Genotype x Environment Interaction and Yield Stability of Bread Wheat Genotypes in Oromia, Ethiopia

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Abstract: Bread wheat is one of the most important cereal crops of Ethiopia grown over wider agro- ecologies mainly between 1900 to 3000 above sea level, Study on genotype by environment interaction and stability of 25 bread wheat genotypes was conducted across six locations 2019/2020 main growing season by Alpha lattice design using three replications at six locations in Oromia, Ethiopia. The main objectives of the present study are to interpret genotype main effect and GE interactions obtained by Additive mean-effect and multiplication Interaction analysis and group the genotypes having similar response pattern over all environments. The AMMI analysis also revealed that bread wheat grain yield was significantly affected by the environment at p < 0.01 and explained 82.44% of the total variation. This indicated existence of high variability among the environments. Comparatively, genotype and GEI captured 6.23% and 11.33% of the total variation, respectively. On the other hand, genotypes BW174463, ETBW9193 and ETBW9087 genotypes are located closer to the origin of the biplot, and this implies that these bread wheat genotypes are stable across environments. In the first quadrant genotypes ETBW9066, ETBWBW174459, ETBW9193, ETBW9087, LEMMU and ETBW9185 are positively associated with locations kulumsa, Debre-Zeit, Holeta and Arsi-Robe are considered adaptable. The genotype with low YSI is considered as high yielding and stable genotypes. Accordingly, BW174466, BW174463, ETBW9094, ETBW9315 and, ETBW9089 were the most stable genotypes which were determined by YSI with mean grain yield of 5.33 t/ha, 5.11 t/ha, 5.41 t/ha, 5.14 t/ha and 6.29 t/ha, respectively.

Keywords: Genotype, Environment, GEI, AMMI, IPCA

1. 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 [1]. 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 [2]. Wheat 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 [2].

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 [3]. 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° and 16° N latitude and 35° and 42° E longitude and altitudes ranging is 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 [4]. 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 [5-7]. An understanding of the effects of environment, genotype and Genotype by environment interaction is important at all stages of crop improvement programs as they have crucial effects on selection and cultivar adaptation trials. GEI studies thus provide a basis for selection of genotypes that are suitable for wider or specific cultivation.

They also provide information about the effect of environment on cultivar performance [8]. Further, the yield plateau in wheat productivity is now of great concern. It necessitates the development of high-yielding genotypes with wide or specific (local) adaptation to the environments within a target area [9].

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 [10]. 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 [11-15]. 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 [16]. GEI in multi-environment trials shows differential responses of wheat genotypes across ranges of environments. Grain yield is quantitative in nature and routinely exhibits GEI [17]. The main objectives of the present study are to interpret genotype main effect and GE interactions obtained by AMMI analysis and group the genotypes having similar response pattern over all environments.

2. Materials and Methods

The experiment was conducted during the 2019/20 main cropping season across six locations. The locations were Kulumsa (L1), Bekoji (L2), Assasa (L3), Arsi-Robe (L4), Debre-Zeit (L5) and Holeta (L6). 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.

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

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

Source: Kulumsa Agricultural Research Center, experimental site description, 2013.

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.

Table 2. The Entry code, Genotype code and pedigree selection history of the genotypes were evaluated in the experiment in 2019/20 cropping season at six locations.

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/TNMU/5/TNMU/6/SITE/7/TNMU
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

Entry Code	Genotype code	Pedigree
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//FN/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	FLORKWA-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)

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 weight (TKW) and grain yield per plot.

3. Data Analysis

Analysis of variance (ANOVA) was made for the six locations separately using SAS software and then combined over six locations for all characters since all showed homogeneity of error variance. Prior to running combined analysis of variance, homogeneity of variance was checked using Bartlett's test. ANOVA was carried out using AMMI model to partition the total variance into genotype, environment and genotype by environment interaction, replication within environment and block within replication. The AMMI analysis was performed using the model suggested by [18]. as:

$$Y_{ij} = \mu + G_i + E_j + \Sigma \lambda_n \alpha_{in} \, y_{jn} \, n = 1 + e_{ijk}$$

Where Y_{ij} is the yield of the ith genotype in the jth environment, μ is the grand mean, G_i is the mean of the ith genotype minus the grand mean, E_j is the mean of the jth environment minus the grand mean, λn is the square root of the Eigenvalue of the principal component analysis (PCA) axis, αin and yjn are the principal component scores for PCA axis n of the ith genotype and j^{th} environment and e_{ijk} is the error term.

