Genotype X Environment Interaction and Stability of Drought Tolerant Bread Wheat (*Triticum Aestivum* L.) Genotypes in 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 1800 to 2500 above sea level, Study on genotype by environment interaction and stability of 20 bread wheat genotypes was conducted across nine locations in 2017 main growing season in a randomized complete block design with three replications. The objectives of this study were to determine the magnitude of GEI for yield and yield components and to identify genotypes for specific or wider adaptation for grain yield under drought prone conditions of Ethiopia. Strong significant environment, genotype and GEI effects were recorded and environment captured the largest portion of the total sum of squares for all of the measured traits, which reveals the influence of the environment in evaluating the genotypes. The maximum mean grain yield value of genotypes due to the mean effect of the environment was obtained from G9 (4.36 ton ha-1) followed by G14 (4.00 ton ha-1) and G17 (3.93 ton ha-1) whereas the least mean grain yield was obtained from G11 (2.48 ton ha-1). The multiplicative variance of the treatment sum of squares due to GEI was partitioned into five significant interaction principal component axes. Cumulatively the two significant IPC explained 68.4% for grain yield. The AMMI1 biplot revealed G12, G17, G15 and G6 were stable genotype across locations. Dhera, Maichew and Korem for grain yield were favorable testing locations. Based on AMMI2 G17 for grain yield were stable genotypes. Kulumsa was the most discriminating environments for grain yield. Considering AMMI Stability Value (ASV), yield stability index (YSI)genotype G17 was the most stable genotypes for grain yield*

Keywords: *AMMI, ASV, Biplot.*

1. INTRODUCTION

Bread wheat is one of the most important cereal crops of Ethiopia grown over wider agro-ecologies mainly at mid and high land areas, commonly known as the east African wheat-belt (Dawit*et al*., 2017). Variations in soil and climate conditions have resulted insignificant variation in yield and yield components of bread wheat, and thus genotype x environment interaction is an important issue facing bread wheat breeders (Mohammadi *et al.*, 2012). In multi-location field experiment a significant G x E interaction reduces the correlation between phenotypic and genotypic values as well as the progress from selection. Plant breeders usually evaluate a series of genotypes across environments before a new improved genotype is released for production (Erkul *et al*., 2010; Kusaksiz and Dere, 2010). A crop is considered the most favorable one if it has a high mean yield and a consistent performance when grown across diverse locations and years. Therefore, identification of genotype(s) that perform consistently across environments should be emphasized.

The genotype by environment interaction (GEI), defined as the variation in relative performance of genotypes in different environments (Cooper and Byth, 1996). In the absence of GEI, the superior genotype in one environment may be regarded as the superior genotype in all, whereas the presence of the GEI confirms particular genotypes being superior in particular environments. Therefore, knowledge of the pattern and magnitude of GEI and stability analysis is important for understanding the response

of different genotypes to varying environments and for identification of stable and widely adapted and unstable but specifically adapted genotypes for countries like Ethiopia where environmental variations are very high and unpredictable (Tesfaye *et. al*., 1998).If GEIs are present, breeders need to identify stable genotypes with relatively consistent performance across a range of environments. Usually a combined analysis of variance is used to identify the presence of GE interaction from replicated multi-environment trials.

Stable yield performance of genotypes under both favorable and drought conditions is vital for plant breeders to identify drought tolerant genotypes. In order to reduce the effect of G x E interaction, crop improvement programs usually run performance trials across a wide range of environments to ensure that the selected genotypes have a high and stable performance across several environments. Stability of yield of a cultivar across a range of production environments is very important for variety recommendation. The cultivars must have the genetic potential for superior performance under ideal growing conditions, and must produce acceptable yields under less favorable environments. In Ethiopia, various studies have been conducted to analyze the effect of GEI on bread wheat varieties. However, the changing environmental conditions of Ethiopia, the expansion of bread wheat to new agro-ecologies coupled with inadequate bread wheat varieties available for the different environments necessitate a rigorous and continuous study of G x E interaction for a dynamic crop improvement program.

Several statistical methods have been proposed to investigate genotype by environment interactions. Among these AMMI is commonly used method in plant breeding for the analysis of genotype by environment interaction (Zobel *et al*., 1988). AMMI model is a hybrid model combine's analysis of variance for the genotype and environment main effects and principal components analysis of the genotype by environment interaction. Lack of high yielding varieties adapted to diverse agro- ecological conditions and limitation of information on GEI of bread wheat genotypes in Ethiopia is the major reason of low productivity. Therefore, this study was conducted to determine the magnitude of genotype by environment interaction for yield and yield components and to identify genotypes adapted to a specific or wider adaptation of bread wheat genotypes for grain yield.

