoji, D-Z = Debre-Zeit, HO=Holeta and KU = Kulumsa.

ETBW9102 were the best performing genotype at Arsi-Robe, Bekoji and Holeta. The vertex genotypes ETBW9313 and BW174465 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. Genotype ETBW9313 ranked 25th at Bekoji and 24th at Arsi-Robe and genotype ETBW9313 ranked 25th at Assasa and Holeta and 24th at Debre-Zeit.

In this study, the environments were grouped under two quadrants while the genotypes were clustered under four quadrants (Figure 1). The first quadrant contained four locations, namely Kulumsa, Assasa, Holeta and Debre-Zeit and six genotypes viz. ETBW9089, BW174464, ETBW9094,

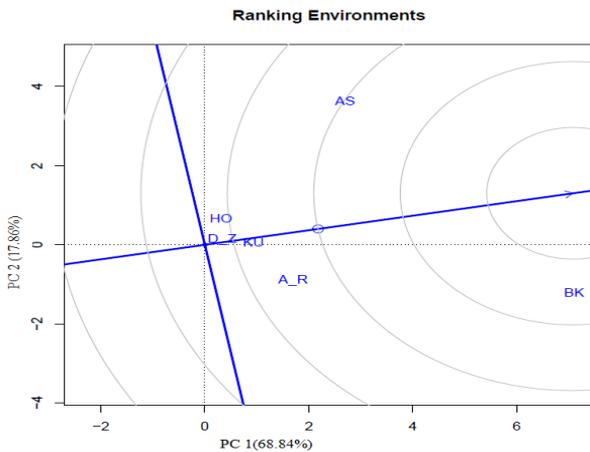


Fig. 3: GGE-biplot view of ranking the test environments based on discriminating ability and representativeness: Key: A-R = Arsi-Robe, AS = Assasa, BK = Bekoji, D-Z = Debre-Zeit, HO = Holeta and KU = Kulumsa.

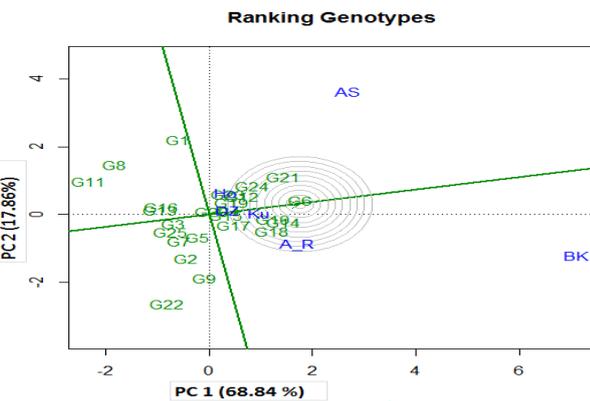


Fig. 4: The average-environment coordination (AEC) of GGE-biplot view to rank genotypes relative to ideal genotypes: NB: A-R = Arsi-Robe, AS = Assasa, BK = Bekoji, D-Z = Debre-Zeit, HO = Holeta and KU = Kulumsa.

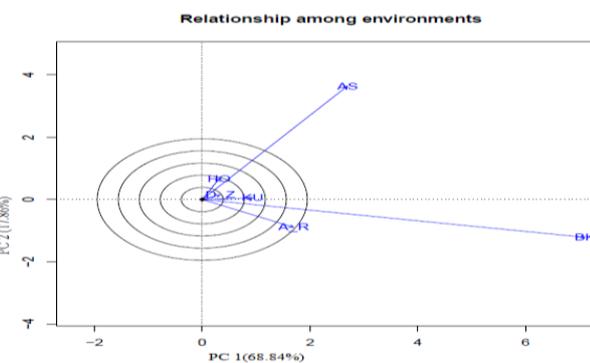


Fig. 5: Relationship among environments: Key: A-R = Arsi-Robe, AS = Assasa, BK = Bekoji, D-Z = Debre-Zeit, HO = Holeta and KU = Kulumsa location.

BW174467, BW174466 and BW174462. The genotype at the vertex, ETBW9089 (G6), was the highest yielding genotype across six testing locations. The 4th quadrant contained two locations, Arsi-Robe and Bekoji with corresponding genotypes ETBW9102, ETBW9304, BW174461, BW174460 and ETBW9315. Under this quadrant, the vertex genotype was ETBW9102.

Environments within the same sector shared the same winning genotype, and environments in different sectors had different winning genotypes.

Average Yield and Stability Performance

Stability and yield performance of the 25 bread wheat genotypes were plotted using average environment coordination (AEC) method as shown in Figure 2. The best genotype is 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 (Yan and Tinker, 2006). A genotype drawn through the average environment and the biplot origin having one direction pointed to a greater genotype main effect. Moving either direction away from AEC and from the biplot origin indicates greater GEI effect and reduced stability. The AEC separates genotypes with below-average means from those with above-average means. Thus, in this study genotypes with above-average means were ETBW9089, ETBW9102, BW174464, BW174461 and BW174467, whereas those with below-average yield means were ETBW9313, ETBW9284, BW174465, ETBW9299 and ETBW9185 as demonstrated in Figure 2. Similar results were reported by Tena et al. (2019); these authors reported that the genotypes on the left side of the ordinate had less yield performance relative to the trial mean grain yield.