4. Ammi Stability Value (Asv)

The AMMI stability value (ASV) as described by [19]. Was calculated as follow

$$ASV = \sqrt{\left[\frac{IPCA1_{sumofsquare}}{IPCA2_{sumofsquare}}(IPCA1_{Score})\right]^2 + (IPCA2_{Score})^2}$$

Where, ASV = AMMI stability value.
IPCA1 = the first interaction principal component analysis.
IPCA2 = the second interaction principal component analysis.

SSIPCA1 = sum of square of the first interaction principal component.

SSIPCA2 = sum of square of the second interaction principal component.

$\frac{IPCA1_{sumofsquare}}{IPCA2_{sumofsquare}}$ Is the weight given to the IPCA1-value by dividing the IPCA1 sum of squares by the IPCA2 sum of squares. Larger the IPCA score, either negative or positive, the more indicates more specific adaptation of a genotype to a certain environment. Smaller ASV score for a given genotype indicates that a given genotype has broad adaptation across variable environments.

5. Yield Stability Index (YSI)

The yield stability index was calculated as:

$$YSI = RASV + RGY.$$

Where RASV is the rank of the AMMI stability value and RGY is the rank of the mean grain yield of genotypes across environments.

6. Results and Discussion

AMMI model showed highly significant main effects (P < differences for environment, genotype and their interactions (Table 3). The AMMI analysis also revealed that bread wheat grain yield was significantly affected by the environment at p < 0.01 under (Table 3) and explained 82.44% of the total variation. This indicated existence of high variability among the environments. Comparatively, genotype and GEI captured 6.23% and 11.33% of the total variation, respectively.

Table 3. *Additive mean-effect and multiplicative Interaction analysis of variance for grain yield of 25 bread wheat genotypes across six locations.*

Source of Variation	df	SS	MS	Explained%
Total	449	1594.5	3.55	
E	5	1261.90	252.38**	82.44
G	24	95.35	3.97**	6.23
G x E	120	173.38	1.44**	11.33
IPCA1	28	111.78	3.99**	62.25
IPCA 2	26	46.23	1.78**	25.74
IPCA3	24	14.34	0.60**	7.99
Error	300	63.87	0.21	

The large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing variation in the grain yield of G across E. "Similar result was reported by Mehari. [20]". Additive mean-effect and Multiplicative Interaction model demonstrated the presence of significant GEI and it was partitioned into IPCA. The first three principal component axises (IPCAs) were highly significant (p<0.01) accounting for 62.25, 25.74 and 7.99% of the total variation attributable to GEI, respectively. The Results from AMMI analysis also showed that the first three principal component axes accounted about 96% of the GEI variation. When looking at the environments, it is clear that there is a good variation in different environments. Assasa and Bekoji were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 1). However, due to their large IPCA2 score, genotypic differences observed at these environments may not exactly show the genotypes with average yield over all locations. Closer relationships were observed between Kulumsa, Arsi-Robe, Debre-Zeit and Holeta.
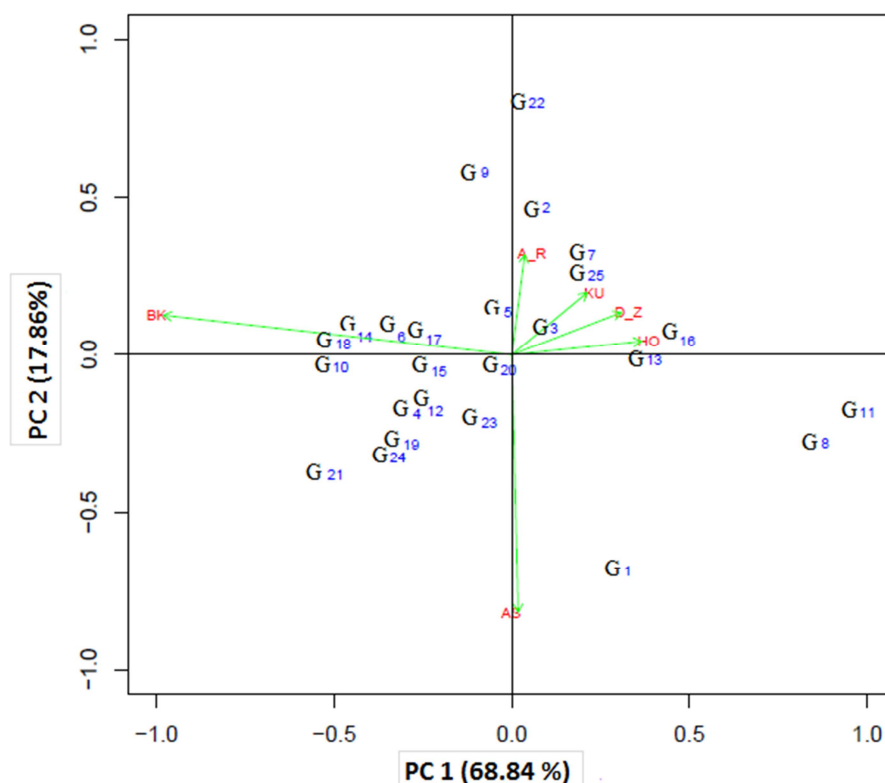
Figure 1. AMMI 2 biplot of IPCA1 against IPCA2 for grain yield of 25 bread wheat genotypes tested across six locations (G stands for genotype as described in Table 2.

