Analysis of Genotype by Environment Interaction for Agronomic Traits of Bread Wheat (*Triticum aestivum* L) Genotypes in Oromia, Ethiopia

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Abstract: Twenty five bread wheat genotypes were tested in 2019/20 cropping season across six environments viz Kulumsa, Bekoji, Assasa, Arsi-Robe, Debre-Zeit and Holeta in alpha lattice design replicated trice. The study cried out with objectives to determine the effect of genotype, environment, and GEI on agronomic traits and to identify stable genotype for specific adaptation. Data was collected for yield and component traits and subjected to different statistical procedures. ANOVA revealed highly significant differences (p < 0.01) among 25 genotypes for grain yield and other studied traits. Combined ANOVA depicted highly significant differences among environments. Genotype ETBW9089 ranked first in mean grain yield in four of the six environments. It showed highest mean grain yield of 9.03 t/ha at Kulumsa, and also showed highest yield (4.00 t/ha) in the lowest yielding environment, Holeta. The proportions total sum of squares for genotype, environment and GEI for grain yield were 5.34%, 84.25% and 10.40%, respectively. Having the largest proportion of sum of squares, the environment had the highest impact on genotype yield performance. The combined ANOVA obtained from AMMI model showed highly significant differences for environment, genotype and GEI. The combined results showed that bread wheat grain yield was significantly affected by the environment (p < 0.01) which explained 82.44% of the total variation, indicating that the environments were highly variable. While genotype and GEI captured 6.23% and 11.33% of the total sum of squares, respectively. The AMMI model demonstrated the presence of significant GEI. The first and second IPCA were highly significantly (p < 0.01) contributed for 88% of the GEI of which PC1 and PC2 accounted for 62.25% and 25.74%, respectively of the variations explained by GEI. Considering both ranks of ASV and grain yield using yield stability index (YSI), BW174466 followed by BW174463) and ETBW9094 were stable genotypes. The results of AMMI's first four selection of genotypes per environments and GGE-biplot revealed that ETBW9089 is an ideal and promising genotype across most test environments. Moreover, Bekoji was the best discriminating environment to screen bread wheat genotypes. ETBW9089 genotype is suggested to be further evaluated for commercial release.

Keywords: Genotype, DH, SL, TKW, Grain Yield

1. Introduction

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]. 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 [2].

Bread 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 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 [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 GEI is important at all stages of crop improvement programs as they have crucial effects on selection and cultivar adaptation trials. Genotype x environment interaction studies thus provides 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 [8]. 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 [9-13]. 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, W. N. *et al.* [14]. 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 [15]. Therefore, GEI has become the major concern in plant breeding for two main reasons; first, it reduces progress from selection of cultivar and second, it makes cultivar recommendation difficult because it is statistically impossible to interpret the main effects [16].

In case of wheat, several environmental factors such as temperature, precipitation and its distribution during the growing season, sowing time, soil type, and nitrogen fertilization influences its yield and associated components [17]. Some genotypes are characterized by a stable performance while others vary considerably with the environment [18]. The main objectives of the present study were to determine the effect of genotype, environment, and GEI on agronomic traits and to identify stable genotype for specific adaptation.

2. Materials and Methods

2.1. Description of the Study Areas

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.

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°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

2.2. 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 Center.

Table 2. 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.

2.3. Experimental Design and Field Management

The trials were planted 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. It used 150kg/ha amount of Seed rate. 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.

2.4. Statistical Analysis

The agronomic traits 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. Agronomic traits data was subjected to combined ANOVA and AMMI analysis. 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 [19] as:

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

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, λ_n is the square root of the Eigen value of the principal component analysis (PCA) axis α_{in} and y_{jn} are the principal component scores for PCA axis n of the ith genotype and j^{th} environment and e_{ijk} is the error term.

3. Results and Discussions

Combined analysis of data over locations revealed significant differences for all traits of the genotypes (Table 3). Also the Genotype by Environment interactions was highly significant for all traits. Moreover, it should be noted that E x Rep and Blocks x Locations had significant influence on some traits though not on all of them (Table 3). Generally, the indication is that all or most traits of bread wheat are highly influenced by the environmental factors (Table 3). [20] Reported high environmental variances on agronomic traits of bread wheat.