2. MATERIALS AND METHODS

2.1. Description of the Study Sites

The experiment was conducted during the 2017 main cropping season at nine rainfed locations. These locations represent the main multi-location variety testing sites for the national bread wheat improvement program for drought stress agro-ecologies i.e., (Alem Tena, Dhera, Maichew Mekan, Mekelle,Minjar and Mainebri) and for optimum agro-ecology i.e.,(Korem and Kulumsa) of Ethiopia. Description of testing locations is provided in (Table 1).

Table1. *Description of Study Sites*

Location	Altitude	Geographical position		Rainfall (mm)	Soil type/texture
		latitude	Longitude		
Kulumsa	2200	08º 01'00''N	39º 09'32'	820	Luvisols
Korem	2490	12º30'21''N	39º 31'22'E	946	Vertisols
Maichew	2419	12o46'47''N	39º32'23''E	657	Vertisols
Mekan	2423	12º44'N	39º 32'	485	Vertisols
AlemTena	1611	08º30'N	38º95'E	728	Haplic andosol
Dhera	1660	08º20'N	39º19'E	680	Andosol
Mekelle	1970	13º14'N	39º 32'E	453.3	Cambisol
Minjar	1810	08º55''N	39º45	867	Vertisols
Mainebri	NA	NA	NA	NA	NA

Source:KARC,DZARC and MARC, NA= not available

2.2. Experimental Materials

Eighteen bread wheat genotypes selected based on their drought performance from moisture stress trials, which was conducted at were agricultural reach center and two standard check varieties were included in this study. Description of bread wheat genotype is provided in (Table 2).

Table2. *Pedigree of the 20 Bread Wheat Genotypes*

Genotype	Pedigree
G1	WBLL1*2/BRAMBLING//ZAFIR-3
G2	CHAMRAN/4/OPATA/BOW//BAU/3/OPATA/BOW/5/SAMIRA-9
G3	CHAMRAN/4/OPATA/BOW//BAU/3/OPATA/BOW/5/SAMIRA-9
G4	ATTILA//PSN/BOW/3/ATTILA/4/ETBW 4919/5/LEITH-1
G5	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/NESMA*2/14-2//2*SAFI-3
G6	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/QAFZAH-4/3/VEE#7//MT773/EMU'S'
G7	RABIH-10/ETBW 4922//KAUZ'S'/FLORKWA-1
G8	THELIN/WAXWING//ATTILA*2/PASTOR/3/INQALAB91*2/TUKURU 9Y-0B
G9	MEX94.27.1.20/3/SOKOLL//ATTILA/3*BCN/4/ZAFIR-3
G10	WBLL1*2/BRAMBLING//ZAFIR-3
G11	QAFZAH-19//HI1077/SR25/3/QADANFER-4
G12	22SAWSN - 142/ETBW 4921/6/HPO/TAN//VEE/3/2*PGO/4/MILAN/5/SSERI1
G13	SHARP/3/PRL/SARA//TSI/VEE#5/5/VEE/LIRA//BOW/3/BCN/4/KAUZ/6/HUBARA-5
G14	SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA//PSN/BOW/3/ATTILA
G15	KAUZ//MON/CROW?S?/3/VEE/PJN//2*KAUZ
G16	SERI.1B//KAUZ/HEVO/3/AMAD/4/ATTILA//PSN/BOW/3/ATTILA
G17	SERI.1B//KAUZ/HEVO/3/AMAD/4/ESDA/SHWA//BCN
G18	KAUZ/FCT//ETBW 4920/3/MILAN/PASTOR
G19	OGOLCHO (CHECK)
G20	KINGBIRD (CHECK)

2.3. Experimental Design and Field Management

The field experiment was laid out in randomized complete block design (RCBD) with three replications in all locations. Each experimental plot had six rows of 2.5 m long spaced 20 cm apart with a plot area of 1.2 m x 2.5 m (3 m^2).The data was collected from the four middle rows. The seed rate was maintained at 150 Kg ha^{-1} .The fertilizer was applied at a rate of 100 kg ha^{-1} DAP and 100 kg ha^{-1} of Urea. Urea was applied at planting and tillering time (top dressing). Weeds grown in the plots were removed manually starting from 2-3 weeks after sowing.

2.4. Data Collection

Data on the following Morpho-agronomic traits were collected:

- **Days to Heading (DH)**

The number of days from date of sowing to 50% of the stand in a plot is headed and 75% of the spikes have fully emerged.

- **Days to Maturity (MD)**

The number of days from sowing to the stage when 75% of the stand in a plot have reached physiologically maturity and ripe, i. e., when the peduncles were turned yellow.

- **Grain-Filling Period (GFP)**

The number of days from heading to maturity, i.e. the number of days to maturity minus the number of days to heading.

