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Stability Performance of Bread Wheat (*Triticum aestivum* L) Genotype for Yield Related Traits

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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 agronomic traits and to identify stable genotype. Fifteen bread wheat genotypes were evaluated by RCBD using four replications at six locations in Ethiopia. Combined analysis of variance showed very highly significant differences (P<0.001) among environments and among genotypes. The GEI was also significant for all agronomic except for tiller number. The Genotype main effect was not significant for grain per spike and tiller number. 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 environments contributed total treatment sum square 80-90% in TILL and BIO, 70-80% in PHT and HI. These traits were determined mainly by the environment. Other yield and yield components contributed 20-60% total sum square of environments. Genotype contributed less than 10% to total treatment sum square in all traits except in GYLD (33.46), HLW (20.4), TKW (38.0) and HI (12.9%). GxE contributed less than 10% to total treatment sum square in BIO. It contributed 10-20% in PHT, TILL and HI, 20-30% in HLW, 30-40% in GYLD, TKW and GNO. The biplot of AMMI revealed clear insight into the specific and general adaptation of genotypes across locations. The AMMI biplot, which accounted for 80.71 PHT, 65.52 TILL, 78.81 GNO, 82.9 BIO, 78.53 HI, 70.1 TKW, 68 HLW and 74.7% GYLD of the GxE interaction, provides the interaction principal component scores of the 1st and 2nd IPCA. High grain yield was harvested from the advanced genotype ETBW9470 and lowest from ETBW8075. The advanced genotype ETBW8427was the tallest genotype and ETBW8078was found to be the shortest plant height. The maximum fertile tiller numbers were obtained from advanced genotype ETBW8070 and minimum tiller number was obtained from the advanced genotype ETBW9464. Advance genotypes ETBW9037 had high number of grain per spike and ETBW8075had low mean number of grains spike^{-1} over locations. Advanced genotype ETBW8070 had high biomass yield over the location and ETBW8075 had low biomass yield. Maximum harvest index was observed for ETBW9470, while minimum harvest index noticed for ETBW8075.

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Keywords

Genotypes, HLW, TKW

Introduction

Bread wheat (*Triticum aestivum L.*), a self-pollinating annual plant in the true grass family Gramineae is extensively grown as staple food sources in the world (Mollasadeghi and Shahryari (2011). Wheat is an important and most widely cultivated food crop in the world and quantity produced is more than that of any other crop, feeding about 40% of the world population. This crop played a central role in combating hunger and improving the global food security. The grains of this plant provide about 20% of all calories and proteins consumed by people on the globe (Shiferaw*et al*.2013).Bread wheat (*Triticum aestivum L.*) and durum wheat (*T. turgidum spp*, *durum* L.) are the two major species of wheat cultivated in Ethiopia. Ethiopia is the first largest wheat producer in sub-Saharan Africa and wheat is one of the major crop among cereals. The current total area devoted to wheat production in Ethiopia is estimated to be over 1.6 million hectare (13% of national cereal acreage); fourth in area coverage and third in amount of grain production (4.2 million tons) following maize and teff (CSA, 2014).

Superior genotypes must be evaluated on the basis of multi-environment trials (MET) and multiple traits to ensure that the selected genotypes have acceptable performance in variable environments within the target region. For this reason, MET are conducted throughout the world for major crops every year in which multiple traits and characteristics are usually recorded (Yan and Rajcan, 2002). Improvement of agronomic traits has been the primary objective of breeders/agronomists for many years under variable environments. Breeders have also measured and selected for grain yield and most related traits such as kernel weight, plant height, and other related traits (Maman *et al.*, 2004). All these traits are affected by the growing environment as well as by genetic factors, and numerous studies have described the genotype-by-environment (GE) interactions (Doehlert *et al.*, 2001). However, evaluation of genotypes across diverse environments and over several years is needed in order to identify spatially and temporally stable genotypes that could be recommended for release as new cultivars and/or for use in the breeding programs (Sharma *et al.*, 2010).

GEI refers to different ranking of genotypes across environments and may complement the selection process and recommendation of a genotype for a target environment (Gauch, 2006). It may also reduce the selection efficiency in different breeding programs because in a GEI, measured traits are less predictable and cannot be interpreted using main effects (genotype or environment) and need more analysis (Gauch *et al.*, 2008). GEI is also one of the most important reasons for the failure or decreased efficiency of breeding efforts to serve small resource poor farmers in different areas (Mitrovic *et al.*, 2012). Plant breeders perform multi-environment trials (MET) to select favourable genotypes based on both mean yield and performance stability and to determine whether a test environment is homogeneous should be divided into various mega-environments (Gauch, 2006).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.

Materials and Methods

Experimental materials and design

Thirteen advanced bread wheat genotype and two recently released varieties were evaluated across six locations in 2017 / 2018 main cropping seasons. Description of test locations and wheat genotype is provided in Table 1 and 2, respectively

The field experiment was laid out in RCBD with four replications. The experimental field plot was 6 rows of 2.5 m long with a 0.2 m inter-row spacing. Each plot was planted at a rate of 150 kg ha^{-1}. The fertilizer application and other crop management practices were done as per recommendations of each test locations. Weeds grown in the plots were removed manually starting from two weeks after sowing.

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 spikelet per spike, plant height, number of tiller per plant, spike length, biomass yield, TKW, HLW and grain yield per plot.