The bread wheat grain yield was significantly affected by environment. It also showed the presence of high genetic variability among the tested genotypes and the inconsistency of their performance over the six locations. This agrees with finding of [21] who reported that genotypes had highly significant differences for grain yield across environments.

Table 3. Combined analysis of variance for phenological traits, growth characters, yield and yield components.

Source of variation							Mean	CV%
Traits	Env't (df=5)	Rep (Env), df=12	BLK (Loc x Rep) df=72	G (df=24)	G x E (df=120)	Error (df=216)		
DH	4696.30**	6.27ns	6.25ns	146.40**	21.20**	7.51	69.05	3.97
SL	33.24**	0.68**	0.34*	3.51**	0.68**	0.22	8.05	5.85
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; DH = days to heading; GY = grain yield; SL= spike length; TKW = thousand kernel weight.

The proportions of sum of squares of different components were determined for the 25 agronomic traits of bread wheat genotypes (Table 4). The environment contributed total treatment sum square more than 79% in DH and 50% SL. These traits were determined mainly by the environment. Genotype's contribution to variation of some of the traits is equal or less than 11.89% as in DH, and GY (Table 4). But contribution from the genotype to some of the traits is considerable as in SL (25.4%) and TKW (30.92%). G x E contributed less than 42.93% to the total treatment sum of square in DH (8.63%), LS (24.46%), GY (10.40%) and TKW (42.93%). The contribution of environment to the total sum of squares of treatment is very high for DH, and GY; moderate for SL, and lower for TKW traits (Table 4). Comparatively, contribution of G x E to the total sum of squares of treatment is moderate for TKW (42.93%); relatively lower for SL (24.46%) and very low proportion to DH and GY as indicated in Table 4.

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

Traits	Total treatment	Genotype (G)	Environment (E)	G x E interaction
DH	29,539.28	11.89	79.49	8.61
SL	331.56	25.40	50.13	24.46
TKW	7517.27	30.92	26.15	42.93
GY	1,497.74	5.34	84.25	10.40

Remark: Description of Abbreviation is given under Table 3.

3.1. Mean Comparison of the Genotypes

Genotypes showed variation for days to heading ranged from 65.06-76.00 days with a mean of 69.05 days. Among the genotypes, ETBW9094 was early to heading which took 65.06 days while LEMMU was late heading which took 71.17 days. The released variety was late headed when compared to 23 advanced genotypes. The result showed that the presence of wide range of variations among the genotypes for days to heading and days to maturity. This result is agreed with the finding of [22] those shown that between the different wheat genotype there was a significant difference on the number of days to heading and days to maturity. Tested genotypes also showed variation for spike length. Spike length ranged from 6.59-9.13cm across environments. The released variety WANE had shorter (6.59cm) mean spike length while ETBW9299 had longer (9.13cm) mean spike length (Table 5).

Similarly, [20] reported the presence of highly significant variations among wheat genotypes for spike length.

Table 5. Mean values of DH, 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

3.2. Difference Between Environments

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 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. 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 heading date was early at Debre-Zeit (54.33 days) and late at Bekoji (89.33 days). Genotypes

headed and matured early at Debre-Zeit as a result of high growing temperatures. Most genotypes matured very late at Bekoji due to the cooler climatic conditions (Table 1). The environments were diverse and caused the greatest variation in agronomic traits. They had high spike length at Kulumsa and highest TKW was obtained from Bekoji, while the lowest was obtained from Holeta (Table 6).

3.3. Ammi Analysis

The results of AMMI model for yield and yield components are presented in Table 3. As it can be seen from the table, the mean square of the two IPCA were highly significant ($p<0.01$). The AMMI biplot, which accounted for 82.27 DH, 66.85 SL, 88 GY, and 72.88 TKW of the G x E interaction, provides the interaction principal component scores of the 1st and 2nd IPCA.

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

Remark: Description of Abbreviation is given under Table 3. G stands for genotype and description of abbreviations on genotypes is presented in Table 2.

