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Research Article

Stability Performance of Bread Wheat (*Triticum aestivum* L.) Genotype for Yield and Yield Components in Oromia, Ethiopia

Berhanu Sime[1]*, Shimelis Tesfaye[2]

[1]Ethiopian Institute of Agricultural Research Center, Ethiopia; [2]Kulumsa Agricultural Research Center, Ethiopia

ABSTRACT

The study of GEI has assumed great importance in genotype testing programs because yield performance of a genotype is a result of the interaction between the genotype and environment. The study cried out with objectives to determine the effect of genotype, environment, and GEI on yield and yield components and to identify stable genotype. Twenty five bread wheat genotypes were evaluated by Alpha Lattice using three replications at six locations in Oromia, Ethiopia. Combined analysis of variance showed very highly significant differences (P<0.01) among environments and among genotypes. Genotype's contribution to variation of some of the traits is equal or more than 30% except NGLS and GY. The contributions of environment to the total sum of squares of treatment is very high for GY and lower for NSLS, NGS, NGSL and TKW traits. Comparatively, contribution of G × E to the total sum of squares of treatment is moderate for NSLS (50.19%), NGSL (52.96%) and TKW (42.93%); relatively lower for NGS (28.32%) and very low proportion to GY (10.4). The biplot of AMMI revealed clear insight into the specific and general adaptation of genotypes across locations. The AMMI biplot, which accounted for 88GY, 72.88TKW, 73.41NGS, 73.67NGSL and 74.19NSLS of the G × E interaction, provides the interaction principal component scores of the 1st and 2nd IPCA. High grain yield was harvested from the advanced genotype ETBW9089 and lowest from ETBW9313.

Keywords: Genotype; GY; TKW; Ethiopia

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 by Mollasadeghi and Shahryari [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 CSA in 2019 [2]. 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 in 2019 [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 by Mulatu in 2015 [3,4]. 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 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 by Bekele et al. [5]. 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 × environment interaction (GEI) as expressed by different authors by Trethowan and Crossa in 2007 [4], Sial et al. [6], Hamam et al. [7]). 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 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 × environment (G × E) interaction by Yan and Kang in 2003 [8]. Though, environment mostly accounts for the major

Correspondence to: Berhanu Sime, Ethiopian Institute of Agricultural Research Center, Ethiopia, Tel: +251223312924; E-mail: birhanume2006@gmail.com

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portion of the total yield variation, only genotype and genotypes × environment interaction are relevant to cultivar evaluation and mega environment classification by Yan et al. [9], Yan [10], Yan and Rajcan [11] Rao et al. [12] and Kaya et al. [13]. Additive Main-effect and Multiplicative Interaction (AMMI) and Genotype main effect and Genotype × 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 × 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. [14]. GEI in multi-environment trials shows differential responses of wheat genotypes across ranges of environments. The main objectives of the present study were to determine the effect of genotype, environment, and GEI on yield and yield components and to identify stable genotype for specific adaptation.

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. 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 × 5 Alpha Lattice design replicated three times during the 2019/20 cropping season. Each treatment was planted on six rows of 2.5 m length with 20 cm 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 yield and yield components 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 AMMI analysis was performed using the model suggested by Crossa et al. [15] as:

$$Y_{ij}=\mu+ G_i+ E_j +\sum_{n=1}^{n}[[\lambda_n \alpha]]_{in} y_{jn}]] + e_{ijk}$$

Where Yij is the yield of the ith genotype in the jth environment, μ is the grand mean, Gi is the mean of the ith genotype minus the grand mean, Ej is the mean of the jth environment minus the grand mean, λn is the square root of the Eigen value of the principal component analysis (PCA) axis αin and yjn are the principal component scores for PCA axis n of the ith genotype and jth environment and eijk is the error term.

RESULTS AND DISCUSSION

Combined analysis of variance for yield and yield components are presented in Table 3. Combined analysis of data over locations revealed significant differences for all traits of the genotypes. Also the G × E interactions was highly significant for all traits except for number of grains per spike which resulted in non-significant difference. Moreover, it should be noted that E × Rep and Blocks × Locations had significant influence on some traits though not on all of them. Generally, the indication is that all or most traits of bread wheat are highly influenced by the environmental factors (Table 3). Alemu et al. [16] reported high environmental variances on agronomic traits of bread wheat. The bread wheat grain yield was significantly affected by environment. It also showed the

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/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
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)

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

Table 3: Combined analysis of variance for yield and yield components.