Statistical analysis

The agronomic traits data for fifteen 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 Crossa *et al.,* (1990) 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 i^{th} genotype in the j^{th} environment, μ is the grand mean, $G_i$is the mean of the i^{th} genotype minus the grand mean, E_j is the mean of the j^{th} 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 i^{th} genotype and j^{th} environment and e_{ijk} is the error term.

Results and Discussions

Combined analysis of variance for agronomic traits over locations

Combined ANOVA depicted highly significant differences among environments and among genotypes except, for grain per spike and tillers plant^{-1} which were non-significant for the genotypes (Table 3). This indicated that agronomic traits of bread wheat were highly influenced by environmental factors. These results were in agreement with the works of Desalegn (2012) and Demelsah *et al.,* (2013) who reported high environmental variance for the agronomic traits. Mohamed and Ahmed (2013.) and Melkamu *et al.,* (2015) reported that 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 Temesgen *et al.,* (2015) who reported that genotype was highly significant difference for grain yield. Similarly Melkamu *et al.,* (2015) reported that the bread wheat genotypes had a wider genetic variability for the entire traits. The present study showed that non-significance difference in number of tiller per plant among tested genotypes. The results of the present study are agree with the findings of Khan (2013) who reported non-significant differences among bread wheat genotypes for number fertile tillers per plant in bread wheat. The GxE interaction was also highly significant for all traits except for tiller number plant^{-1}(Table 3). This result is in agreement with the findings of Trakanovas and Ruzagas, (2006) and Temasgen *et al.,* (2015) who reported that the GEI was highly significant reflecting the differential response of genotypes in various environments.

The proportions of sum of squares of different components were determined for the 15 agronomic traits of bread wheat genotypes (Table 4). The environments contributed total treatment sum square 80-90% in TILL and BIO, 70-80% in PHT and HI. These traits were determined mainly by the environment. Other yield and yield components contributed 20-60% total sum square of environments. Genotype contributed less than 10% to total treatment sum square in all traits except in GYLD (33.46), HLW (20.4), TKW (38.0) and HI (12.9%). GxE contributed less than 10% to total treatment sum square in BIO. It contributed 10-20% in PHT, TILL and HI, 20-30% in HLW, 30-40% in GYLD, TKW and GNO. G, E and GxE had similar effect on GYLD and TKW. Both G and GxE had moderate contribution to the determination of HI and HLW although the environment contributed more than 50% to total treatment sum square of these traits. GxE was more important in the determination of agronomic traits; its contribution was always higher than the contribution of the genotype.

Mean comparison in agronomic traits

Tested genotype showed variation for yield and yield components. High grain yield was harvested from the advanced genotype ETBW9470 followed by the advanced genotype ETBW8070 and Hiddase. The low yield was obtained from the genotype ETBW8075 only two advanced genotype were greater than the released varieties in grain yield across environments. These two advanced genotype ETBW9470 and ETBW8070 are recommended to be included in variety verification trials

for further release. The advanced genotype ETBW8427was the tallest genotype and ETBW8078was found to be the shortest plant height (Table 5). The maximum fertile tiller number were obtained from advanced genotype ETBW8070 and minimum tiller number was obtained from the advanced genotype ETBW9464 (Table 5). With regard to tiller number about 53.33% of the genotypes exceeded the overall mean (5.11 tiller plant^{-1}) of the genotypes while, advanced genotypes exceeded 40% and 80% of the released variety Lemu and Hidasse respectively. Similar results were reported by several investigators (Desalegn, 2012; Degewione *et al.,* 2013; Wani *et al.,* 2013). These authors reported the presence of highly significant variation among the studied wheat genotypes for plant height.

Advance genotypes ETBW9037 had high number of grain per spike and ETBW8075had low mean number of grains spike^{-1} over locations (Table 5). This study genotype showed high variability in the number of grains per spike. These result was in agreement with those obtained by (Ali *et al.,* 2008; Zecevic *et al.,* 2010) who investigated that genotype showed high variability in the number of grains per spike in wheat. Advanced genotype ETBW8070 had high biomass yield over the location and ETBW8075 had low biomass yield.

The present study result shows that biomass yield for most of the studied characters were >3.1 indicating genotypes had high yield. With regard to biomass yield about 53.33% of the genotypes exceeded the overall mean (3.01 kg plot^{-1}) of the genotypes while, genotypes exceeded 13.33% and 26.66% of the released variety Lemu and Hidasse respectively. Accordingly, there is plenty of variability among the genotypes for selection designed for improvement of this trait. This finding is in agreement with Mollasadeghi*et al.,* (2012) which stated the existence of variability for biomass yield among bread wheat genotypes. Harvest index exhibited significant difference among genotypes having the range of 0.15 to 0.33 with a mean value of 0.28. Demelash*et al.,* (2013) reported highly significant differences among bread wheat varieties for harvest index with the range of 0.31-0.45. Maximum harvest index was observed for ETBW9470, while minimum harvest index noticed for ETBW8075 (Table 5). In this result the genotype that had highest harvest index had high grain yield over locations while, genotype that had low harvest index had low grain yield. The present study result shows that harvest index for most of the studied characters were >0.28 indicating genotypes had high yield.

