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Multi-Location Evaluation of Yield and Yield Related Trait Performance in Bread Wheat Genotypes at Western Oromia, Ethiopia

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Abstract: Wheat (*Triticum aestivum* L.) is an important cereal crop, which receives the most attention of specialists in plant breeding and production worldwide. Knowledge of the interaction between genotypes and environment with yield and yield components is a principal aspect of effective selection in crop improvement. Therefore, the objective of this study was: to identify bread wheat genotypes with high level of grain yield and yield stability and insect pest tolerant across locations. The study used 15 bread wheat genotypes, against one local and two standard checks (Liban and Kingbird) at Haro Sabu Agricultural Research Center (HSARC) in 2017-2018 cropping season. Ten agronomic traits and four economically important disease reaction data were evaluated. Analysis of variance detected significant difference, among genotypes in both separated and combined analysis of variance. The combined ANOVA and the additive main effects and multiplicative interactions (AMMI) analysis for grain yield across environments exhibited significantly affected by environments, which explained 65.06% of the total variation. The genotype and genotype environmental interation were significant and accounted for 13.34 and 9.44%, respectively. Pricipal component (PCA) 1 and 2 accounted for 7.88 and 1.15% of the GEI, respectively, with a total of 9.03% variation. Generally, G6 and G3 were identified as ideal genotypes for yielding ability and stability, tolerant to diseases and use as parents in future breeding programs.

Keywords: AMMI, GGEI, Performance, Stability, *Triticum aestivum*

1. Introduction

World wide, wheat (*Triticum aestivum* L.) is an important cereal crop, which receives the most attention of specialists in plant breeding and production. Yet, its production is limited by the adverse environmental conditions. Environmental fulactuation and interaction with crop plant are the major limitation to wheat production and productivity. Genotype x environment (GE) interaction reduces genetic progress in plant breeding programmes through minimising the association between phenotypic and genotypic values [2]. Therefore, multi-environment yield trials are essential in estimation of genotype by environment interactionn (GEI), identification of superior and stable genotypes in the final selection cycles [11, 12]. Phenotypes are a mixture of genotype (G) and environment (E) components, and their interactions (G x E). Genotype by environment interactionn (GEI) complicate process of selecting genotypes with superior performance. Accordingly, Multi-environment trails (METs) are widely used by plant breeders to evaluate the relative performance of genotypes for target environments [4]. The additive main effects and multiplicative interaction (AMMI) model have led to more understanding of the complicated patterns of genotypic responses to the environment [8]. These patterns have been successfully related to biotic and abiotic factors. Yan et al. [20], proposed

another methodology known as GGE-biplot for 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 the GE interactions. The first two principle 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 [19]. 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 interaction [22].

Therefore, the objective of this study was: to identify bread wheat genotypes with high level of grain yield and yield stability and insect pest tolerant across locations.

2. Materials and Methods

2.1. Study sites

The multi-location yield study (MLYT) was conducted at three locations in Kellem and west Wollega zones of Haro-Sabu Agricultural Research Center at Belem sub site (altitude 1759 masl, 09° 02' N, 035° 104'E), Mata (altitude 2016 masl, 08° 34' N, 034° 44'E) and Badesso (altitude 2054 masl, 08° 40' N, 034°47'E) in western Oromia, Ethiopia, during the 2017-2018 main cropping season.

2.2. Breeding materials and experimental design

A total of 15 genetically diverse bread wheat genotypes (Table1) was evaluated against the checks (Liban, Kingbird and one local check). Arandomised complete block design (RCBD), with three replications, were used. Six rows per plot of 0.2 m spacing between rows and 2.5 m row length, and harvestable plot size was 2 m^2 (four harvestable rows per plot). A seed rate of 150 kgha^{-1} and fertiliser rate of 100 kg ha^{-1} DAP and 150 kg ha^{-1} Urea were used.

2.3. Statistical analysis

Analysis of variance was calculated using the model:

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

Where:

Y_{ij} is the corresponding variable of the i-th genotype in j-th environment, μ is the total mean, G_i is the main effect of i-th genotype, E_j is the main effect of j-th environment, GE_{ij} is the effect of genotype x environment interaction.

The AMMI model used was:

$$Y_{ij} = \mu + g_i + e_j + \sum_1^N \Lambda_k \Upsilon_{ik} \delta_{jk} + \varepsilon_{ij}$$

Where:

Y_{ij} is the grain yield of the i-th genotype in the j-th environment, μ is the grand mean, g_i and e_j are the genotype

and environment deviation from the grand mean, respectively, Λ_k is the eigenvalue of the principal component analysis (PCA) axis k, Υ_{ik} and δ_{jk} are the genotype and environment principal component scores for axis k, N is the number of principal components retained in the model, and ε_{ij} is the residual term.