	Source of variation							
Traits	**Env't (df=5)**	**Rep (Env), df=12**	**BLK(Loc × Rep) df=72**	**G (df=24)**	**G × E (df=120)**	**Error (df=216)**	**Mean**	**CV%**
NSLS	8.71**	1.24ns	0.96ns	9.14**	2.21**	1.01	17.05	5.90
NGS	1004.28**	95.85**	31.61ns	213.92**	33.44ns	29.02	48.92	11.01
NGSL	5.99**	0.14ns	0.13ns	0.40**	0.37**	0.13	3.79	9.35
TKW	393.18**	23.10**	6.87ns	96.84**	26.89**	7.49	35.65	7.68
GY	252.38**	0.32ns	0.27**	3.33**	1.30**	0.19	**5.11**	8.53

CV=Coefficient of Variation; GY=Grain Yield; NGS=Number of Grains per Spike; NSLS=Number of Spikelets Per Spike; NGSL=Number of Grains per Spikelet; TKW=Thousand Kernel Weight.

presence of high genetic variability among the tested genotypes and the inconsistency of their performance over the six locations. This agrees with finding of Temesgen et al. [17], who reported that genotypes had highly significant differences for grain yield across environments. This study showed non-significant G × E interaction differences in number of grains per spike. The results of the present study are in agreement with the findings of Temesgen et al. [17], who reported non-significant differences among bread wheat genotypes for number of grains per spike. The genotypes showed inconsistent performances across the tested environments.

The proportions of sum of squares of different components were determined for the yield traits of bread wheat genotypes (Table 4). Genotype's contribution to variation of some of the traits is equal or more than 30% except NGLS and GY (Table 4). But contribution from the genotype to some of the traits is considerable as in NSLS (41.56%), NGS (35.44%) and TKW (30.92%). The contributions of environment to the total sum of squares of treatment is very high for GY and lower for NSLS, NGS, NGSL and TKW traits (Table 4). Comparatively, contribution of G × E to the total sum of squares of treatment is moderate for NSLS (50.19%), NGSL (52.96%) and TKW (42.93%); relatively lower for NGS (28.32%) and very low proportion to GY (10.4) as indicated in Table 4.

Mean comparison of the genotypes

Grain yield is an important trait in any crop improvement. In this experiment, the highest yielders across environments were ETBW9089 with 6.29 t/ha followed by ETBW9102, BW174464, ETBW9304 and BW174461 with 5.87, 5.76, 5.58 t/ha and 5.54 t/ha, respectively. The check varieties WANE and LEMMU, with 4.88 and 4.75 t/ha, gave lower mean grain yield than the overall grand mean. The lowest mean yield was obtained from ETBW9313 with 4.25 t/ha. Across environments, about 64% and 76% of the advanced genotypes had significantly higher yield than check varieties WANE and LEMMU respectively (Table 5). Higher performances of advanced wheat genotypes than the best check indicates that much progress have been made on wheat improvement. From twenty five genotypes three of them, which means the higher grain yield then the others are ETBW9089, ETBW9102 and BW174464 are recommended to be included in variety verification trials for further release. The advanced genotype, BW174467, had maximum spikelets per spike, while minimum number of spikelets per spike is recorded for WANE over six locations. BW174463 had high number of grains per spike while and ETBW9089 had low mean number of grains per spike over locations (Table 5). This study genotype showed high variability in the number of spikelets per spike and number of grains per spike,

Table 4: Proportion of sum of squares of treatment (G+E+GEI), Genotype, Environment and G × E interaction of studied traits.

Traits	Total treatment	Genotype (G)	Environment (E)	G × E interaction
NSLS	527.60	41.56	8.25	50.19
NGS	14,168.12	35.44	36.24	28.32
NGSL	83.84	11.33	35.71	52.96
TKW	7517.27	30.92	26.15	42.93
GY	1,497.74	5.34	84.25	10.40

GY=Grain Yield; NGS=Number of Grains per Spike; NSLS=Number of Spikelets per Spike; NGSL=Number of Grains per Spikelet; TKW=Thousand Kernel Weight.