Table 6. *Mean values of agronomical traits at six locations.*

Traits	Kulumsa	Bekoji	Assasa	A-Robe	D-Zeit	Holeta	Mean	LSD (0.05%)
DH	72.88	82.93	68.00	61.19	63.24	66.04	69.05	1.80
SL	9.16	8.05	8.29	7.87	6.89	8.25	8.05	0.31
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

Remark: Description of Abbreviation is given under Table 3.
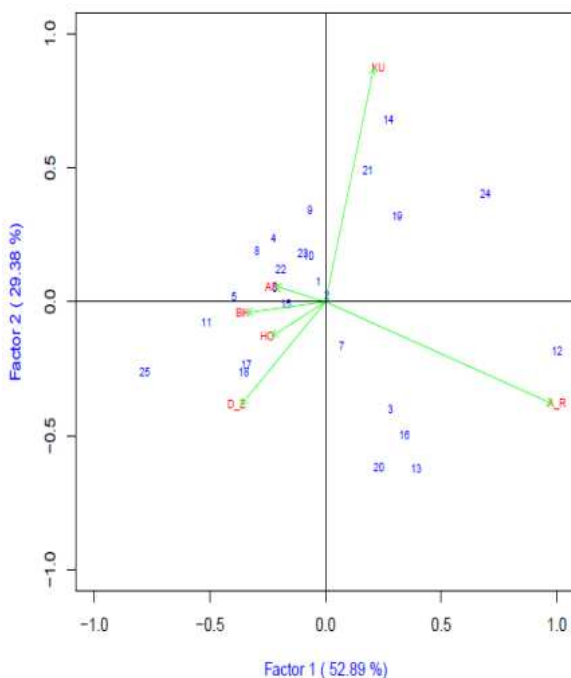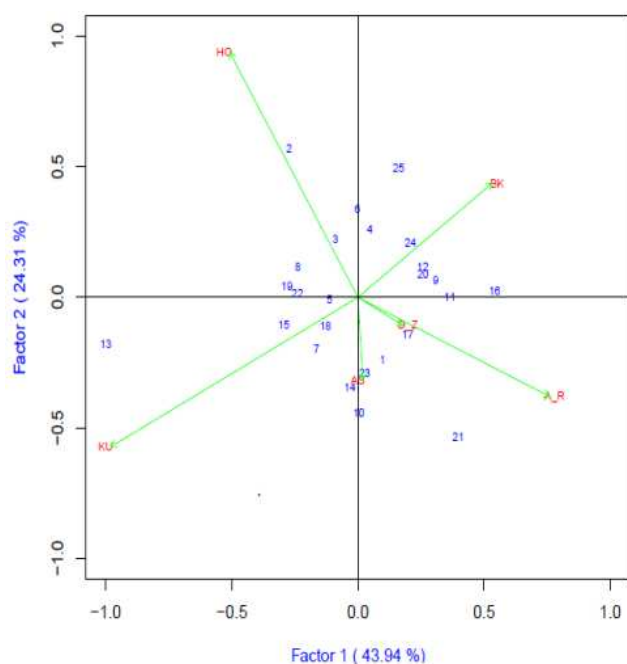
3.4. Days to Heading

Figure 1. *AMMI 2 Biplot of IPCA 1 against IPCA 2 for Days to heading 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).*

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for days to heading (Figure 1). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 52.89% and the IPCA2 explained 29.38% and the two IPCs cumulatively captured 82.27% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Arsi-Robe (A_R) and Kulumsa (KU) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 1). Assasa (AS), Bekoji (BK), Debre-Zeit (D_Z) and Holeta (HO) were least discriminating environments. Genotypes ETBW 9066, BW174463, BW174459, LEMMU, ETBW 9094 and BW174467 were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The WANE and ETBW 9109 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 1).

3.5. Spike Length

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for spike length (Figure 2). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 43.54% and the IPCA2 explained 24.31% and the two IPCs cumulatively

