Available Online at ESci Journals
Journal of Plant Breeding and Genetics
ISSN: 2305-297X (Online), 2308-121X (Print)
http://www.escijournals.net/JPBG

SEASONAL VARIABLITY AND GENETIC RESPONSE OF ELLITE BREAD WHEAT LINES IN DROUGHT PRONE ENVIRONMENTS OF ETHIOPIA

[a]Dawit A. Tigabu*, [a]Zerihun Tadesse, [a]Habtemariam Zegeye, [b]Alemayehu Assefa
[a] *National Wheat Research Program, Kulumsa Agricultural Research Center, Assela, Ethoipia.*
[b] *Ethiopian Agricultural Research Institute, Addis Ababa, Ethiopia.*

A B S T R A C T

Development and deployment of wheat varieties having desirable traits for drought prone wheat growing environments of Ethiopia, where unpredictable climate variability across seasons and locations is the predominant challenge, is the priority tasks of breeders. Hence, this study was aimed to evaluate the performance of 12 bread wheat genotypes across 14 environments and; assess the nature and magnitude of genotype by environment interaction (GEI) in moisture-limited environments. The field trial was conducted in a Randomized Complete Block Design with 4 replications in 2011 and 2012. Stability and GEI analysis were done using Additive Main effect and Multiplicative Interactive (AMMI) model. AMMI analysis of grain yield data revealed highly significant ($p < 0.001$) variation among tested genotypes, environments and GEI; and accounted for 2.9%, 80.8%, and 16.3 % of the observed significant variation in grain yield, respectively. Besides, 64% of the interaction pattern was explained by the first two principal component axes. The AMMI biplots revealed genotype ETBW6095 (G6) is the most stable and well adapted for commercial cultivation across moisture limited environments. This genotype out yielded the average of the checks by 9 %. In summary, the existence of inconsistent performance of genotypes due to temporal and spatial variability clearly confirmed the necessity of multi-environmental trials. Use of AMMI potentially enabled identification of sub-regions and selection of best genotypes for wide and specific adaptation while conducting METs.

Keywords: bread wheat, drought, Ethiopia, interaction, stability, yield.

Abbreviations: AMMI, GEI, METs, IPCA

INTRODUCTION

Wheat is grown as a rain-fed crop in the Ethiopian highlands, commonly known as the east African wheat-belt. It ranks third in terms of area after teff and maize, and second in terms of production after maize. The area coverage under wheat production reaches nearly 1.7 m ha which is 12.9% of the area under cereals production; and wheat contributed 15.60% (4.5 m MTs) of the cereal grain production with an average productivity of 2.5 ton/ha (CSA, 2014/15). This makes the country the leading wheat producer in Sub-Saharan Africa.

Despite the huge production potential, an increase in production and productivity in the last two decades, the annual grain production still lagged far behind its consumption. To bridge the gap in the demands of the rapid population growth and supply, its productivity should consistently be increased. Therefore, wheat breeders carry out rigorous germplasm screening aiming at developing high yielding varieties with reasonable combined resistance to both biotic and abiotic stresses. However, selection of genotypes having high yield potential and stable performance has usually been hindered by the existence of significant genotype by environment interaction (GEI). The existence of variability in wheat grain yield response can be attributed to genotypic (phenology, growth habit) and the prevailing environmental variations (vernalization and photoperiodic requirements) (Van Oosterom et al., 1993). As a consequence, consistent development and provision of suitable/best bread wheat cultivars requires stratification of environments and conducting multi-environmental trials (METs) (Basford and Cooper, 1998). The stability of a genotype

* Corresponding Author:
Email: apari199@yahoo.com

across environments is defined as the consistent performance of a genotype across different environments and/or years for a given character (Tadesse et al., 2010).

Identifying stable and high yielding genotypes in METs requires two important approaches that should be addressed by breeders. First, the prevailing GEI in MET's should be quantified using appropriate statistical tools. Secondly, keen observation on the nature and magnitude of GEI in the METs is of great value to describe the stable performance of genotypes under evaluation. GEI is composed of both additive and multiplicative components, it would have been important to use statistical methods which enables estimate and quantify various GEI variance components (Fernandez, 1991). AMMI model is among the multivariate statistical analysis techniques which partition both the additive and multiplicative variance components of GEI (Gauch and Zobel, 1997). Therefore, this study was conducted to evaluate the phenotypic performance of elite bread wheat lines and assess the nature and magnitude of GEI an under diverse moisture limited environments.

MATERIALS AND METHODS

Ten advanced bread wheat lines and two check genotypes, one standard check (Kakaba) and one local check (Hawi) cultivars were evaluated across eight locations in 2011 and 2012 main cropping seasons. Description of wheat lines and test locations is provided in Table 1 and Table 2, respectively.

Table 1. Characteristic features of the testing locations.