Table 5: Mean values of yield and yield components of bread wheat genotypes tested across six locations.

Entry code	Genotype	NSLS	NGS	NGSL	TKW	GY
G1	WANE	16.04h	46.63gj	3.74de	35.50eg	4.88hk
G2	ETBW 9185	17.04df	45.24gj	3.65de	33.89gj	4.83ik
G3	ETBW 9193	16.58fh	45.51gj	3.72de	32.78ij	4.62kl
G4	ETBW 9086	17.86ac	54.25ac	3.83cd	34.56fi	5.08gi
G5	ETBW 9087	17.49be	50.38df	3.77de	35.39eg	4.92hj
G6	ETBW 9089	17.43ce	43.32j	3.66de	42.89a	6.29a
G7	ETBW 9109	16.62fh	47.73ei	3.59e	34.67fh	4.86hk
G8	ETBW 9284	16.97eg	46.72gj	3.73de	32.94hj	4.54l
G9	ETBW 9299	18.07ac	48.53eg	3.57e	35.44eg	4.91hk
G10	ETBW 9304	16.13h	47.08fi	3.84bd	36.83ce	5.58cd
G11	ETBW 9313	18.13ab	44.93hj	3.63de	33.78gj	4.25m
G12	ETBW 9094	16.91eg	46.18gj	3.78de	36.50ce	5.41df
G13	ETBW 9066	16.68fh	46.71gj	3.64de	34.00gj	4.74jl
G14	ETBW 9102	16.12h	55.24ab	4.24a	37.33cd	5.87b
G15	ETBW 9315	16.14h	44.63ij	3.59e	36.94ce	5.14fh
G16	BW174459	17.83ac	47.86ei	3.76de	35.94df	4.92hj
G17	BW174460	17.72bc	54.81ab	4.06ac	38.11bc	5.27eg
G18	BW174461	16.57fh	52.76bd	3.83cd	37.94c	5.54ce
G19	BW174462	16.39fh	52.25bd	3.83cd	37.50cd	5.14fh
G20	BW174463	17.66bd	56.91a	4.02ac	32.67j	5.11gi
G21	BW174464	16.31gh	46.61gj	3.86bd	36.11df	5.76bc
G22	BW174465	17.02df	54.41ac	3.78de	30.11k	4.51lm
G23	BW174466	16.56fh	45.07gj	3.66de	35.50eg	5.33dg
G24	BW174467	18.39a	51.01ce	4.07ab	39.83b	5.43de
G25	LEMMU	17.47ce	48.33eg	3.83cd	34.00gj	4.75jl
	Mean	**17.05**	**48.92**	**3.79**	**35.65**	**5.11**
	Minimum	16.04	46.63	3.57	30.11	4.25
	Maximum	18.39	56.91	4.24	42.89	6.29
	LSD (0.05)	0.66	3.54	0.23	1.80	0.91

Within the same column, values with the same letter are not significantly different, GY=Grain Yield; LSD=Least Significant Difference; NGS=Number of Grains per Spike; NSLS=Number of Spikelet's per Spike; NGSL=Number of Grains per Spikelet and TKW=Thousand Kernel Weight (G).

similar result was found by Ali et al. [18] and Zecevic et al. [19], those investigated that genotype showed high variability in the number of spikelets per spike and number of grains per spike in wheat.

When locations were compared, the high mean grain yields of 7.61 and 7.22 t/ha were obtained at Kulumsa and Assasa, respectively; on the other hand, Debre-Zeit (3.78 t/ha) and Holeta (3.37 t/ha) gave the lowest mean location yields. Relatively, Bekoji (4.11 t/ha) and Arsi-Robe (4.55 t/ha) resulted in moderate grain yield performances (Table 6). High rainfall that occurred at seedling stage of the crop development and water logged condition at Holeta, Debre-Zeit, Bekoji and Arsi Robe when the crop reached knee height resulted in poor stand and low grain yield at the respective locations. On the other hand, Kulumsa and Assasa have obtained relatively high rainfall during the growing season (Table 6). Generally, the grain yield obtained from Holeta, Debre-Zeit, Bekoji and Arsi-Robe were below the overall location mean grain yield (5.11 t/ha), whereas the grain yield of genotypes at Kulumsa and Assasa were better than that at Holeta, Debre-Zeit, Bekoji and Arsi-Robe (Table 6). For most genotypes, the spikelets per spike had high at Bekoji and at Assasa. The highest TKW was obtained from Bekoji, while the lowest was obtained from Holeta (Table 6).