- **Plant Height (PH)**

The average height of five (5) plants in cm from ground level to the tip of the spike excluding the awns, at maturity was measured.

- **Spike Length (SL)**

The average spike length in cm measured at physiological maturity on five (5) random samples taken from each genotype.

- **Number of Spikelet per Spike (NSS)**

The average number of spikelets per spike counted from main tiller of each of the spike of five (5) randomly selected plants.

- **Number of kernels per spike (NKS)**

The average number of kernels per spike counted from main tiller of each of the spike of five (5) randomly selected plants.

- **Effective Tillers**

The average number of effective tillers counted from five (5) randomly selected plants was recorded at physiological maturity.

- **Thousand- Kernel Weight (TKW)**

The grain weight (g) of 1000 seeds sampled at random from total grain harvest of the experimental plot was recorded, when 12.5% of moisture content and measured by using sensitive balance.

- **Grain Yield (YLD)**

The grain yield per plot was measured in grams using sensitive balance after moisture of the seed is adjusted to 12.5%. Total dry weight of grain was harvested from the middle four rows and were converted to tonnes per hectare

- **Above Ground Biomass Yield (BY)**

Was determined as the weight (grams) of the biomass yield from a plot and converted to tonnes per hectare.

- **Harvest index (HI)**

Was determined as ratio of grain yield per hectare to total biological yield per hectare.

2.5. Data Analyses

Different statistical software packages were used to analyze the data; combined analyses of variance and mean comparison with LSD test were done using the General Linear Model (GLM) procedure of the Statistical Analysis System (SAS) software 9.0 (SAS Institute Inc., 2002). The chi-square test for homogeneity of variances was significant; however no site has a CV value that is greater than 20% so that all nine sites are included in the combined analysis of variance. The additive main effect and multiplicative interaction (AMMI) analysis and was performed using GEA-R software version 4.0. AMMI analysis

The Additive Main effect and Multiplicative Interaction (AMMI) model analysis was performed for grain yield and above ground biomass yield. The AMMI model equation is given as*:*

$$y_{ij} = \mu + G_i + E_j + (\sum K_n V_{ni} S_{nj}) + Q_{ij} + e_{ij}$$

Where,

y_{ij} = is the observed yield of genotype i in environment j, μ = is the grand mean, G_i= the additive effect of the ith genotype (genotype means minus the grand mean), E_j=is the additive effect of the jth environment (environment mean deviation), K_n= is the eigenvalues of the PCA axis n, V_{ni} and S_{nj} = are scores for the genotype **i** and environment **j** for the PCA axis n, Q_{ij} = is the residual for the first n multiplicative components, e_{ij} = is the error

AMMI stability value (ASV)

The AMMI stability value (ASV) as described by Purchase *et al*. (1997) was calculated as follows:

$$ASV = \sqrt{\left[\left[\frac{IPCA\ 1\ Sum\ of\ squares}{IPCA\ 2\ Sum\ of\ squares}(IPCA\ 1\ scores)\right]^2 + [IPCA\ 2\ scores]^2\right]}$$

Where;

ASV= AMMI stability value, IPCA1 = interaction principal component analysis 1, IPCA2 = interaction principal component analysis 2, SSIPCA1 = sum of square of the interaction principal component one and SSIPCA2 = sum of square of the interaction principal component two.

2.6. Yield Stability Index (YSI) Analysis

The yield stability index was calculated using the following formula: YSI = RASV + R, where RASV is the ranking of the AMMI stability value and RY is the rank of the genotypes based on yield across environments.(Mkumbira *et al.*, 2003). YSI incorporates both mean yield and stability in a single criterion. Low values of both parameters show desirable genotypes with high mean yield and stability (Olivera *et al.*, 2014;).

3. RESULTS AND DISCUSSION

3.1. Combined Analysis of Variance

The combined analysis of variance (Table3) revealed that main effects of genotype (G), environment (E), and G × E interaction were highly significant (P ≤ 0.01) for all traits.The significant interactions of genotypes × environments suggest that agronomic traits of the genotypes varied across the tested environments. These results were in agreement with the works of Mohammadi *et al.* (2011) who reported for thousand- kernel weight, plant height, days to heading and days to maturity. Alemu*et al.*(2018) also reported similar results for all of these traits except for the productive tiller number.The significant difference of genotypes, environments and their interactions was attributed to variations in different climatic and edaphic conditions across the locations.