G1=WANE, G2=ETBW9185, G3=ETBW9193, G4=ETBW9086, G5=ETBW9087, G6=ETBW9089, G7=ETBW9109, G8=ETBW9284, G9=ETBW9299, G10=ETBW9304, G11=ETBW9313, G12=ETBW9094, G13=ETBW9066, G14=ETBW9102, G15=ETBW9315, G16=BW174459, G17=BW174460, G18=BW174461, G19=BW174462, G20=BW174463, G21=BW174464, G22=BW174465, G23=BW174466, G24=BW174467, G25=LEMMU A-R=Arsi-Robe, AS= Assasa, BK= Bekoji, D-Z=Debre-Zeit, HO=Holeta and KU=Kulumsa).

Closer IPCA Score to Zero, the more adaptable is the genotype across all test locations by [20]. Similarly location scores from AMMI analysis regarding to interaction also interpreted as location with large IPCA scores are more discriminating the genotypes. While locations with low IPCA scores or near zero revealed small interactions with the genotypes and have low discrimination power on the genotypes [21]. Accordingly, genotype BW174465, ETBW9313, ETBW2884 and WANE are considered unstable as they located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores (Figure 1). On the other hand, genotypes BW174463, ETBW9193 and ETBW9087 genotypes are located closer to the origin of the biplot, and this implies that these bread wheat genotypes are stable across environments. The rest of the bread wheat genotypes are unstable as they are located distant from the origin. In the first quadrant genotypes ETBW9066, ETBWBW174459, ETBW9193, ETBW9087, LEMMU and ETBW9185 are positively associated with locations kulumsa, Debre-Zeit, Holeta and Arsi-Robe as indicated by the vector lines and are considered adaptable (Figure 1).

7. Additive Mean-Effect and Multiplicative Interaction Stability Value

Additive mean-effect and multiplication interaction stability values revealed variations in yield stability among

the 25 genotypes (Table 4). According to [22]. The genotype with least ASV score is the most stable across environments and the larger the ASV value, either negative or positive; the more specifically adapted a genotype is to certain environments. Consequently, genotypes with lower ASV values were BW174463, ETBW9087 and BW174466 which are considered more stable than the rest of the genotypes (Table 4). On the other hand, genotypes which showed larger values were unstable, and only adaptable to specific areas. Hence, genotypes with larger ASV values include ETBW9313, ETBW9284, BW174461 and BW174459. Accordingly, these last three genotypes have been picked for the Debre-Zeit, Bekoji and Holeta types of specific environments by AMMI ranking.

Table 4. Mean grain yield, ASV and YSI of 25 bread wheat genotypes across six locations.