Difference between environments

When locations were compared, the highest mean grain yield (5.15 t/ha) was obtained at Kulumsa, and the lowest (2.86 t ha^{-1}) was obtained from Bekoji. Arsi robe (3.32 t/ha) and Dhera (3.17 t/ha) were also poor yielding locations (Table 6). The grain yield obtained from Bekoji, Dhera, Arsi Robe were below the overall location mean grain yield (3.77 t/ha), whereas the grain yield of genotypes at Kulumsa, Asasa and Holeta were better than that at Bekoji, Dhera, Arsi Robe (Table 6). Highest plant height was recorded at Asasa, and the lowest at Dhera. Obtained values of plant height indicated that environment had higher influence than genotype on expression of plant height. Fertile tiller numbers were high at Bekoji, while low at Arsi Robe. Genotype had highest average value of biomass yield at Kulumsa when compared with other five locations and lowest at Arsi Robe. The highest harvest index was obtained from Arsi Robe, while lowest obtained from Asasa. The highest hectolitre weight was obtained from Holeta and lowest one was obtained from Asasa. The highest TKW was obtained from Arsi Robe, while the lowest obtained from Asasa (Table 6).

AMMI analysis

The results of AMM 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 ($p<0.001$). AMMI multiplicative component further partitioned the GE interaction into five interaction principal component axes (IPCAs). However, only the first two axes showed significant contribution to the GEI in the AMMI model (Table 3). The remaining three principal components contributed insignificant portion of the variation. The AMMI biplot, which accounted for 80.71 PHT, 65.52 TILL, 78.81 GNO, 82.9 BIO, 78.53 HI, 70.1 TKW, 68 HLW and 74.7% GYLD of the GxE interaction, provides the interaction principal component scores of the 1st and 2nd IPCA with 34 degrees of freedom.

Grain yield

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 8). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 46.1% and the IPCA2 explained 28.6% and the two IPCs cumulatively captured 74.7% of the sum of

square the GEI of bread wheat genotypes(Table 4). There is a good variation in the different environments. Holeta (HL), Bekoji (BJ) and Dhera (DH) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 8). Closer relationships were observed between Kulumsa (KU), Arsi Robe (AR) and Asasa (AS).Genotypes ETBW8075 (#11), ETBW8070 (#2) and ETBW9470 (#14) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores.

The ETBW8078 (#3), ETBW8459 (#8) and Hidase (#15) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments. The genotype ETBW8070 (#2) positively interact at Bekoji and Holeta. This two location are highland wheat production locations. The genotype with highest positive interaction with location Kulumsa (KU) was ETBW9470 (#14); ETBW8075 (#11) interacted positively with Dhera (DH), while ETBW8070 (#2) had high interaction with Holeta (HL) while ETBW9466 (#13) was the best genotype for Arsi Robe (AR) (Figure 8).

Plant height

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 1). The AMMI analysis for the IPCA1 captured 47.25% and the IPCA2explained 33.46% and the two IPCs cumulatively captured 80.71% of the sum of square the GEI of bread wheat genotypes. Genotypes ETBW9466 (#13), ETBW8065 (#6), ETBW8070 (#2), ETBW4427 (#7), ETBW9045 (#10) andETBW9464 (#12), were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8311 (#5), ETBW8459 (#8) and Hidase (#15) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments.

The genotype ETBW9466 (#13), positively interact at Bekoji (BJ). The genotype with highest positive interaction with location ArsiRobe (AR) and Dhera(DH) was ETBW8070 (#2); ETBW9464(#12), interacted positively with Holeta(HL) while ETBW8311 (#5) had high interaction with Kulumsa (KU) and Asasa (AS) while ETBW9466 (#13) was the best genotype for Arsi Robe (AR) (Figure 1).

Tiller number

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 33.18% and the IPCA2 explained 29.34% and the two IPCs cumulatively captured 65.52% of the sum of square the GEI of bread wheat genotypes. Genotypes ETBW9464 (#12), ETBW8070 (#2), Lemu (#1)ETBW9037 (#9), ETBW9470 (#14) and Hiddase (#15) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9045 (#10), ETBW8459 (#8) and ETBW8070 (#3) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 2).

Grain 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 59.28% and the IPCA2 explained 20.53% and the two IPCs cumulatively captured 78.81% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Holeta (HL), Bekoji (BJ) and Dhera (DH) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 8). Kulumsa (KU), Arsi Robe (AR) and Asasa (AS) were least discriminating environments. Genotypes ETBW8075 (#11), ETBW8070 (#2), ETBW9470 (#14), ETBE9037 (#9), ETBW9466(#13) and ETBW8311 (#5) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9045 (#10) and Lemu (#1) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 3).

Biomass yield

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 66.98% and the IPCA2 explained 15.92% and the two IPCs cumulatively captured 82.9% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Genotypes ETBW9464 (#12), ETBW8070 (#2), ETBW9037 (#9) and ETBW9470 (#14) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW9045 (#10), Hidase (#15), ETBW8078 (#3), ETBW8084 (#4) and ETBW8427 (#7) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Table 4).

Harvest index

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 39.39% and the IPCA2 explained 39.15% and the two IPCs cumulatively captured 78.53% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Arsi Robe (AR), Bekoji (BJ) and Dhera (DH) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 5). Kulumsa (KU), Holeta (HL) and Asasa (AS) were least discriminating environments.Genotypes ETBW8075 (#11), ETBW8065 (#6),ETBW9464 (#12), and Lemu (#1) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8084 (#4), ETBW8459 (#8) and Hidase (#15) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments. The genotype ETBW9470 (#14) positively interact at Bekoji. The genotype with highest positive interaction with location Kulumsa (AR) was Lemu (#1); ETBW8075 (#11) interacted positively with Dhera (DH), while ETBW8078(#3) had high interaction with Holeta (HL) while Hiddase (#15) was the best genotype for Asasa (AS) and Kulumsa (KU) (Figure 5).