Table 1. List of bread wheat genotypes evaluated for two years at Western Oromia in Ethiopia.

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

G=genotype, ETBW=Ethiopia bread wheat, KARC=Kulumsa Agricultural Reaserch center

GGE-biplot methodology, which is composed of two concepts, the biplot concept [7] and the GGE concept [20] was used to visually analyse 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 sources of variation in GEI analysis of METs data [18]. 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 [20].

2.4. 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 [14]. 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:

$$ASV = \sqrt{[(SSIPCA1 + SSIPCA2)(IPCA1score)]^2 + (IPCA2score)^2}$$

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 [14].

2.5. 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 rank of AMMI stability value RASVi), genotype selection index (GSI) was calculated for each genotype as:

GSIi=RASVi + RYi

A genotype with the least GSI is considered as the most stable [5]. Analysis of variance was carried out using Statistical Analysis System (SAS) version 9.2 Software [15]. Additive Main Effect and Multiplicative Interaction (AMMI) analysis and GGE bi-plot analysis were performed using Gen Stat 15th edition statistical package [17].

2.6. Data collection method

Ten plants were selected randomly before heading from each row (four harvestable rows) and tagged with thread and plant-based data were collected from the sampled plants.

2.6.1. Plant-based

Plant height, Spike length, and spike weight, spike lets per spike, grain per spike and grain per spikelet. Plant height (cm); was measured and recorded when reached at 90% physiological maturity from the ground level to the base of the spike of plant. Spike length (cm); was measured from the base of the spike to the tip of the highest spikelet excluding awns. Spike weight (g); is the average weight of spike of the ten plants randomly selected. Spikelets per spike; is the average number of spikelets of the ten plants randomly selected. Grain per spike; is the average number of grains of the ten plants randomly selected. Grain per spikelet; was calculated by dividing grain per spike by the spikelets per spike.

$$\text{Grain per spikelet} = \frac{\text{Grain per spike}}{\text{Spikelets per spike}}$$

2.6.2. Plot Based

Days to heading, days to maturity, thousand seed weight, grain yield and four economically important disease reactions like stem rust, leaf rust, septoria and fusarium head blight. Days to heading; was recorded by counting the number of days from sowing to the time when at least 50% of the heads of the plot fully exerted from the boom or flowered. Days to maturity; was recorded by counting the number of days from sowing to the days when 95% of the heads of the plot were physiologically matured. Thousand seed weight (g); fife hundred wheat grains were counted and weighed then multiplied by two to obtain thousand seed weight. Grain yield per plot (g); yield per plot was taken and moisture was adjusted to the standard moisture content of 12% moisture basis after threshing the crop using moisture tester by the following formula. It was calculated as:

Adjusted yield per plot=Actual yield per plot (100-Y/100-X)

Where=Actual yield is yield per a given area in a unit at threshing

Y=is moisture in % age at threshing

X=is standard moisture in % age

The disease severity score rated for each pathogen reaction was conducted as per the established procedures for each disease using CIMMYT's method (www.CIMMYT.org).

Table 2. Analysis of variance (ANOVA) for grain yield and yield related traits of bread wheat genotypes evaluated in 2017-2018 main cropping season.

S. variation	DF	DH	DM	SR	LR	SEP	FHB	PH
Rep	2	12.68**	12.86	0.22**	0.03	0.02	7.37**	13.08
Gen	14	265.24**	340.90**	0.05*	0.05	0.01	1.53**	578.88**
Loc	2	832.68**	5506.27**	0.11*	0.13*	0.03	1.30*	7274.29**
Yr	1	963.33**	3998.23**	0	0.49**	0.07*	76.80**	338.08**
Gen.*loc.	28	12.30**	47.71**	0.02	0.03	0.01	0.15	59.27**
Gen.*yr.	14	46.97**	122.82**	0.02	0.05	0.01	1.37**	14.19
Loc.*yr.	2	106.68**	3232.78**	0.11*	0.13*	0.03	1.30*	351.89**
Gen.*loc.*yr.	28	12.3	48.52**	0.02	0.03	0.01	0.15	8.2

Table 2. Continued.