The total sum of squares was partitioned into components to estimate the magnitude of GEI. For all measured traits, the explained percentage sum of square for environments took the largest portion, accounting 48.39% to days to maturity to 90.86% for plant height of total variance (Table 3). 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 and the measured agronomic traits contributing in large to the genotype by environment interaction. In this regard, for grain yield environments took the largest portion (72.07%), followed by GEI which had (20.91 %). Environment and GEI together captured the largest portion of the total sum of squares (92.98%). The partitioning of total sum of squares indicated that the environment effect was a predominant source of variation followed GEI and genotype effect.This result was in agreement with the reports of Somayeh *et al.*(2019). Delacy *et al.* (1996) also indicated that environment and interaction effects are much more than the effects of the genotypes in most variety trials. It is clearly seen that the contribution of environmental variation to the sum of squares is considerable, and this means that the environment in which the experiments was undertaken were significantly different.

In the case of grain filling period, plant height, spike length, spikelets per spike, thousand- kernel weight, above ground biomass yield and harvest index, environments took the largest portion (67.54,90.86,64.55,53.63,68,67.4 and 68.35%,respectively) followed by GEI (19.5,4.88,21.67,28.37, 22.91, 24.22 and 27.30%, respectively)(Table 3).While in the case of days to heading, days to maturity and kernels per spike environments took the largest portion (71.60, 48.39 and 85.65%, respectively) followed by genotype (15.32, 28.88 and 11.81%, respectively). This result was in agreement with the reports of Alemu *et al.* (2018) in bread wheat and Tadele *et al.* (2016) in barley.

Mean comparison for the tested genotypes (Table 4) indicated that the environmental mean grain yield varied from the lowest 1.47 ton ha^{-1} at Mainebri to highest 5.07 ton ha^{-1} at Dhera. Thus, the variations among the testing environments revealed the existence of considerable variability for wheat production in the drier parts of the country. Moreover, the presence of interaction effect would imply inconsistent response of genotypes across the test environments. The maximum mean grain yield value of genotypes due to the mean effect of the environment was obtained from G9 (4.36 ton ha^{-1}) followed by G14 (4.00 ton ha^{-1}) and G17 (3.93 ton ha^{-1}) whereas the least mean grain yield was obtained from G11 (2.48 ton ha^{-1}). The significant GEI could be due to rank changes of the genotypes across the environment, and /or due to change of magnitude in the differences between the genotypes over the Environment. However, Yan *et al.* (2000) reported that selection of best lines both for specific and wide adaptation based on the mean results was misleading.

Table3. *ANOVA of Morphological Traits between Genotypes (G), Environment (E) and GE Interaction for 20 Bread Wheat Genotypes Across Nine Location*

Triat		HD		MD		GFP		PHT	
Source of variation	df	MS	Percent	MS	Percent	MS	Percent	MS	Percent

Environment(E)	8	3174.35**	71.60	1828.32**	48.39	1929.36**	67.54	16460.6**	90.86
Genotype (G)	19	285.92**	15.32	459.38**	28.88	35.69**	2.97	324.68**	4.26
GxE interactions	152	30.53**	13.08	45.2**	22.73	44.35**	29.50	46.52**	4.88
Trait		SL		NSS		NKS		TKW	
Source of variation	df	MS	Percent	MS	Percent	MS	Percent	MS	Percent
Environment(E)	8	50.68**	64.55	153.38**	53.63	3128.19**	85.65033	2492.51**	68.00
Genotype (G)	19	4.55**	13.77	21.68**	18.00	431.36**	11.8107	140.25**	9.09
GxE interactions	152	0.89**	21.67ns	4.27**	28.37	92.73**	2.53ns	44.2**	22.91
Trait		GY		BY		HI			
Source of variation	df	MS	Percent	MS	Percent	MS	Percent		
Environment(E)	8	89.04**	72.08	500.15**	67.14	4071.62**	68.35		
Genotype (G)	19	3.64**	7.01	27.08**	8.63	108.95**	4.3		
GxE interactions	152	1.36**	20.91	9.5ns	24.22	85.77**	27.30ns		

** Highly significant at 1% level of probability, ns: non-significant, DH: days to heading, DM: days to maturity, GFP: grain filling period, PHT: plant height, SL: spike length: NSS: spikelets per spike NKS: kernels per spike, TKW: thousand- kernel weight, GY: grain yield, BY: above ground biomass yield and HI: harvest index.