SN	Genotype	GY (t/ha)	RGY	RASV	YSI	ASV	IPCA1	IPCA2
1	WANE	4.88	17	19	36	1.36	0.3255	-0.6843
2	ETBW 9185	4.83	19	5	24	0.60	0.0974	0.4707
3	ETBW 9193	4.62	22	4	26	0.39	0.1183	0.0853
4	ETBW 9086	5.08	13	11	24	0.81	-0.2663	-0.1874
5	ETBW 9087	4.92	15	2	17	0.24	-0.0114	0.1342
6	ETBW 9089	6.29	1	15	16	1.05	-0.3100	0.0580
7	ETBW 9109	4.86	18	9	27	0.75	0.2253	0.3179
8	ETBW 9284	4.54	23	24	47	2.82	0.8817	-0.2810
9	ETBW 9299	4.91	16	10	26	0.80	-0.0751	0.5800
10	ETBW 9304	5.58	4	21	25	1.56	-0.4823	-0.0401
11	ETBW 9313	4.25	25	25	50	3.13	1.0000	-0.1819
12	ETBW 9094	5.41	7	7	14	0.63	-0.2156	-0.1790
13	ETBW 9066	4.74	21	17	38	1.25	0.4003	-0.0160
14	ETBW 9102	5.87	2	18	20	1.36	-0.4146	0.0571
15	ETBW 9315	5.14	10	6	16	0.61	-0.2057	-0.0551
16	BW174459	4.92	14	22	36	1.61	0.4933	0.0420
17	BW174460	5.27	9	8	17	0.66	-0.2203	0.0468
18	BW174461	5.54	5	23	28	1.63	-0.4746	0.0335
19	BW174462	5.14	11	13	24	0.83	-0.2835	-0.2860
20	BW174463	5.11	12	1	13	0.09	-0.0095	-0.0487
21	BW174464	5.76	3	20	23	1.56	-0.4958	-0.3819
22	BW174465	4.51	24	14	38	1.02	0.0695	0.8040
23	BW174466	5.33	8	3	11	0.33	-0.0633	-0.2145
24	BW174467	5.43	6	16	22	1.06	-0.3203	-0.3257
25	LEMMU	4.75	20	12	32	0.82	0.2370	0.2520

Note: ASV = AMMI Stability Value, IPCA = Interaction Principal Component Axes, RASV = Rank of ASV, RGY = rank of grain yield of genotypes across environments and YSI = Yield Stability Index.

8. Yield Stability Index (YSI)

Yield stability index (YSI) proposed by [23]. Includes both stability (ASV) rank and combined grain yield rank simultaneously. ASV takes into consideration both IPCA1 and IPCA2 which consider most of the variations in the GE interaction. Therefore, the genotypes with smallest ASV takes the rank one, while the genotype with the highest mean grain yield takes the rank one and then the ranks are summed in a single simultaneous selection index of yield and yield stability called yield stability index (YSI). The genotype with low YSI is considered as high yielding and stable genotypes. Accordingly, BW174466, BW174463, ETBW9094, ETBW9315 and, ETBW9089 were the most stable genotypes which were determined by YSI with mean grain yield of 5.33 t/ha, 5.11 t/ha, 5.41 t/ha, 5.14 t/ha and 6.29 t/ha, respectively. On the other hand, less stable genotypes, also with lower yields were ETBW9313, ETBW9284, ETBW9066, BW174465 and BW174459; these gave 4.25 t/ha, 4.54 t/ha, 4.74 t/ha, 4.51 t/ha and 4.92 t/ha, respectively.

9. Conclusion

Bread wheat genotypes are generally evaluated in multi-environment trials to test their performance across environments and to select the best genotypes for specific environments. The AMMI analysis for the additive main-effect and multiplicative interaction effect revealed significant variance for Genotype, location and genotype by location interaction. Genotypes BW174463, ETBW9193 and ETBW9087 genotypes are located closer to the origin of the biplot, and this implies that these bread wheat genotypes are stable across environments. Some selected genotypes showed similar ranking in different locations while other selected genotypes showed different rankings over different locations. For example, genotypes ETBW9089 ranked first at four of the six environments (Kulumsa, Bekoji, Debre-Zeit and Holeta), and 2nd at Arsi-Robe and 3rd at Assasa. ETBW9102 was picked by the AMMI model as 1st rank at Arsi-Robe and genotype, BW174464 ranked 1st at Assasa. Accordingly, ETBW9089 was 1st at Kulumsa, Bekoji, Debre-Zeit and

Holeta, 2nd at Arsi-Robe and 3rd at Assasa. It showed good performance in grain yield across most locations with variable performances and adaptation under two locations.

Acknowledgements

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