S. variation	SL	SW	STPS	GPS	GPST	TSW	Kg/ha
Rep	3.29**	0.41	21.25*	364.69**	2.12**	198.23	42646.84
Gen	11.37**	5.72**	35.06**	597.59**	1.31**	513.13*	1831217.12**
Loc	28.99**	2.48**	293.70**	433.04**	2.72**	2741.55**	13090998.64**
Yr	101.14**	27.60**	64.68**	3229.91**	5.18**	4066.07**	89102882.12**
Gen.*loc.	0.71**	0.25	11.54**	93.93*	0.41	242.62	376887.84**
Gen.*yr.	0.51	0.96**	2.99	72.64	0.31	287.65	206156.52
Loc.*yr.	202.90**	11.45**	176.97**	4456.30**	4.96**	261.09	4874484.92**
Gen.*loc.*yr.	0.47	0.41*	8	95.65*	0.37	352.59	167928.97**

ns * ** non –significant, significant at 5% and 1% respectively, Loc *gen=location by genotype, Yr*Loc*gen=year by location by genotype, DF=degree of freedom, DH=Days to Heading, DM=Days to Maturity, PH=Plant Height; SL=spike Length, SW=Spike Weight, STPS=Spikelets per spike; GPS=-Grain per spike, GPST=Grain per spikelets, TSW=Thousand Seed Weight, YLD kgha[-1]=Yield in kilogram per hectare

3. Results and Discussion

3.1. Combined Analysis of Variance (ANOVA)

Mean square of analysis of variance for all genotypes at different environmental conditions, for grain yield and yield related traits, are presented in Table 2. Highly significant differences were detected among years ($P \leq 0.01$) for all parameters, except for stem rust and septoria. The combined analysis of variance revealed that year and location effects were significant for all parameters, except septoria and thousand seed weight. Year*genotypes effects were not significant for all parameters, excluding days to heading, days to maturity, fusarium head blight and spike weight. Year*location *genotypes were significant for some traits such as days to maturity, spike weight, grain per spike and yield. Genotype by environment interaction mean square was highly significant ($P \leq 0.01$) for days to maturity, days to heading, plant height, and spike length, spikelets per spike and grain yield.

3.2. Yield Across Environments

The performance of the tested bread wheat genotypes for grain yield across location and year are presented in Table 3. Some genotypes (e.g., G6 and G3) are constantly performed best in a group of environments, while other genotypes (such as G14 and G13) are fluctuated across location. The average grain yield ranged from the lowest (3524.47 kgha⁻¹) at Belem site in 2017 to the highest (5520.17kgha⁻¹) at Bedesso site in 2018, with grand mean of 4479.47 kgha⁻¹ (Table 3) The grain yield across environments ranged from the lowest of 3925 kgha⁻¹ for local check to the highest of 5069 kgha⁻¹ for genotype (G6) (Table3). This wide variation might be due to

their genetic potential of the genotypes. Genotype (G6) was the top-ranking pipeline in all environments, except at Belem in 2018. Similarly, genotype (G3) ranked first at all sites, except at Bedeso in 2017 and 2018 cropping season. However, genotype (G8) ranked the least in all environmental sites throughout cropping season (Table3). The difference in yield rank of genotypes across the environments exhibited the high crossover type of genotypes x environmental interaction [21].

3.3. Agronomic Performance

Combined mean grain yield and other agronomic traits are presented in Table 4. High mean of spike length, spike weight, spikelets per spike, grain per spike, grain per spikelets, thousand seed weight and grain yield and medium days to heading and days to maturity were recorded by genotypes (G6). These offer great flexibility for developing improved varieties suitable for various agro-ecologies with variable length of growing period and high in grain yield status. However, G2, G10 and G14 were with short mean of days to heading and days to physiological maturity, indicating that early maturing genotypes were desirable when moisture was the limiting factors of production. Similarly, the local check was recorded with high plant height, indicating that the variety might be susceptible to lodging. Genotypes (G6) and (G3) were with medium plant height indicated, and the possibility for developing resistant varieties against lodging problems. Moreover, genotypes (G6, G3 and G2) recorded the highest grain yield and had 21.3, 10.9 and 4.4% yield advantages over the best standard check (Liban), respectively (Table 4).

Table 3. Mean grain yield (kgha⁻¹) of bread wheat genotypes evaluated at three environments.