captured 66.85% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Holeta (HO) and Kulumsa (KU) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 2). Bekoji (BK), Arsi-Robe (A-R), Assasa (AS) and Debre-Zeit (D_Z) were least discriminating environments. Genotypes ETBW9066, BW174464, ETBW9304, LEMMU, 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 ETBW9087 and BW174461 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 2).
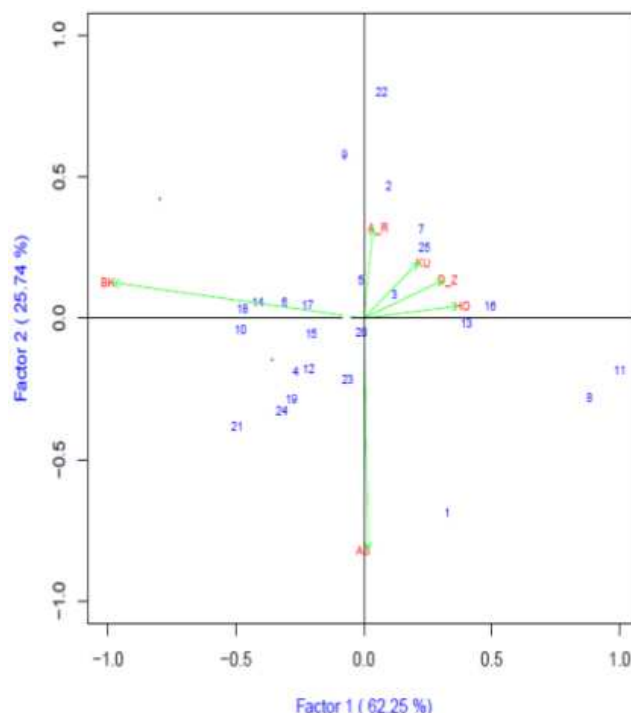

Figure 2. AMMI 2 Biplot of IPCA 1 against IPCA 2 for Spike length of 25 bread wheat genotypes tested across six locations (A-R=Arsi-Robe, AS=Assasa BK=Bekoji, HO=Holeta, D_Z=Debre-Zeit and KU=Kulumsa).
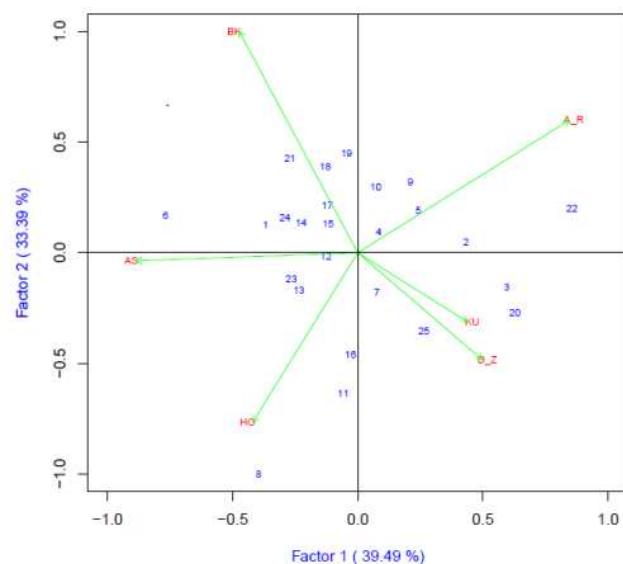
3.6. Grain Yield

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield (Figure 3). 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 distance between their marker and the origin (Figure 3). Closer relationships were observed between Kulumsa (KU), Arsi-Robe (AR) and Holeta (HO). Genotypes ETBW 9313, 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 ETBW 9193, 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 3).

Figure 3. AMMI 2 Biplot of IPCA 1 against IPCA 2 for Grain Yield of 25 wheat genotypes tested across six locations (A-R=Arsi-Robe, BK=Bekoji, HO=Holeta, D_Z=Debre-Zeit and KU=Kulumsa).

Figure 4. AMMI 2 Biplot of IPCA 1 against IPCA 2 for Thousand kernel weight of 25 bread bread wheat genotypes tested across six locations (A-R=Arsi-Robe, AS=Assasa AS=Assasa, BK=Bekoji, HO=Holeta, D_Z=Debre-Zeit and KU=Kulumsa).

3.7. Thousand Kernel Weight

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 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 4). Genotypes ETBW 9066, BW174464 and ETBW 9185 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 ETBW 9087 were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 4).

4. Conclusion

Genotype x environment 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 significant GEI indicated that performance of the genotypes in agronomic was not consistent over environments; some genotypes performed well at some locations but poorly at other locations. The environment contributed total treatment sum square 79.49 in DH, 50.13 in SL, 26.15 in TKW and 84.25 in GY. These traits were determined mainly by the environment. Genotype contributed less than (12%) to total treatment sum square in all traits except in SL (25.40) and TKW (30.92). G x E contributed less than 25% to total treatment sum square except in TKW (42.93). The biplot of AMMI revealed clear insight into the specific and general adaptation of genotypes across locations. The AMMI biplot, which accounted for 82.27 DH, 66.85 SL, 88 GY and 72.88 TKW of the G x 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.

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