Ideal test environments for selecting adapted genotypes

Figure 3 shows an ideal test environment which is the center of the concentric circles. It is a point on the Average Environment Coordinate (AEC) in the positive direction with a distance to the biplot origin equal to the longest vector of all environments (Tena et al., 2019). Thus, Kulumsa is closer to this point (AEC) with small GEI, and is considered the best representative of the location for selecting superior genotypes. On the other hand, Assasa and Bekoji was the least representative, but the most discriminative environments in this study. The result is in agreement with the fact that Kulumsa is the best representative location confirmed for the national bread wheat breeding program to develop and disseminate appropriate bread wheat technologies (varieties) nationally.

Ranking of genotypes relative to the ideal genotypes

An ideal genotype has the highest grain yield and stable across environments (Yan and Kang, 2003; Farshadfar et al., 2012). Desirable genotypes are those located close to the ideal genotype. The ideal genotype is located in the middle of the concentric circle. From the origin through the middle of concentric circle is drawn a line to visualize the distance between genotypes and the ideal genotype (Yan and Tinker, 2006). The ideal genotype which is found at the centre of the concentric circles 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). The ideal genotype (the center of concentric circles) is a point on Average Environment Coordinate (AEC) in the positive direction and has a vector length equal to the longest vector of the genotypes on the positive side of the AEC (“highest mean performance”). As a result, a genotype located closer

to the “ideal genotype” is more desirable than the others located farther away. Hence, the GGE biplot in Figure 4 showed ETBW9089 as an ideal genotype, while genotypes BW174464, ETBW9102, ETBW9304 and BW174461 were desirable genotypes as they were closer to the ideal genotype. Conversely, genotypes ETBW9313, ETBW9284, BW174465 and variety WANE were the least desirable genotype as indicated by the GGE biplot.

Relationship among environments

The GGE biplot in Figure 5 accounted for about 87% of the total variation related to genotype and GEI and suggested the possibility of extracting interrelationships among the test environments. To visualize the relationship between environments, environment vectors are drawn to connect the test environments to the biplot origin. 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. The cosine of the angle between two environments is used to approximate the correlation between them as described and used in Kaya et al., (2006) and Dehghani et al. (2010).

According to the angles between test location vectors, the six locations are divided into two major groups. The smallest angle group include locations Kulumsa, Holeta and Arsi-Robe, implying that there is very high association among them. Hence, they provide redundant information and have less capacity in discriminating among the genotypes (Figure 5). Debre-Zeit had a very short vector and stands alone. Obtaining reliable information on the similarity of environments and their subdivision into groups can enable breeders to use fewer test environments, hence reducing the cost of testing and increasing breeding efficiency (Alemu et al., 2019). The second group included Assasa and Bekoji locations. With the longest vectors from the origin, environments Bekoji and Assasa were the most discriminating environments. Kulumsa, Holeta and Arsi-Robe were moderately discriminating while Debre-Zeit was a least discriminating location.

Conclusion

A GGE biplot model is an excellent tool for visual MET data analysis. The visualization of "which won where" pattern is important to know the existence of different mega environments within an agro-ecology. The results of combined analysis of variance for grain yield of 25 bread wheat genotypes indicated that genotype, environment and GEI were highly significant ($P < 0.01$). The factors explained showed that bread wheat genotypes grain yield was affected by environment (82.44%), genotype (6.23%) and GEI (11.33%). In this GGE biplot, a polygon was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. The vertex genotypes were ETBW9089, BW174464, WANE, ETBW9313, ETBW9102 and genotype BW174465 having the largest distance from the origin. These genotypes are the best or poorest in some or all environments because they are farthest from the origin of biplot which were more responsive to environmental change and are considered as

specially adapted genotypes. They are best in the environment lying within their respective sector in the polygon view of the GGE-biplot. Thus, these genotypes are considered specifically adapted. Locations within the same group were closely correlated and provided redundant information about the genotypes. Testing can be performed in any one of the locations within a group. As a result, a genotype located closer to the “ideal genotype” is more desirable than the others located farther away. Hence, the GGE biplot showed genotype ETBW9089 as an ideal genotype, while genotypes BW174464, ETBW9102, ETBW9304 and BW174461 were desirable genotypes as they were closer to the ideal genotype. Conversely, genotypes ETBW9313, ETBW9284, BW174465 and variety WANE were the least desirable genotype as indicated by the GGE biplot. Based on yield performance advanced lines ETBW9089, ETBW9102 and BW174464 are recommended to be included in variety verification trials for further release.

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