Thousand kernel weight

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 6). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 39.1% and the IPCA2 explained 30.99% and the two IPCs cumulatively captured 70.1% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Arsi Robe (5), Bekoji (4) and Dhera (3) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 6). Closer relationships were observed between Holeta (6) and Asasa (2). Genotypes ETBW8075 (#11), ETBW9466 (#13), ETBW9470 (#14) and ETBW8427 (#7) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8078 (#3) and ETBW8311 (#5) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 6).

Hectolitre weight

The IPCA1 was plotted on x-axis whereas IPCA2 was plotted on y-axis for grain yield and yield components (Figure 7). AMMI2 analysis positioned the genotypes in different locations, indicating the interaction pattern of the genotypes. The AMMI analysis for the IPCA1 captured 44.88% and the IPCA2 explained 23.1% and the two IPCs cumulatively captured 68% of the sum of square the GEI of bread wheat genotypes. There is a good variation in the different environments. Holeta (HL), Bekoji (BJ) and Dhera (DH) were the most discriminating environments as indicated by the long distance between their marker and the origin (Figure 7). Closer relationships were observed between Kulumsa (KU), Arsi Robe (AR) and Asasa (AS).Genotypes ETBW8459 (#8), ETBW8065 (#6), ETBW9466 (#13) and ETBW9464 (#12) were unstable as they were located far apart from the other genotypes in the biplot when plotted on the IPCA1 and IPCA2 scores. The ETBW8078 (#3) andETBW8075 (#11) were genotype located near to the origin of the biplot which implies that they were stable bread wheat genotypes across environments (Figure 7).

Figure of AMMI 2 Biplot of IPCA 1 against IPCA 2 for agronomic traits of 15 bread wheat genotypes tested across six locations are listed below. For all figure where; 1=Lemu, 2=ETBW8070, 3=ETBW8078, 4=ETBW8084, 5=ETBW8311, 6=ETBW8065, 7=ETBW8427, 8=ETBW8459, 9=ETBW9037, 10=ETBW9045, 11=ETBW8075, 12=ETBW9464, 13=ETBW9466, 14= ETBW9470, 15=Hidasse,

Table.1 Location and descriptions of weather condition for six locations.

Location	Geographic position		Altitude	Soil pH	Soil type	Temperature(°c)		Rainfall (mm)
	Latitude	Longitude				Min	Max	
Kulumsa	08°01'10"N	39°09'11"E	2200	6	Luvisol	10.5	22.8	820
Asasa	07°07'09"N	39°11'50"E	2000	6.5	Gleysol	5.8	24	620
Dhera	08°19'10"N	39°19'13"E	1650	7	Andosol	14	27.8	680
Bekoji	07°32'37"N	39°15'21"E	2780	5	Nitosol	7.9	18.6	1020
Arsi Robe	07°53'02"N	39°37'40"E	2420	5.6	Vertisol	6	21.1	890
Holeta	NA	NA	2400	5	Nitosol	6.2	22.1	1044

Table.1 The names, pedigree and selection history of the genotypes were evaluated in the experiment in 2017/18 cropping season at six locations.

Name	Pedigree
Lemu	WAXWING*2/HEILO
ETBW8070	Line 1 Singh/ETBW4919
ETBW8078	Line 1 Singh/(Cham6/WW1402)
ETBW8084	Line 3 Singh/(Cham6/WW1402)
ETBW8311	ND643/2*WBLL1/3/KIRITATI//PRL/2*PASTOR/4/KIRITATI//PBW65/2*SERI.1B
ETBW8065	Line 1 Singh/ETBW4919
ETBW8427	SERI.1B//KAUZ/HEVO/3/AMAD/4/PYN/BAU//MILAN/5/ICARDA-SRRL-1
ETBW8459	CHIL-1//VEE'S'/SAKER'S'
ETBW9037	SWSR22T.B./2*BLOUK #1//WBLL1*2/KURUKU
ETBW9045	KINDE/4/CMH75A.66//H567.71/5*PVN/3/SERI
ETBW8075	Line 1 Singh/(Cham6/WW1402)
ETBW9464	MARCHOUCH*4/SAADA/3/2*FRET2/KUKUNA//FRET2*2/4/TRCH/SRTU//KACHU
ETBW9466	ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA//TSI/VEE#5/4/CROC_1/AE.SQUARROSA(224)//2*OPATA*2/6/HUW234+LR34/PRINIA//UP2338*2/VIVITSI
ETBW9470	BAVIS#1/5/W15.92/4/PASTOR//HXL7573/2*BAU/3/WBLL1
Hidasse	YANAC/3/PRL/SARA//TSI/VEE#5/4/CROC-1/AE.SQUAROSA(224)//OPATTA

Table.3 Combined analysis of variance for agronomic traits

Traits	Source of Variation							
	Environment (5)	Gen(E) (18)	Genotype (14)	GEI(70)	PCA1 (18)	PCA2 (16)	Error (267)	CV%
GYLD	43.51***	1.05	14.74***	2.75***	4.94***	3.45***	0.43	16.55
PHT	6281.53***	89.38	211.82***	75.67***	139.03***	110.77***	22.36	5.23
TILL	79.20***	3.70	0.98ns	1.03ns	1.33ns	1.32ns	0.95	19.04
GNO	1681.82***	145.56	92.37ns	94.19***	217.15***	84.58**	32.17	12.85
BIO	106.8***	2.40	2.51***	0.59***	1.54***	0.4*	0.20	14.94
HI	0.65***	0.02	0.04***	0.01***	0.015***	0.017***	0.003	19.12
TKW	505.64***	11.38	295.19***	60.39***	91.84***	81.91***	7.88	8.06
HLW	648.09***	8.29	84.20***	19.9***	17.43***	10.1***	2.57	2.26

***very highly significant p<0.001 ns= non-significant

Where; PHT = plant height, GNO=grain per spike, TILL=number of tiller per plant, BIO=biomass yield, HI=harvest index, TKW= thousand kernel weight, HLW= hectolitre weight, GYLD= grain yield and CV= coefficient of variation.