Table4. *Mean Grain Yield (Ton Ha-1) of 20 Bread Wheat Genotypes across Nine Different Test Locations*

Genotype	Alem Tena	Dhera	Korem	Kulumsa	Maichew	Mekan	Mekelle	Mainebri	Minjar	Mean
G1	2.52[e]	4.74[a-f]	5.26[a]	5.60[a]	5.06abc	4.34[def]	1.19[ijk]	2.04[d]	3.39[b]	3.79
G2	3.63[bcd]	5.57[a-d]	3.01[f]	3.63[gh]	3.48ef	3.77[f]	2.05[e-h]	0.86[ij]	3.85[ab]	3.32
G3	3.42[bcd]	4.61[def]	3.30[ef]	4.69[bcd]	4.61a-d	4.69[c-f]	1.76[fgh]	0.87[ij]	2.95[bc]	3.44
G4	3.30[cde]	5.40[a-d]	4.84[ab]	5.34[ab]	4.85a-d	4.38[def]	1.84[fgh]	0.74[ij]	3.58[ab]	3.81
G5	2.86[ed]	5.59[a-d]	5.25[a]	4.56[cde]	4.77a-d	4.49[c-f]	1.65[ghi]	0.87[ij]	3.60[ab]	3.74
G6	3.80[abc]	5.04[a-e]	4.49[a-e]	4.67[bcd]	4.32b-e	5.20[bcd]	1.25[ijk]	1.20[fg]	3.39[b]	3.71
G7	3.68[bc]	4.62[c-f]	4.68[a-d]	1.40[j]	3.92de	5.46[abc]	1.85[fgh]	0.76[ij]	3.77[ab]	3.35
G8	3.66[bcd]	5.54[a-d]	3.73[b-f]	3.70[fgh]	3.45ef	4.63[abc]	2.34[cde]	2.48[b]	3.46[b]	3.67
G9	4.51[a]	5.85[a]	3.52[c-f]	5.76[a]	4.61a-d	4.55[c-f]	3.68[a]	3.13[a]	3.60[ab]	4.36
G10	4.14[ab]	5.16[a-e]	4.46[a-e]	3.31[ih]	4.20b-e	5.23[a-d]	2.90[b]	1.38[f]	3.11[bc]	3.77
G11	3.31[cde]	3.44[g]	3.48[def]	0.77[j]	2.54f	3.82[ef]	1.20[ijk]	0.68[j]	3.07[bc]	2.48
G12	3.89[abc]	3.64[fg]	4.22[a-f]	3.93[e-h]	4.23b-e	4.55[c-f]	2.19[def]	2.15[cd]	4.37[a]	3.69
G13	3.65[bcd]	4.66[b-f]	4.70[a-d]	4.60[cde]	4.68a-d	3.93[ef]	2.13[d-g]	1.71[e]	3.44[b]	3.72
G14	3.55[bcd]	5.61[a-d]	4.28[a-e]	4.80[bc]	4.61a-d	4.76[c-f]	2.60[bcd]	2.39[b]	3.41[b]	4.00
G15	3.63[bcd]	5.16[a-e]	4.75[abc]	4.05[d-g]	5.23ab	5.98[a]	1.16[jk]	1.16[g]	3.52[ab]	3.85
G16	4.53[a]	5.26[a-e]	4.73[abc]	2.81[i]	5.55a	6.21[cde]	1.05[k]	0.94[hi]	3.90[ab]	3.89
G17	3.79[abc]	5.75[ab]	4.73[abc]	4.40[c-f]	4.64a-d	4.79[bcd]	2.74[bc]	0.76[ij]	3.79[ab]	3.93
G18	3.23[cde]	4.26[efg]	3.66[b-f]	4.79[bc]	4.66a-d	5.16[bcd]	2.34[cde]	2.34[bc]	3.87[ab]	3.81
G19	3.46[bcd]	5.74[abc]	4.39[a-e]	2.59[j]	4.13cde	4.75[c-f]	1.81[fgh]	1.74[e]	3.17[b]	3.53
G20	3.59[bcd]	5.69[a-d]	3.90[b-f]	2.80[i]	3.94de	4.82[cde]	1.57[hij]	1.11[gh]	3.74[ab]	3.46
Mean	3.61	5.07	4.27	3.91	4.37	4.78	1.96	1.47	3.55	3.66

3.2. AMMI Analysis

The results of AMMI model for grain yield is presented in (Table 5). The classical analysis of variance showed that the GEI was significant. So the multiplicative variance of the treatment sum of squares due to GEI was further partitioned by principal component analysis. The ordination technique revealed significant differences for IPC1, IPC2 and IPC3, IPC4 and IPC5. The first interaction principal component (IPC1) captured 42.81% of the variability in the genotype by environment interaction and the second interaction principal component explained 25.59 %, cumulatively the two significant interaction principal components explained 68.4%. Many researchers witnessed that the best accurate AMMI model prediction can be made using the first two IPCA (Yan *et al*., 2000).Similar findings have been reported in previous studies(Bavandpori *et al*., 2015; Melkamu *et al*., 2015).