| Genotypes | Grain yield (kgha⁻¹) | | | | | | Com. mean |
| | 2017 | | | 2018 | | | |
	Belem	Bedesso	Mata	Belem	Bedesso	Mata	
ETBW7052	3426.5c	3780.6cd	3894.8d	4477.5c-f	5394.6d	4707.4cd	4280ef
ETBW7056	4057.2a	4896a	4744.4ab	3830f	6348.5a	5387.8ab	4877c
ETBW7068	3531.3bc	3689.5cd	4634.2abc	4790.3a-d	5459.4cd	5308.6ab	4568cd
ETBW7069	3278.1cd	3395.1d	3841.1d	4442.3c-f	5132de	4711.1cd	4133fg
ETBW7071	3282.6cd	3735.3cd	4060.6bcd	4466.7c-f	5295.7de	4835.9bcd	4280ef
ETBW7072	3006.9d	3268.7d	3811d	4029.2ef	4889.9e	4636.4d	3940g
ETBW7075	3902.5a	4490ab	4315.8a-d	4353.3c-f	6030.6ab	5056.2a-d	4691c
ETBW7076	4119.9a	4942a	4848.1a	4633.5b-e	6400.2a	5468.4a	5069a
ETBW7077	3228cd	3583.5cd	4436a-d	4477.5c-f	5141.7de	5152.3a-d	4337def
ETBW7088	3320.3cd	3463d	4488.2a-d	5219.3ab	5205.7de	5173.1a-d	4478cde
ETBW7092	3525bc	3668.3cd	4613.9abc	5420a	5429.4cd	5275.7abc	4655bc
ETBW7104	3795.4ab	4125.3bc	4819.6a	5260.8ab	5840.9bc	5430.2a	4880b
kingbird	3295.3cd	3634.5cd	4361.1a-d	4863.7abc	5219.6de	5066a-d	4407de
Liban	3846.8ab	3761.5cd	4663.7ab	4351.8c-f	5834.7bc	5572.4a	4672bc
Local	3251.1cd	3567.4cd	3926.3cd	4107.2def	5179.7de	4721cd	3925fg
Mean	3524.47	3866.71	4363.90	4581.54	5520.17	5100.16	4479.47
R² (%)	82	77	54	67	85	55	88
CV%	5.63	9.24	9.73	9.49	4.46	6.87	8.05
LSD 5%	331.85	597.27	710.29	727.53	411.72	585.82	237.98
F test	**	**	**	**	**	**	**

ETBW=Ethiopia bread wheat, R²=R-squire, CV=coefficient of variation, LSD=least significant different

Table 4. Combined mean grain yield and other agronomic traits of bread wheat genotypes.

Genotypes	DH	DM	PH	SL	SW	STPS
ETBW7052 (G13)	80.2a	121.3c	78.1c	9.6bc	2.14c	16.4bcd
ETBW7076 (G6)	77.8b	118.2ef	75.04de	10.4a	3.7a	19.02a
ETBW7092 (G11)	76.1c	119.5de	81.9b	7.9hi	1.69de	15.01d
ETBW7069 (G12)	75.9c	117.2fg	74.06def	8.5fg	1.9cde	15.36cd
ETBW7071 (G15)	75.9cd	118.7e	73.54ef	8.8ef	1.9cd	16.26cd
ETBW7072 (G8)	75de	120.5cd	76.19cd	8.3gh	1.99cd	15.73cd
Liban (G9)	74.8e	121.3c	74.05def	8.4fg	2.12c	16.69bc
Local (G1)	72.6f	123b	93.18a	7.6i	1.3f	12.79e
ETBW7104 (G3)	71.6g	113.4h	75.3de	9.2d	3.02b	17.85ab
ETBW7077 (G7)	71.4g	126.5a	73.47ef	9.1de	2.03c	15.90cd
ETBW7068 (G5)	70.9g	114.2h	78.18c	9.8b	2.02c	15.05d
ETBW7056 (G2)	70.3i	116.3g	76.48cd	9.8b	2.06c	16.29cd
ETBW7075 (G10)	69.7i	114.1h	71.8f	9.4cd	1.98cd	15.58cd
ETBW7088 (G14)	69.6i	114.5h	68.46g	9.2cd	1.87cde	15.52cd
kingbird (G4)	65.3j	109.6i	72.04f	7.9hi	1.6ef	14.98d
Mean	73.13	117.89	76.12	8.92	2.09	15.9
CV%	1.91	1.85	5.23	6.71	23.36	14.65
R^2%	96	97	90	92	0.8	0.69
LSD 5%	0.9	1.43	2.62	0.39	0.32	1.53
F test	**	**	**	**	**	**

Table 4. Continued.