Table.4 Proportion of Total Treatment (G+E+GEI) contributed by G, E and GxE Interaction and PCA In Agronomic traits

Traits	Genotype	Environment	GEI	PCA1%	PCA2%
Grain yield	33.46	35.28	31.45	46.1	28.6
Plant height	7.5	79.2	13.4	47.25	33.46
Tiller number	2.8	82.2	14.9	33.18	29.34
Grain per spike	7.9	51.6	40.5	59.28	20.53
Biomass yield	5.8	87.4	6.8	66.98	15.92
Harvest index	12.9	71.5	15.6	39.39	39.15
Hectolitre weight	20.4	56.1	23.5	44.88	23.1
Thousand kernel weight	38.0	23.2	38.8	39.1	30.99

Table.5 Mean values of agronomic traits of bread wheat genotypes tested across six locations

Genotype	PHT	TILL	GNO	BIO	HI	HLW	TKW	GYLD
Lemu	91.97^{a-c}	5.1^{abc}	44.59^{bc}	3.28^{bc}	0.28^{c-f}	69.62^{d-f}	31.93^{e}	3.93^{b-d}
ETBW8070	92.39^{a-c}	5.4^{a}	45.84^{a-c}	3.62^{a}	0.28^{c-f}	73.38^{ab}	35.45^{b-e}	4.60^{ab}
ETBW8078	86.08^{e}	5.1^{abc}	42.9^{b-d}	3.07^{c-f}	0.24^{g}	69.75^{de}	33.82^{de}	3.39^{cd}
ETBW8084	87.56^{e}	5.2^{abc}	45.36^{a-c}	3.17^{b-e}	0.27^{de-g}	70.18^{c-e}	35.71^{b-e}	4.05^{a-d}
ETBW8311	87.12^{e}	5.3^{ab}	44.4^{bc}	2.73^{gh}	0.26^{e-g}	70.62^{b-e}	31.4^{ef}	3.11^{d}
ETBW8065	88.04^{e}	4.82^{bc}	43.39^{b-d}	3.35^{ab}	0.25^{fg}	73.02^{ab}	34.56^{e}	3.91^{b-d}
ETBW8427	94.62^{a}	5.1^{abc}	42.76^{cd}	3.1^{c-f}	0.31^{a-c}	72.69^{a-c}	39.22^{ab}	4.16^{a-c}
ETBW8459	91.06^{cd}	5.0^{abc}	44.54^{bc}	2.77^{gh}	0.28^{c-f}	71.13^{a-e}	33.18^{e}	3.45^{cd}
ETBW9037	91.26^{b-d}	5.3^{ab}	48.4^{a}	2.95^{e-g}	0.32^{ab}	72.04^{a-d}	35.32^{b-e}	4.11^{a-c}
ETBW9045	94.06^{ab}	5.26^{ab}	43.68^{bc}	2.85^{f-h}	0.3^{abc}	73.56^{a}	38.66^{a-c}	3.90^{b-d}
ETBW8075	86.76^{e}	5.13^{abc}	39.94^{d}	2.31^{i}	0.15^{h}	67.06f	27.32^{f}	1.53^{e}
ETBW9464	94.15^{ab}	4.65^{c}	42.5^{cd}	2.67^{h}	0.29^{b-e}	66.58^{ef}	34.7^{c-e}	3.35^{cd}
ETBW9466	88.93^{de}	5.12^{abc}	46.52^{ab}	3.0^{d-g}	0.3^{a-d}	69.73^{de}	31.93^{e}	3.91^{b-d}
ETBW9470	88.74^{de}	5.22^{abc}	43.17^{b-d}	3.27^{b-d}	0.33^{a}	70.31^{a-e}	40.89^{a}	4.93^{a}
Hidasse	93.48^{a-c}	4.86^{abc}	44.21^{bc}	3.16^{b-e}	0.29^{a-d}	69.76^{de}	38.21^{a-d}	4.29^{a-c}
Mean	90.41	5.11	44.16	3.02	0.28	70.56	35.07	3.77
LSD0.5	2.91	0.57	3.6	0.28	0.03	2.71	4.47	

Values with the same letter in a column are not significantly different

Where; NSPPSP=number of spikelet per spike, NGPPL= grain per spike, BIO=biomass yield, HI=harvest index, TKW= thousand kernel weight, HLW= hectolitre, GYLD= grain yield and LSD%= Least Significant Difference