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

AMMI Analysis

The AMMI model showed highly significant main effects (P<differences for environment, genotype and their interactions (Table 7). The AMMI analysis also revealed that bread wheat grain yield was significantly affected by the environment at p<0.01 level (Table 7) 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. In line with the current findings, previous studies also indicated the existence of significant GEI in wheat genotypes and high environmental variation by Mehari et al. [20], Temesgen et al. [17], Kendal and Tekdal [21], Jeberson et al. [22], Mehari et al. [23] and Mizan et al. [24], indicating the challenges presented by GEI in crop breeding. A 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 genotypes across environments. Similar result was reported by Mehari et al. [23].

The AMMI model demonstrated the presence of significant GEI and it was partitioned into IPCA (Interaction Principal Components Axes). 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. 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.

Grain Yield

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 1). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 62.25% and the IPCA2 explained 25.74% and the two IPCs cumulatively captured 88% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Bekoji (BK) and Assasa (AS) were the most discriminating environments as indicated by the long

Table 6: Mean values of Yield and yield components at six locations.

Traits	Kulumsa	Bekoji	Assasa	A-Robe	D-Zeit	Holeta	Mean	LSD (0.05%)
NSLS	17.12	17.39	17.49	16.79	16.67	16.81	**17.05**	0.66
NGS	50.47	52.41	49.83	50.67	47.65	41.97	**48.92**	3.54
NGSL	3.88	3.93	3.92	3.64	4.07	3.29	**3.79**	0.23
TKW	36.00	38.29	35.12	36.99	35.95	31.53	**35.65**	1.80
GY	7.61	4.11	7.22	4.55	3.78	3.37	**5.11**	0.28

GY=Grain Yield; NGS=Number of Grains per Spike; NGSL=Number of Grains per Spikelet; NSLS=Number of Spikelet's per Spike and TKW=Thousand Kernel Weight.

Table 7: AMMI 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	
Environment (E)	5	1261.90	252.38**	82.44
Genotype (G)	24	95.35	3.97**	6.23
Interactions (G × 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	

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

distance between their marker and the origin (Figure 1). Closer relationships were observed between Kulumsa (KU), Arsi-Robe (AR) and Holeta (HO). Genotypes ETBW9313, BW174465, ETBW 9284 and WANE were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9193, BW174463 and ETBW 9087 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 1).

Thousand Kernel Weight

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 2). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 39.49% and the IPCA2 explained 33.39% and the two IPCs cumulatively captured 72.88% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Kulumsa, Arsi-Robe and Holeta were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 2). Genotypes ETBW 9066, BW174464 and ETBW9185 were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The BW174461 and ETBW9087 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 2).

Number of grains per spike

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 3). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 45.2% and the IPCA2 explained 28.21% and the two IPCs cumulatively captured 73.41% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Arsi-Robe (A-R) was the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 3). Genotypes ETBW9086, ETBW9284 and BW174465 were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9185, BW174459 and BW174466 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 3).

Number of spikelets per spike

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 4). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 47.82% and the IPCA2 explained 26.37% and the two IPCs cumulatively captured 74.19% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Assasa (AS) was the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 4). Genotypes BW174465, BW174467, ETBW9089 and LEMMU were unstable as they were located far apart from the other genotypes in the biplot when plotted on