Genotypes	GPS	GPST	TSW	Kgha	YAD
ETBW7052 (G13)	43.09bc	2.64b-f	24.37cd	4280ef	-8.4
ETBW7076 (G6)	55.51a	2.97ab	36.54ab	5669a	21.3
ETBW7092 (G11)	33.82f	2.29fgh	36.83a	4655bc	-0.4
ETBW7069 (G12)	37.05def	2.48c-h	25.48bcd	4133fg	-11.5
ETBW7071 (G15)	40.48cd	2.46c-h	25.56bcd	4280ef	-8.4
ETBW7072 (G8)	37.08def	2.41d-h	25.61a-d	3940g	-15.7
Liban (G9)	45.75b	2.78a-d	22.64cd	4672bc	0
Local (G1)	33.76f	2.67b-e	19.48d	3925fg	-15.9
ETBW7104 (G3)	39.75cde	2.21gh	33.13abc	5179b	10.9
ETBW7077 (G7)	33.59f	2.12h	22.06cd	4337def	-7.2
ETBW7068 (G5)	35.44ef	2.39e-h	29.60a-d	4568cd	-2.2
ETBW7056 (G2)	41.21bcd	2.52c-g	27.04a-d	4877c	4.4
ETBW7075 (G10)	37.62def	2.45c-h	28.28a-d	4691c	0.4
ETBW7088 (G14)	41.63bcd	2.81abc	22.54cd	4478cde	-4.2
kingbird (G4)	43.90bc	3.06a	21.18d	4407de	-5.7
Mean	39.98	2.55	26.69	4492.83	
CV%	19.06	21.92	63.93	8.05	
R^2%	0.73	0.55	0.43	88	
LSD 5%	5.01	0.37	11.22	237.98	
F test	**	**	**	**	

ETBW=Ethiopia bread wheat, DH=Days to heading, DM=Days to maturity, PH=Plant height, SL=spike length, SW=spike weight, STPS=spikelets per spike, GPS=grain per spike, GPST=grain per spikelet, TSW=Thousand seed weight, YLD kgha^{-1}=Yield in kilogram per hectare, YAD=yield advantage, CV=Coefficient of variation, R^2=R-square, LSD=least significant

3.4. Major Disease Reactions

Most genotypes evaluated had significantly low scores for their corresponding economically important disease reactions (Table5). However, some genotypes (G10) and (G12) were less tolerant to stem and leaf rust and septoria. Similarly, genotypes (G12, G15, G5, G2 and G10) were less tolerant to fusarium head blight (Table 5). On the other hand, genotypes (G6 and G3) were better tolerance to stem and leaf rust and fusarium head blight (Table 5).

Table 5. Combined mean of disease reactions (1-5 scale) of bread wheat genotypes evaluated in 2017-2018 main cropping season.

Genotypes	SR	LR	SEP	FHB
ETBW7052 (G13)	1c	1b	1.03ab	1.8b-e
ETBW7076 (G6)	1.1bc	1.08ab	1.03ab	1.9b-e
ETBW7092 (G11)	1c	1b	1b	1.3f
ETBW7069 (G12)	1.13ab	1.03b	1b	2.4a
ETBW7071 (G15)	1c	1b	1b	2.2ab
ETBW7072 (G8)	1.03c	1.06ab	1b	1.8b-e
Liban (G9)	1.03c	1b	1b	1.9b-e

Genotypes	SR	LR	SEP	FHB
Local (G1)	1c	1b	1.03ab	1.8cde
ETBW7104 (G3)	1.04bc	1b	1.07a	1.6ef
ETBW7077 (G7)	1c	1.08ab	1.03ab	1.7de
ETBW7068 (G5)	1.13ab	1.03b	1.03ab	2.1abc
ETBW7056 (G2)	1.06bc	1.11ab	1.06ab	2.4a
ETBW7075 (G10)	1.17a	1.17ab	1.03ab	2.0bcd
ETBW7088 (G14)	1c	1.03b	1b	1.8b-e
kingbird (G4)	1c	1.06ab	1b	1.9b-e
Mean	1.04	1.04	1.02	1.91
CV%	14.14	17.29	9.25	30.15
R^2%	42	41	38	71
LSD 5%	0.097	0.12	0.062	0.38
F test	**	**	**	**

ETBW=Ethiopia bread wheat, CV=Coefficient of variation, LSD=least significant difference, R^2=R-Square, SR=stem rust, LR=leaf rust, SEP=septoria, FHB=fusarium head blight. 1-5 scale where 1=resistant, 5=susceptible

3.5. Additive Main Effects and Multiplicative Interaction (AMMI) Model

The combined ANOVA and AMMI analysis for grain yield at six environments exhibited by bread wheat grain yield (Table 6), was significantly affected by environments. This explained 65.06% of the total treatment variation, while the G and GEI were significant and accounted for 13.34 and 9.44%, respectively (Table 6). Similar findings have been reported in previous studies [6, 11]. A study by Gauch and Zobel [9], reported in standard multi-environment trials (METs), environment effect contributes 80% of the total sum of treatments and 10% effect of genotype and interaction. In additive variance, the portioning of GEss data matrix using AMMI analysis, indicated the first PCAs were significant (P < 0.01). PCA 1 and 2 accounted for 7.88 and 1.15% of the GE interaction, respectively; representing a total of 9.03% of the interaction variation (Table 6). Similar results have been reported in earlier studies [13].