Table.6 Mean values of agronomic traits of six locations

Traits	Kulumsa	Asasa	Dhera	Bekoji	A.Robe	Holeta	Mean	LSD
PHT	96.74^{ab}	97.94^{a}	70.56^{e}	95.8^{b}	92.03^{c}	89.42^{d}	90.42	3.63
TILL	4.32^{d}	5.97^{b}	5.08^{c}	6.97^{a}	4.21^{d}	4.13^{d}	5.11	0.57
NGPPL	48.36^{ab}	49.61^{a}	36.46^{e}	46.92^{ab}	39.1^{d}	44.5^{b}	44.16	4.63
BIO	4.92^{a}	4.35^{b}	2.74^{c}	2.27^{d}	1.43^{e}	2.43^{d}	3.02	0.4
HI	0.21^{cd}	0.20^{d}	0.24^{cd}	0.25^{c}	0.48^{a}	0.31^{b}	0.28	0.05
HLW	70.90^{c}	66.42^{e}	70.04	69.51^{cd}	72.64^{b}	76.13^{a}	70.67	1.14
TKW	36.64^{b}	30.89^{e}	34.89^{c}	35.14^{c}	38.97^{a}	32.37^{d}	34.82	1.29
GYLD	5.15^{a}	4.33^{b}	3.17^{de}	2.86^{e}	3.32^{d}	3.82^{c}	3.77	0.39

Values with the same letter in a column are not significantly different

Where; PHT=plant height, GNO= grain per spike, TILL=number of tiller per plant, BIO=biomass yield, HI=harvest index, TKW= thousand kernel weight, HLW= hectolitre, GYLD= grain yield

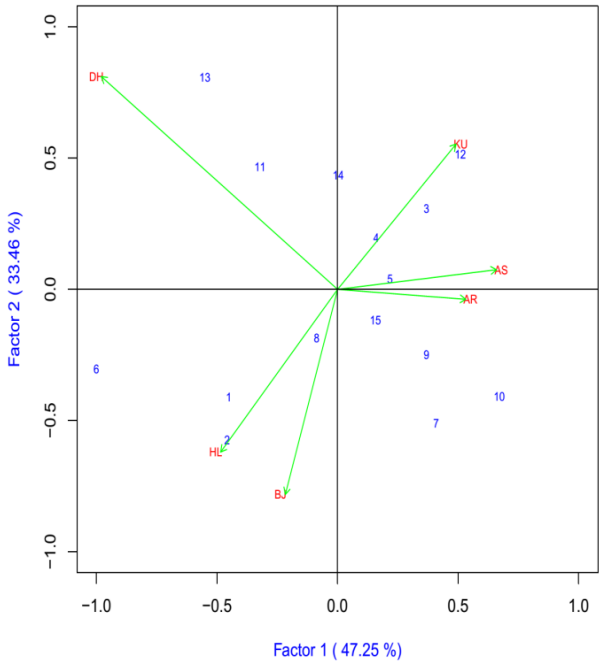

Figure.1 AMMI 2 Biplot of IPCA 1 against IPCA 2 for plant height of 15 bread wheat genotypes tested across six locations (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

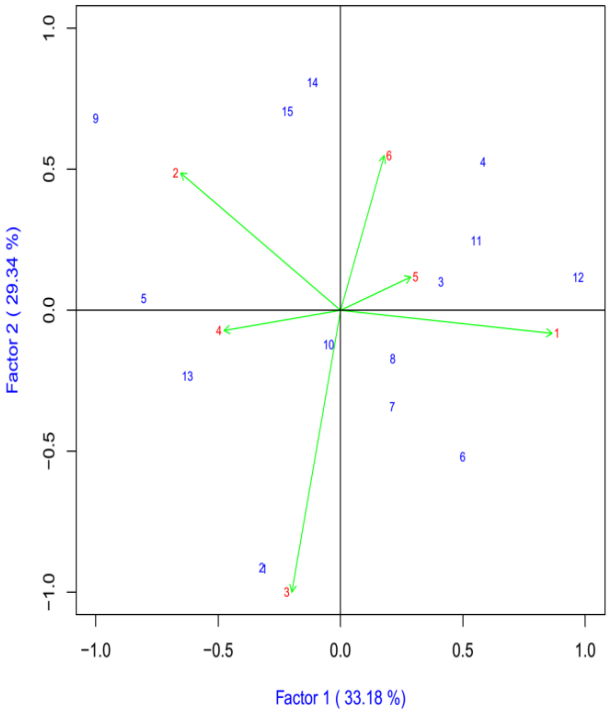

Figure.2 AMMI 2 Biplot of IPCA 1 against IPCA 2 for tiller number of 15 bread wheat genotypes tested across six locations (1=Kulumsa, 2=Asasa, 3=Dhera, 4=Bekoji, 5=Arsi Robe and 6=Holeta)

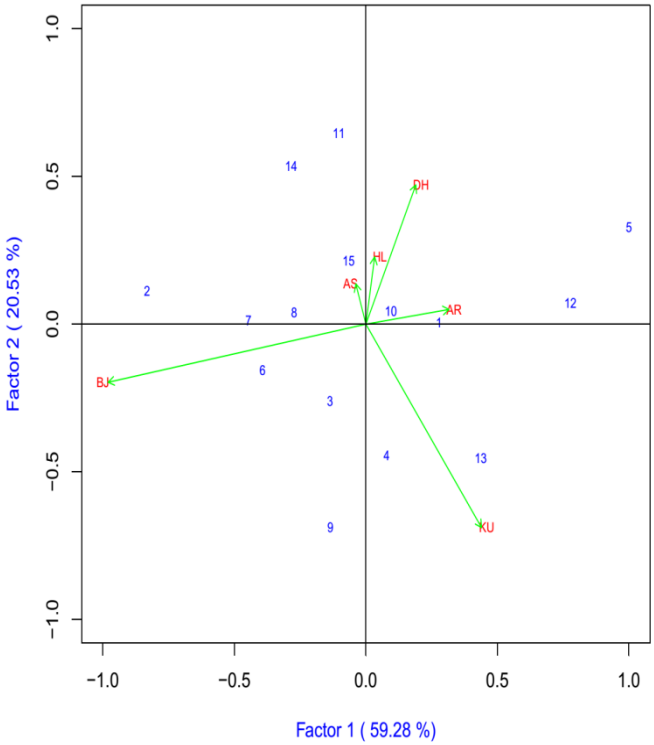

Figure.3. AMMI 2 Biplot of IPCA 1 against IPCA 2 for grain per spike of 15 bread wheat genotypes tested across six locations (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