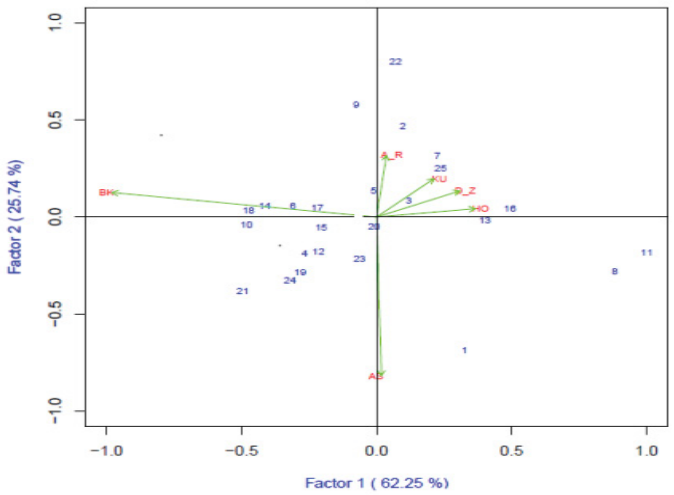

Figure 1: AMMI 2 Biplot of IPCA 1 against IPCA 2 for Grain Yield of 25 bread wheat genotypes tested across six locations (A-R=Arsi-Robe, AS=Assasa, BK=Bekoji, HO=Holeta, D_Z=Debre-Zeit and KU=Kulumsa).

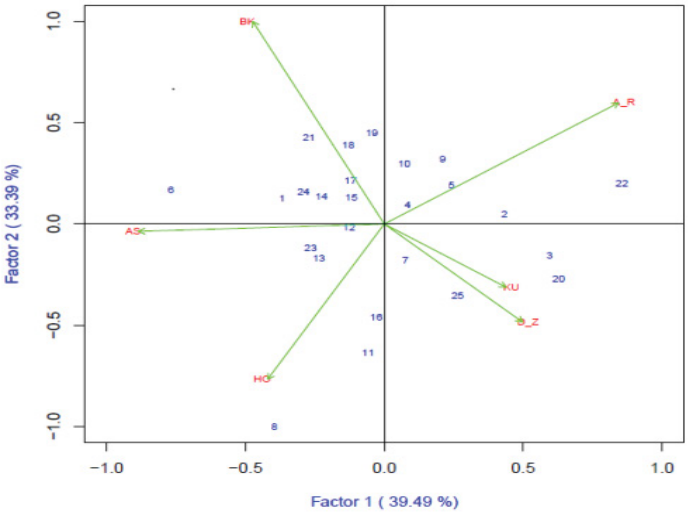

Figure 2: AMMI 2 Biplot of IPCA 1 against IPCA 2 for Thousand kernel weight of bread wheat genotypes tested across six locations (A-R=Arsi-Robe, AS=Assasa BK=Bekoji, HO=Holeta, D_Z=Debre-Zeit and KU=Kulumsa).

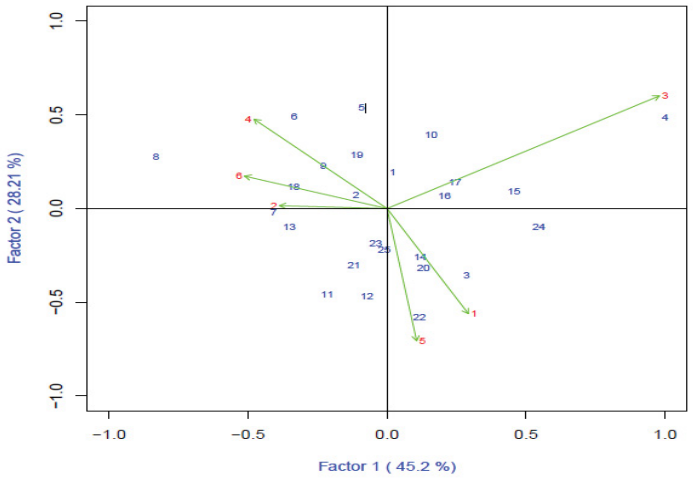

Figure 3: AMMI 2 Biplot of IPCA 1 against IPCA 2 for Number of Grains per Spike of bread wheat genotypes tested across six locations (1=Kulumsa, 2=Bekoji, 3=Arsi-Robe, 4=Assasa 5=Holeta and 6=Debre-Zeit).

the IPCA1 and IPCA2 scores. The ETBW9284, ETBW9066 and BW174463 were genotype located near to the origin of the biplot