Table5. *Analysis of the Multiplicative Model Using Principal Components*

Source of variation	df	MS	Percent	Accumulated
Genotype	19	3.64**	7.01	7.01
Environment	8	89.04**	72.08	79.09

Interactions	152	0.89**	21.67	100
IPC1	26	3.40**	42.81	42.81
IPC2	24	2.20**	25.59	68.4
IPC3	22	1.11**	11.79	80.19
IPC4	20	0.79**	7.61	87.8
IPC5	18	0.64*	5.56	93.36
IPC6	16	0.46[ns]	3.56	96.93
IPC7	14	0.26[ns]	1.79	98.72
IPC8	12	0.2204[ns]	1.28	100
Residuals	102	0.64		
Error	342	0.34		
Total	539	2.07		

*, significant at 5% ; **, highly significant at 1% probability level; ns, non-significant

3.3. AMMI1 Biplot

AMMI1 biplot is glance for displaying genotype main effect and interaction effect of the genotype and environment simultaneously. The closeness between pairs of environments or pairs of genotypes in the biplot is proportional to the response they have to the genotype by environment interaction effects (Crossa *et al.*,1990). X-axis is designated for mean grain yield while Y-axis for IPCA1 scores (Figure 1). This biplot helped in the interpretation of the interaction effects among genotypes and environments, and in the assessment of the adaptability of genotypes.

The Genotypes of G8, G12, G2, G17, G15 and G6 were located near to the origin with lower contribution to the magnitude genotype by environment interaction, implying that these genotypes were stable, however, G8 and G2 did not perform well, whereas G12, G17, G15 and G6 had high grain yield (Figure 1). Genotypes that are characterised by means greater than grand mean and the IPCA scores nearly zero are considered as generally adaptable to all environment. However, the genotype with high mean performance and with large value of IPCA scores are considered as having specific adaptability to the environments. In this case, G9 and G16 were specifically adapted genotypes. Similarly Muez and Assefa (2018)used this model to assessthe adaptability of bread wheat genotypes.

Genotypes or locations located in the right side of the midpoint of the perpendicular line have higher yields than those on the left side; hence, genotypes G9, G10,G14,G16,G2,G17,G6,G5,G18,G4 and G1 were higher grain yielder genotypes while genotypes G7, G11, G20,G19, G2 and G3 were genotypes with lower grain yield.

The testing locations, Dhera, Maichew, Korem and Kulumsa were favorable testing location located to the right side of the grand mean whereas testing locations Mekelle, Mekan, Mainebri, Minjar and Alem Tena were unfavorable testing location placed to the left side of the perpendicular line (Figure 5.1). The testing location Mainebri, Mekelle and Mekan were located distant from the origin implying the testing locations had higher contribution to the magnitude of GEI and caused unstable genotype performance.The testing locations Minjar, Korem and Maichew were nearly placed to the origin with lower contribution to GEI and implying the testing locations had less contribution to the genotype by location interaction and contributes to the stable performance of the genotypes. The genotypes G9 and G14 had higher mean grain yield under environment Maichew and Kulumsa, hence they were the best adaptedgenotypes for these locations. Crossa (1990) also indicated that Genotype and location combinations with IPCA1 scores of the same sign produced positive specific interaction effects; whereas combinations of opposite sign had negative specific interactions.
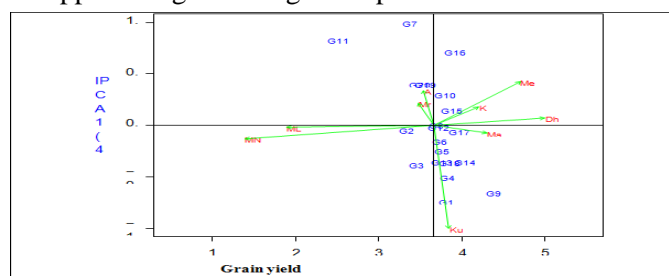

Figure1: *AMMI1 Biplot Of IPCA 1 Against Grain Yield for 20 Bread Wheat Genotypes Tested Across Nine Locations (AT: Alem Tena, DH: Dhera, K: Korem, Ku: Kulumsa Ma: Maichew, MN: Mainebri, Me: Mekan, ML: Mekelle And Mr: Minjar).*