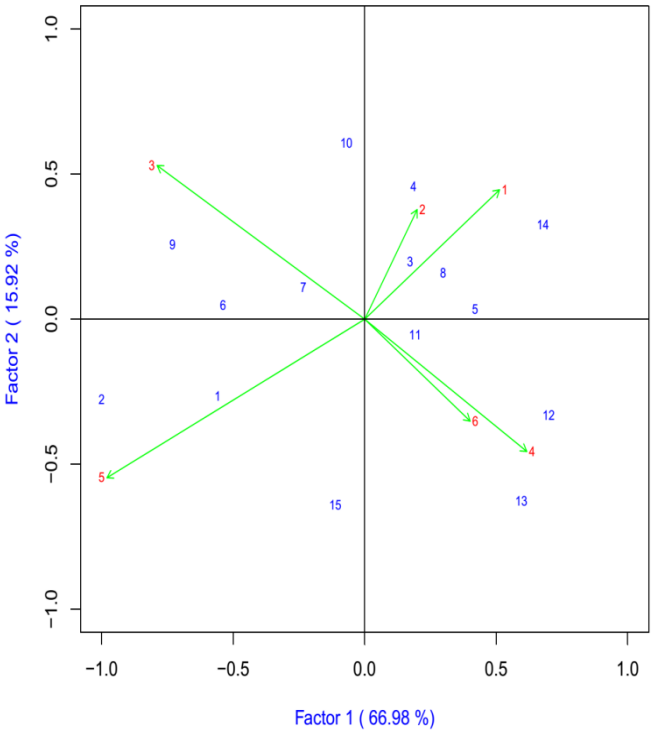

Figure.4 AMMI 2 Biplot of IPCA 1 against IPCA 2 for biomass yield of 15 bread wheat genotypes tested across six locations (1=Kulumsa, 2=Asasa, 3=Dhera, 4=Bekoji, 5=Arsi Robe and 6=Holeta)

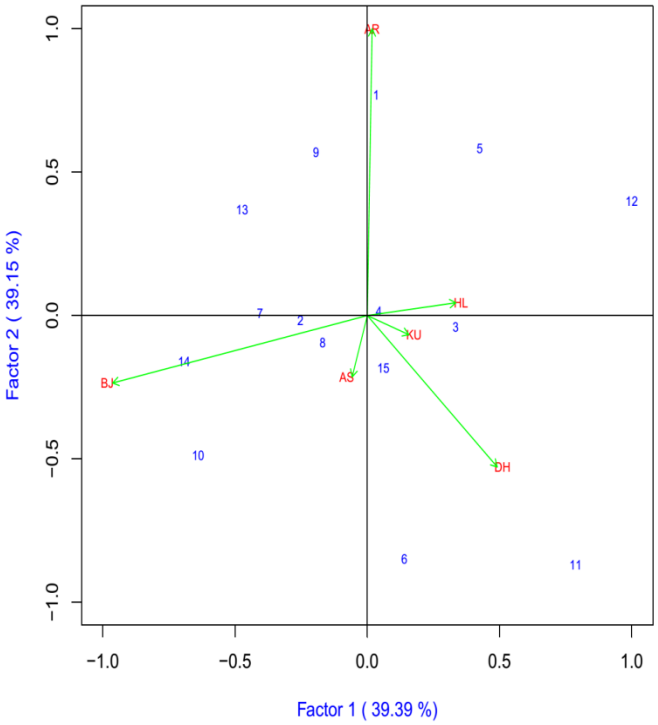

Figure.5 AMMI 2 Biplot of IPCA 1 against IPCA 2 for harvest index of 15 bread wheat genotypes tested across six locations (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

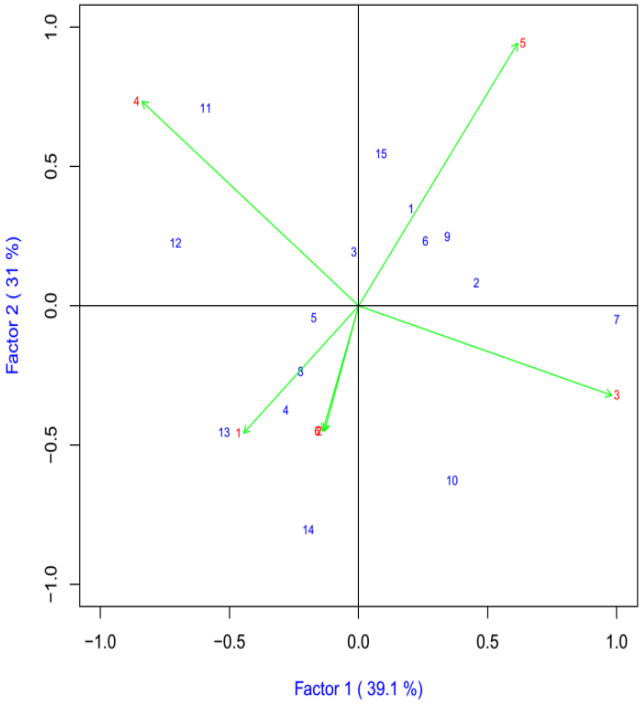

Figure.6 AMMI 2 Biplot of IPCA 1 against IPCA 2 for TKW of 15 bread wheat genotypes tested across six locations (1=Kulumsa, 2=Asasa, 3=Dhera, 4=Bekoji, 5=Arsi Robe and 6=Holeta)