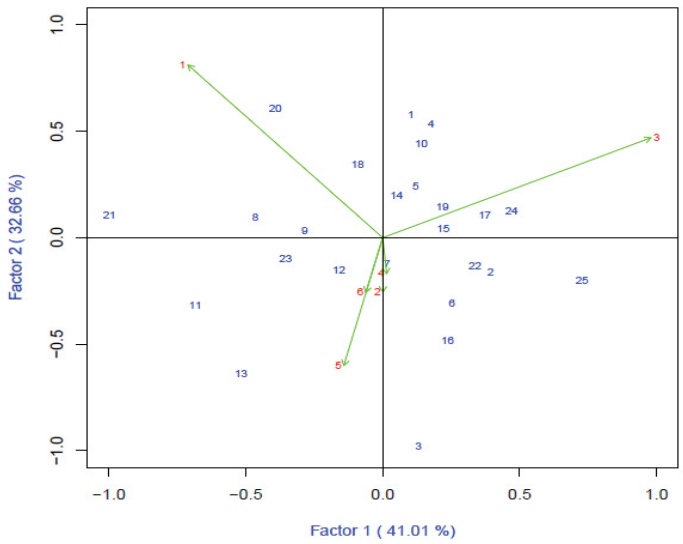

Figure 4: AMMI 2 Biplot of IPCA 1 against IPCA 2 for Number of Grains per Spikelets of bread wheat genotypes tested across six locations (1=Kulumsa, 2=Bekoji, 3=Arsi-Robe, 4=Assasa, 5=Holeta and 6=Debre-Zeit).

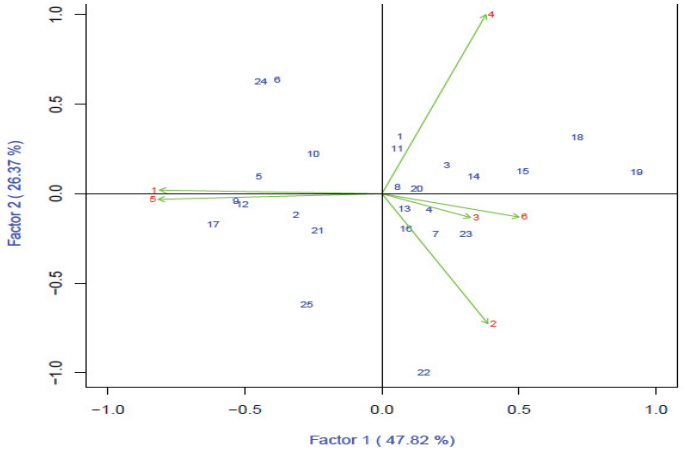

Figure 5: AMMI 2 Biplot of IPCA 1 against IPCA 2 for Number of spiklets per spike of bread wheat genotypes tested across six locations (1=Kulumsa, 2=Bekoji, 3=Arsi-Robe, 4=Assasa, 5=Holeta and 6=Debre-Zeit).

which implies that they were stable bread wheat genotypes across environments (Figure 4).

Number of grain per spikelets

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 5). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 41.01% and the IPCA2 explained 32.66% and the two IPCs cumulatively captured 73.67% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Kulumsa (KU) and Arsi-Robe (A-R) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 5). Closer relationships were observed between Bekoji (BK), Assasa (A-R) and Debre-Zeit (D-Z). Genotypes ETBW9193, ETBW9066 and BW174464 were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9109 and ETBW9315 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 5).

CONCLUSION

Genotype × environmental interaction is an important consideration in plant breeding programs because it reduces the progress from selection in any one environment. Crop breeders have been striving to develop genotypes with superior grain yield and yield components over a wide range of different environmental conditions. The Genotype's contribution to variation of some of the traits is equal or more than 30% except NGLS and GY. The contributions of environment to the total sum of squares of treatment is very high for GY and lower for NSLS, NGS, NGSL and TKW traits. Comparatively, contribution of G × E to the total sum of squares of treatment is moderate for NSLS (50.19%), NGSL (52.96%) and TKW (42.93%); relatively lower for NGS (28.32%) and very low proportion to GY (10.4). The biplot of AMMI revealed clear insight into the specific and general adaptation of genotypes across locations. The AMMI biplot, which accounted for 88 GY, 72.88 TKW, 73.41 NGS, 73.67 NGSL and 74.19 NSLS of the G × E interaction, provides the interaction principal component scores of the 1st and 2nd IPCA. High grain yield was harvested from the advanced genotype ETBW9089 and lowest from ETBW9313. The advanced genotype, BW174467, had maximum spikelets per spike, while minimum number of spikelets per spike is recorded for WANE over six locations. BW174463 had high number of grains per spike while and ETBW9089 had low mean number of grains per spike over locations. This study genotype showed high variability in the number of spikelets per spike and number of grains per spike .

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