Large yield variation explained by environments indicated that environments were diverse, with large differences between environmental means contributing maximum of the variation in grain yield (Table 7). Grain yield of environments ranged from 3524 kgha^{-1} in E3 to 5520 kg ha^{-1} in E2. Genotype mean grain yield varied from 3940 kg ha^{-1} for (G8) to 5069 kg ha^{-1} in (G6), with the over all mean of 4493 kg ha^{-1} (Table 7).
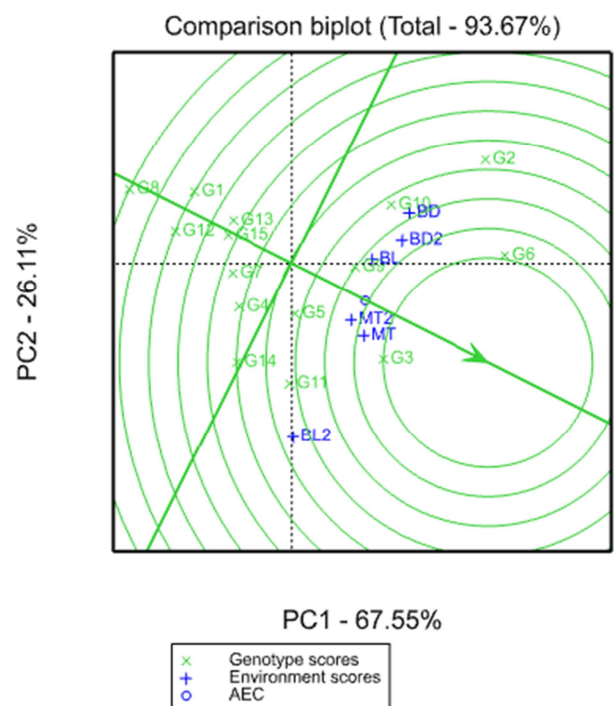

Figure 1. GGE bi-plot based on genotype-focused scaling for comparison of genotypes for their yield potential and stability of bread wheat varieties at Western Oromia in Ethiopia.

Table 6. Additive main effect and multiplicative interaction analysis of variances (AMMI) for grain yield of 15 bread wheat genotypes evaluated at six environments.

Source of variation	DF	SS	EX. SS%	MS
Total	269	192196683	100	714486
Treatments	89	168813778	87.83	1896784**
Genotypes	14	25637440	13.34	1831246**
Environments	5	125035456	65.06	25007091**
Block	12	3230047	1.68	269171*
GxE	70	18140883	9.44	259155**
IPCA 1	18	15142869	7.88	841271**
IPCA 2	16	2201589	1.15	137599^{ns}
Residuals	36	796424	0.41	22123
Error	168	20152857		119957

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

Table 7. *Average grain yield (kg ha^{-1}) of 15 bread wheat genotypes tested across six environments in 2017-2018 main cropping seasons.*

Gen/Env	E1	E2	E3	E4	E5	E6	Mean
Local (G1)	3582	5209	3183	4112	3966	4701	4125
ETBW7075 (G10)	4532	6007	3856	4354	4340	5060	4691
ETBW7092 (G11)	3676	5398	3555	5417	4576	5310	4655
ETBW7069 (G12)	3485	5108	3140	4447	3946	4674	4133
ETBW7052 (G13)	3843	5370	3340	4480	3965	4683	4280
ETBW7088 (G14)	3442	5200	3369	5217	4452	5190	4478
ETBW7071 (G15)	3707	5312	3313	4465	4076	4804	4279
ETBW7056 (G2)	4836	6381	4129	3829	4674	5416	4877
ETBW7104 (G3)	4126	5795	3859	5256	4752	5485	4879
kingbird (G4)	3564	5268	3362	4864	4323	5060	4407
ETBW7068 (G5)	3688	5458	3537	4791	4595	5344	4569
ETBW7076 (G6)	4885	6393	4237	4628	4771	5497	5069
ETBW7077 (G7)	3464	5244	3313	4480	4383	5135	4337
ETBW7072 (G8)	3256	4941	2960	4034	3856	4596	3940
Liban (G9)	3915	5720	3713	4350	4785	5548	4672
Mean	3867	5520	3524	4582	4364	5100	4493

Gen=genotype; Env=environment, E1-BD-2017 (Bedesso), E2-BD-2018, E3-BL-2017 (Belem), E4-BL-2018, E5-MT-2017 (Mata), E6-MT-2018, the number following each location indicates the year, E=environment