3.4. AMMI2 Biplot

The AMMI2 biplot for grain yield was presented in Figure(2). De Oliveira et al. (2014) pointed out that the stability information that is drawn using AMMI2 biplot is more precise than AMMI1 biplot because AMMI2 model contains information from IPCA1 and IPCA2.The AMMI2 analysis positioned the genotypes in to different locations, indicating the interaction pattern of the genotypes. Kulumsa was the most discriminating environments for grain yield as indicated by the long distance from the origin whereas the testing locations Dhera and Minjar with short vector length indicated the less discriminating power of genotypes. Genotypes or environments, which are very close to the vertex are more stable than those genotypes or environments away from the vertex. Accordingly, G17 was stable for grain yield across locations whereas G9, G11, G7, G1 and G16 were unstable as they were located far apart from the other genotypes in the biplot (Figure2).
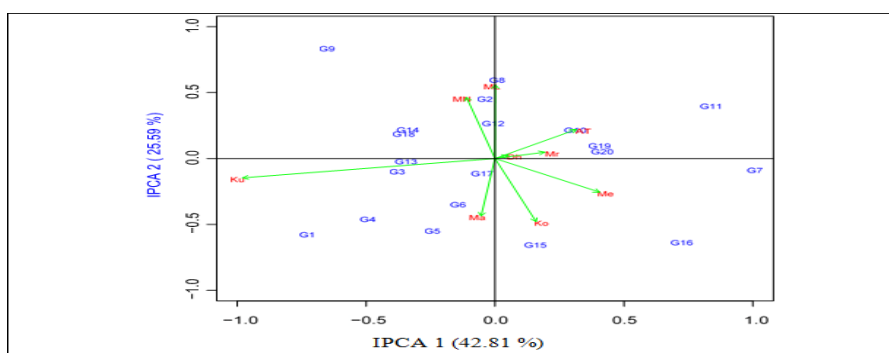

Figure 2: *AMMI 2 Biplot of IPCA 1 Against IPCA 2 for Grain Yield of 20 Bread Wheat Genotypes Tested Across Nine Locations (AT: Alem Tena, Dh: Dhera, Ko: Korem, Ku: Kulumsa Ma: Maichew, MN: Mainebri, Me: Mekan, ML: Mekelle And Mr: Minjar)*

3.5. AMMI Stability Value (ASV)

The interaction principal component one (IPCA1) scores and the interaction principal component two (IPCA2) scores in the AMMI model are indicators of stability. The AMMI stability value (ASV) is a balanced measure of stability (Purchase, 1997). Genotypes with lower ASV values is considered more stable and genotypes with higher ASV are unstable. According to the ASV (Table 6) G17 was the most stable with ASV value of (0.11) followed by genotype G12 (0.28), G6 (0.35) and G14 (0.36). G7(3.62) and G13(2) were the most unstable genotypes for grain yield. The stable genotypes (G17,G12, G6 and G14) was followed with mean grain yield above the grand mean and this result was in agreement with Bavandpori *et al.*(2015) and Melkamu *et al.*(2015) who has used ASV as one method of evaluating grain yield stability of bread wheat varieties.

3.6. Yield Stability Index (YSI) Analysis

The yield stability index method incorporates both yield and stability into a single index, reducing the problem of using only yield stability as the sole criterion to select genotypes. Genotypeswith lower YSI are desirable since they combine high mean yield performance with stability, Based on the YSI (Table 6), genotypes G17, G14, 16, 18 and 10 were selected as the most stable varieties combining high grain yield performance with stability, hence these can be selected to advanced yield trials for wide adaptable variety development. Although genotypes G9 and G15 were high yielding genotypes had high ASV scores resulting in high YSI scores, however, they can be recommended for specific environments where they performed well. This method has been successfully used in wheat (Farshadfar et al., 2011).

Table4. *Mean Grain Yield, AMMI Stability Value and Yield Stability Index for the 20 Bread Wheat Genotypes Tested Across Nine Locations*

	Mean	RY	ASV	RASV	YSI	Rank
G1	3.79	7	1.01	16	23	10
G2	3.32	18	0.46	8	26	11
G3	3.44	16	0.80	15	31	14
G4	3.81	6	0.69	13	19	9
G5	3.74	9	0.56	9	18	8

G6	3.71	11	0.35	3	14	6
G7	3.35	17	3.62	20	37	16
G8	3.66	13	0.61	10	23	10
G9	4.36	1	0.62	11	12	4
G10	3.77	8	0.42	5	13	5
G11	2.48	19	1.25	18	37	16
G12	3.69	12	0.28	2	14	6
G13	3.72	10	2.01	19	29	13
G14	4.00	2	0.36	4	6	2
G15	3.85	5	0.64	12	17	7
G16	3.89	4	0.45	7	11	3
G17	3.93	3	0.11	1	4	1
G18	3.81	6	0.43	6	12	4
Ogolcho	3.53	14	0.79	14	28	12
Kingbird	3.46	15	1.02	17	32	15

REFERENCES

[1] Alemu, G., Mohammed, H., and Asnake, D. 2018. Analysis of genotype by environment interaction for agronomic traits of bread wheat (*Triticum aestivum* L.) genotype in Ethiopia. *Journal of Agricultural Research*, 3(8):000191.

[2] Bavandpori, F., Ahmadi, J. and Mohssen, S.H. 2015. Yield stability analysis of bread wheat lines using AMMI model. Agricultural Communications, 3(1):8-15.