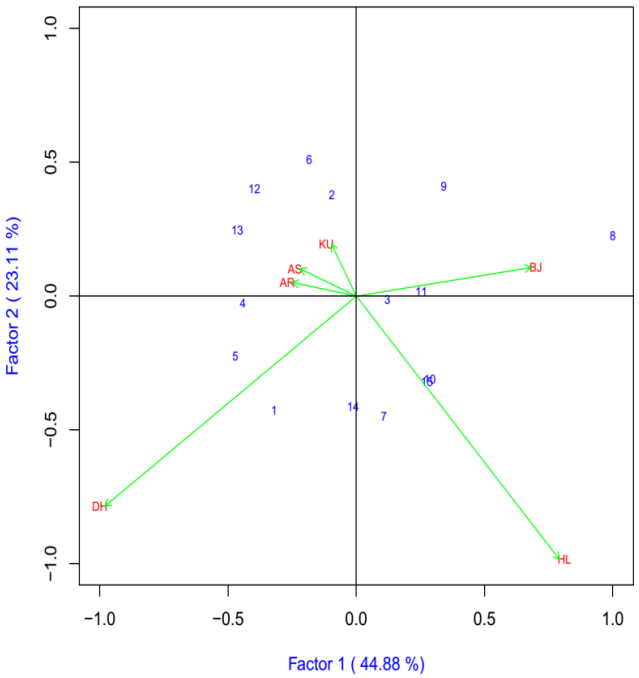

Figure.7 AMMI 2 Biplot of IPCA 1 against IPCA 2 for HLW of 15 bread wheat genotypes tested across six locations (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

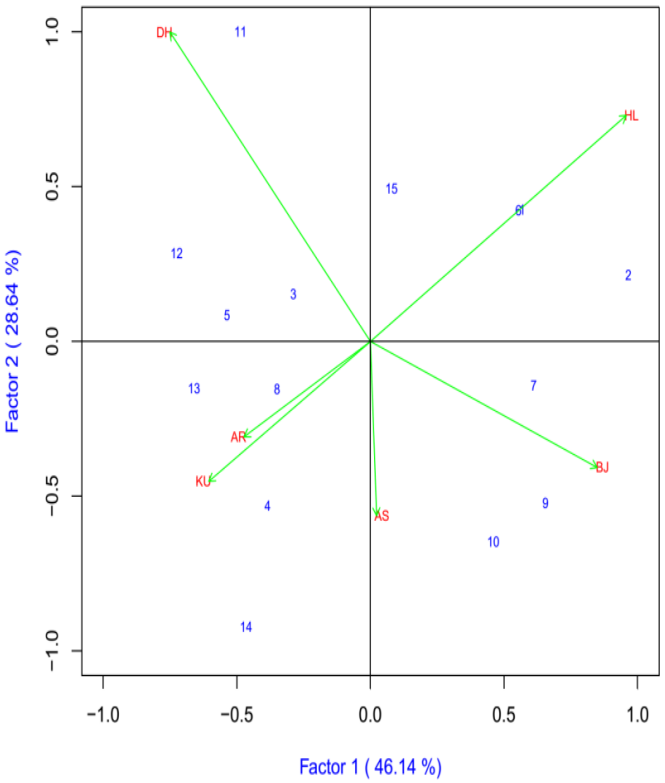

Figure.8 AMMI 2 Biplot of IPCA 1 against IPCA 2 for grin yield of 15 bread wheat genotypes tested across six locations (AR=Arsi Robe, AS=Asasa, BJ=Bekoji, DR=Dhera, HL=Holeta and KU=Kulumsa)

In 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 main effect was not significant for grain per spike and tiller number. 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 environments contributed total treatment sum square 80-90% in PHT, TILL and BIO, 70-80% in HI. These traits were determined mainly by the environment. Other yield and yield components contributed 20-60% total sum square of environments. Genotype contributed less than 10% to total treatment sum square in all traits except in GYLD (33.46), HLW (20.4), TKW (38.0) and HI (12.9%). GxE contributed less than 10% to total treatment sum square in BIO. It contributed 10-20% in PHT, TILL and HI, 20-30% in HLW, 30-40% in GYLD, TKW and GNO. The biplot of AMMI revealed clear insight into the specific and general adaptation of genotypes across locations. The AMMI biplot, which accounted for 80.71 PHT, 65.52 TILL, 78.81 GNO, 82.9 BIO, 78.53 HI, 70.1 TKW, 68 HLW and 74.7% GYLD of the GxE interaction, provides the interaction principal component scores of the 1st and 2nd IPCA. High grain yield was harvested from the advanced genotype ETBW9470 and lowest from ETBW8075. The advanced genotype ETBW8427was the tallest genotype and ETBW8078was found to be the shortest plant height. The maximum fertile tiller numbers were obtained from advanced genotype ETBW8070 and minimum tiller number was obtained from the advanced genotype ETBW9464. Advance genotypes ETBW9037 had high number of grain per spike and ETBW8075had low mean number of grains spike^{-1} over locations. Advanced genotype ETBW8070 had high biomass yield over the location and ETBW8075 had low biomass yield. Maximum harvest index was observed for ETBW9470, while minimum harvest index noticed for ETBW8075.

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