The average environment is defined by the average values of PC1 and 2 for the all environments, and it is presented with a circle [14]. The average ordinate environment (AOE) is defined by the line which is perpendicular to the AEA (average environment axis) line and pass through the origin. This line divides the genotypes in to those with higher yield than average and in to those lower yield than average. By projecting the genotypes on AEA axis, the genotypes are ranked by yield; where the yield increases in the direction of arrow. In this case, the highest yield had genotypes G6, G3 and G2, but the lowers had G8, G1 and G12 (Figure 1). Stability of the genotypes depends on their distance from the AE abscissa. Genotypes closer to or around the center of concentric circle indicated these genotypes are more stable than others. Therfore, the greatest stability in the high yielding group had genotypes G6, G3 and G2, whereas the most stable and yielder of all was G6 (Figure 1)

The genotype ranking is shown on the graph of genotype so-called "ideal" genotype (Figure 1). 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; such as genotypes G6, G3 and G2 [6, 19], Even though such an "ideal" genotype may not exist in reality, it could be used as a reference for genotype evaluation [12].

A genotype is more appropriate if it is located closer to "ideal" genotype [6, 11]. So, the closer to the "ideal" genotype in this study was G6 (Figure 1). 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 2). Actually, 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 [22]. Accordingly, E3 (BL-2017=Belem), 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 (Figure 2).
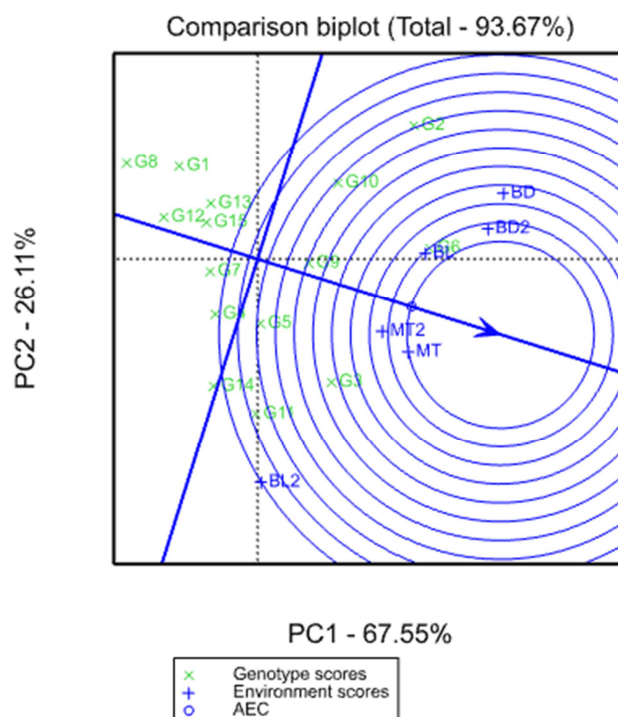

Figure 2. *GGE bi-plot based on tested environments-focused comparison for their relationship E1-BD-2017 (Bedesso), E2-BD-2018, E3-BL-2017 (Belem), E4-BL-2018, E5-MT-2017 (Mata), E6-MT-2018, the number following each location indicates the year, E=environment.*
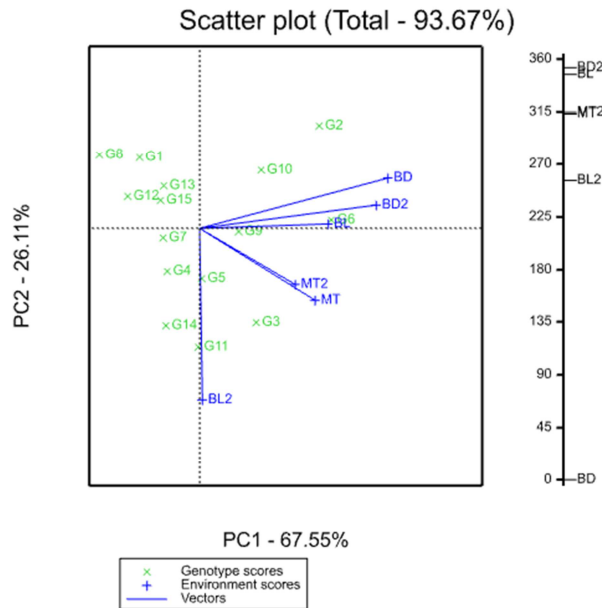
Figure 3. GGE bi-plot based on tested environments-focused comparison for their relationships. E1-BD (Bedesso), E2-BD-2018, E3-BL-2017 (Belem), E4-BL-2018, E5-MT-2017 (Mata), E6-MT-2018, the number following each location indicates the year, E=environment.