[3] Cooper, M. and Byth, D.E. 1996. Understanding plant adaptation to achieve systematic applied crop improvement-a fundamental challenge, in: M. Cooper, G.L. Hammer (Eds.), plant adaptation and crop improvement, CABI Publishing, Wallingford, pp 5-23.

[4] Crossa, J. 1990. Statistical analysis of multi-location trials. Advances in Agronomy, 44:55-85.

[5] Crossa, J., H.G. Gauch and R.W. Zobel. 1990. Additive main effect and multiplicative interaction analysis of two international maize cultivar trials. Crop Science, 30:493-500.

[6] Dawit Asnake, Zerihun Tadesse, Habtemariam Zegeye and Alemayehu Assefa. 2017. Seasonal variablity and genetic response of elite bread wheat lines in drought prone environments of Ethiopia. Journalof Plant Breeding and Genetics, 5(1):15-21.

[7] DeLacy, I.H., Basford, K.E., Kooper, M., Bull, J.K. and McLaren, C.G. 1996. Analysis of multi environment trials - An historical perspective. In: Cooper, M. and Hammer, G.L. (Eds.). Plant Adaptation and Crop Improvement, 39-124.

[8] De Oliveira, E.J., de Freitas, J.P.X. and de Jesus, O.N. 2014. AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. Scientia Agricola, 71(2):139-145.

[9] Erkul, A., Ünay, A. and Konak, C. 2010. Inheritance of yield and yield components in a bread wheat (Triticum aestivum L.) Cross. Turkish Journal of Field Crops, 15(2):137-140.

[10] Farshadfar, E., Mahmodi, N.and Yaghotipoor, A.2011. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (TriticumaestivumL.), Australian Journal of Crop Science, 5(13):1837-1844.

[11] Kusaksiz, T. and Dere, S. 2010. A study on the determination of genotypic variation for seed yield and its utilization through selection in durum wheat (Triticum durum Desf.) mutant populations. Turkish Journal of Field Crops, 15(2):188-192.

[12] Melkamu Temesgen, Sentayehu Alamerew, Firdissa Eticha and Muez Mehari. 2015. Genotype x environment interaction and yield stability of bread wheat genotypes in south east Ethiopia. World Journal of Agricultural Sciences, 11(3):121-127.

[13] Mohammadi, R., Armion, M., Sadeghzadeh, D., Amri, A. and Nachit, M. 2011. Analysis of Genotype by environment interaction for agronomic traits of durum wheat in Iran. *Plant Production Science*, 14:1, 15-21.Mohammadi, M., Karimizadeh, R., Hooseinpou, T., Falahi, H.A., Khanzadeh, H., Sabaghnia,

[14] N., Mohammadi, P., Armion, M. and Hosni, M.H. 2012. Genotype x environment interaction and stability analysis of seed yield of durum wheat genotypes in dryland conditions. Notulae Scientia Biologicae, 4(3):57- 64.

[15] Muez Mehari and Assefa Workineh. 2018. Adaptation study and genotype by environment interaction of bread wheat genotypes in Tigray, North Ethiopia.Basic Research Journal of Agricultural Science and Review, 6(2):09-14.

[16] Mkumbira, J., Mahungu, N.M. and Gullberg, U. 2003. "Grouping locations for efficient cassava evaluation in Malawi," Experimental Agriculture, 39(2):167–179.

[17] Olivera, E.J., Frietas, J.P.X. and Jesus, O.N. 2014. AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. Scientia Agricola, 71 (2):139-145.

[18] Purchase, J.L. 1997. Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. Ph.D. Thesis, Department of Agronomy, Faculty of Agriculture of the University of the Free State, Bloemfontein, South Africa.

[19] SAS Institute. 2002. Statistical Analysis Software version 9.0 Cary, NC,SAS Institute Inc USA.

[20] Somayeh, S. Ghasem, M. and Babak, N. 2019. Yield stability in bread wheat germplasm across drought stress and non stress conditions. Agronomy Journal, 111(1):175-181.

[21] Tadele Tadesse, Amanuel Tekalign, Gashaw Sefera and Behailu Muligeta. 2016. AMMI model for yield stability analysis of linseed genotypes for the highlands of Bale, Ethiopia. Plant, 5(6)93-98.

[22] Tesfaye Tesema., Seifu Tsegaye., Getachew Belay., Efrem Bechere. and Demissie Mitiku.1998. stability of performance of wheat landraces in Ethiopian highland. Euphytica, 102:301-308.

[23] Yan, W., Hunt, L.A., Sheng, Q. and Szlavnics, Z. 2000. Cultivar evaluation and mega environment investigation based on the GGE biplot. Crop Science, 40:597-605.