The correlation coefficients among the six test environments and the vector view of the GGE-bi-plot delivered a brief summary of the interrelationship between the environments and correlation coefficients were significant (Figure 3). Most environments were positively correlated since the angles among them were smaller than 90°, apart from environment E4 (Belem-2018), which had negatively correlated with E1 (BD-Bedesso-2017) and E2 (BD-Bedesso-2018) since obtuse angles between them (Figure 3). Similarly, Farshadfar et al. [6], reported environments ER3 and EI3 which represented rain fed and irrigated conditions in 2011 cropping seasons, respectively, made an obtuse angle with each other, indicated 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 indirect response to selection [3]. Indirect selection for grain yield can be partial across the tested environments. This means, for instance, the genotypes adaptable or higher productivity in E4 may also show similar responses to E5 and E6 as well.

Table 8. Correlation coefficients among six test environments.

Environment	E1	E2	E3	E4	E5
E2	0.984**				
E3	0.936**	0.977**			
E4	0.197ns	-0.134ns	0.066ns		
E5	0.571*	0.701**	0.82**	0.387ns	
E6	0.554*	0.687*	0.806**	0.378ns	0.999**

ns,*, ** non- Significant, significant at the 0.05 and 0.01 probability level, respectively.

3.6. Additive Main Effects and Multiple Interactions (AMMI)

3.6.1. AMMI Stability Value (ASV)

Genotypes exhibited significant genotype by environment interaction effects and the additive and multiplicative interaction effect stability analysis (ASV) implied splitting the interaction effect. In view of the mean grain yield as a first criterion for evaluating, G6 was the highest mean grain yield (5069 kgha^{-1}), followed by the genotypes G3 and G2 with the mean grain yield of (4879 and 4877kgha^{-1}, respectively). Whereas, genotypes G8, G12 and G1 were with low mean grain yields across the testing locations (Table 9). The IPCA1 and 2 scores in the AMMI model are indicators of stability [14]. Considering IPCA1, G6 was the most stable genotype with IPCA1 value (-16.65), followed by G3 with IPCA1 value of (6.95). Likewise, in IPCA2, G9 was the most stable with interaction principal component value (-18.03). The two principal components have their own extremes; however, calculating the AMMI stability value (ASV) is a balanced measure of stability [14]. Genotypes with lower ASV values are considered more stable and genotypes with higher ASV are unstable. According to the ASV ranking in the (Table 9), G8 was the most stable with an ASV value of 1 followed by G1 with

Table 9. AMMI stability value, AMMI rank, yield, yield rank and genotype selection index and principal component axis.

Genotypes	ASV	ASV rank	YLD	YLD rank	GSI	IPCAg1	IPCAg2
G6	144.3	10.0	5069	1.0	11.0	-16.65	5.04
G3	61.4	5.0	4879	2.0	7.0	6.95	2.55
G2	245.6	15.0	4877	3.0	18.0	-28.98	-6.11
G10	148.8	12.0	4691	4.0	16.0	-15.43	9.17
G9	153.4	14.0	4672	5.0	19.0	-4.16	-18.03
G11	145.9	11.0	4655	6.0	17.0	17.29	3.27
G5	86.4	7.0	4569	7.0	14.0	6.82	-7.88
G14	149.0	13.0	4478	8.0	21.0	17.97	-0.03
G4	82.2	6.0	4407	9.0	15.0	9.88	0.72
G7	92.9	8.0	4337	10.0	18.0	5.42	-9.80
G13	100.3	9.0	4280	11.0	20.0	-1.71	11.97
G15	44.1	3.0	4279	12.0	15.0	0.58	5.29
G12	56.6	4.0	4133	13.0	17.0	4.02	5.51
G1	27.2	2.0	4125	14.0	16.0	-3.16	0.86
G8	23.2	1.0	3940	15.0	16.0	1.16	-2.54

ASV value 2. However, G2 was the most unstable since higher ASV value of 15. The stable genotype was followed with mean grain yield above the grand mean and this result was in agreement with Hintsa and Abay [10], who has 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 [1]; Sivapalan et al. [16] in barley in Tigray and bread wheat using AMMI stability value. A genotype with the least of genotype selection index (GSI) is considered as the most stable genotype [5]. Accordingly, G6 was the most stable genotype since with the low of genotype selection index (GSI) and the highest mean grain yield of all (Table 9).

4. Conclusion

Based on the two analyses of AMMI and GGE-bi-plot models, G6 and G3 considered by high yield and more stability, consequently, G6 close to ideal genotype, so this genotype is adaptable to a wide range of environmental conditions. Therefore, G6 was identified as ideal genotypes in terms of yielding ability and stability, tolerant to diseases for advancement, release and use as parents in future breeding programs.

Acknowledgements

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