Location	Altitude	Soil type	LATI	LONG	Temperature		Rainfall (mm)
					Min.	Max.	
Alem Tena	1611	Haplic Andosol	08°.30N	38°.95E	-	-	728.0
Dera	1660	Silty loam	08°.20N	39°.19E	6.6°c	26.2°c	680.0
Geregera	2804	Lithosol	11°.41N	38°.45E	3.8°c	23.4°c	1104.0
Mekelle	1970	Cambisol	13°.14N	39°.32E	12.3°c	27.1°c	453.3
Melkassa	1550	Sandy-loam	08°.24'N	39°.12'E	13.6°c	28.6°c	763.0
Sinana	2400	NA	07°.05'N	40°.12'E	7.9°c	24.3°c	791.0
Kulumsa	2200	Luvisol	08°.01'N	39°.09'E	10.5°c	22.8°c	820.0
Alem Ketema	1685	NA	NA		NA		NA

The field experiment was laid out in a Randomized Complete Block Design (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.

Table 2. Test entries for multi-location experiment with code, designation, pedigree and origin.

Code	Designation	Pedigree/Cross	Origin
G1	Kakaba	KIRITATI//SERI/RAYON	CIMMYT
G2	ETBW6082	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2	CIMMYT
G3	ETBW6083	KS82W418/SPN/3/CHEN/AE.SQ//2*OPATA/4/FRET2	CIMMYT
G4	ETBW6093	CROC_1/AE.SQUARROSA(205)//KAUZ/3/ENEIDA/4/PSN/BOW//MILAN	CIMMYT
G5	ETBW6094	TC870344/GUI//TEMPORALERA M 87/AGR/3/2 *WBLL1	CIMMYT
G6	ETBW6095	PASTOR//HXL7573/2*BAU/3/WBLL1	CIMMYT
G7	ETBW6098	TC870344/GUI//TEMPORALERA M 87/AGR/3/2 *WBLL1	CIMMYT
G8	ETBW5798	WAXWING*2/TUKURU	CIMMYT
G9	ETBW5827	SAMAR-8/KAUZ'S'//CHAM-4/SHUHA'S'	CIMMYT
G10	ETBW5834	WEEBILL- 1/4/CMH82.17/KAUZ// CMH83.30/3/ VEE#5//DOBUC'S'	CIMMYT
G11	ETBW5801	WAXWING*2/TUKURU	CIMMYT
G12	Hawi	CHIL/PRL	CIMMYT

Data Collection: Data was collected on the following traits: days to heading, days to maturity, grain filling period, thousand kernel weight, and hectoliter weight (HLW) and grain yield per plot. Moreover, disease scores on stripe rust, stem rust, leaf rust and septoria was also made.

Statistical analysis: The grain yield data from each location were subjected to analysis of variance (ANOVA) using the General Linear Model (GLM) procedure of the Statistical Analysis System (SAS) software (SAS Institute Inc., 2002). Prior to combined analysis, the experimental error variance from each location was tested for homogeneity using Bartlett test. For the combined analysis of variance, each year x location combination was considered as an environment (E). Since the residual variances homogeneous, the following model was employed to perform the subsequent combined ANOVA:

$$Y_{\cdot ijk} = m + G_{\cdot i} + E_{\cdot j} + R(E)_{\cdot jk} + (GxE)_{\cdot ij} + e_{\cdot ijk}$$

Where,

Yijk is the observation of the ith variety G in the jth environment E in the kth replication R nested within environment E; m is the general mean, e.ijk is the variation due to random error, associated with ith genotype, in the kth block of the jth environment and (G x E) ij is the genotype by environment interaction (Shukla, 1972). Based on grain yield data, G× E interaction was also partitioned using joint regression (Finlay and Wilkinson, 1963; Eberhart, and Russell, 1966) and the additive main effect and multiplicative interaction (AMMI) models (Gauch and Zobel, 1997). In addition, AMMI biplot (Site Regression) analysis was used to assess similarity and dissimilarity among ten environments and interaction patterns between genotypes and environments (Hernandez and Crossa, 2000; Burgeno et al., 2001). The biplots from the AMMI analysis were used to visualize the pattern of response of genotypes, environment and their interaction; and also, to identify genotypes with broad or specific adaptations to the target agro-ecologies.

RESULTS AND DISCUSSIONS

Mean Genotypic Performance: AMMI analysis of variance from the grain yield data set of this trial showed highly significant ($p \leq 0.0001$) variation among tested genotypes, environments and genotype by environment interaction (Table 3). Partitioning of the total sum of squares revealed that 80.76% was due to environmental effects, 2.94% to genotypic effects and 16.3% was due to genotype by environment interaction effects (Table 3). This is an indication that the test environments were very diverse, causing most of the variation in grain yield. DeLacy et al. (1996) and Gauch (1992) also indicated that environment and interaction effects are much more than the effects of the genotypes in most variety trials.

Table 3. AMMI Model analyses of the genotype x environments interaction of grain yield of 12 wheat lines grown at 14 Rainfed Environments across Ethiopia.

Source of variation	DF	SS	MS	F-Value	%SS
Total	671	720.5	1.074		
Treatments	167	524.3	3.139	8.86***	
Genotypes	11	15.4	1.398	3.94***	2.94
Environments	13	423.4	32.567	42.1***	80.76
Block	42	32.5	0.773	2.18***	
Interactions	143	85.5	0.598	1.69***	16.3
IPCA	23	27.5	1.195	3.37***	32.13
IPCA	21	19.2	0.915	2.58***	22.46
IPCA	19	14.7	0.775	2.19**	17.22
Residuals	80	24.1	0.301	0.85ns	
Error	462	163.7	0.354		
R2=76.3	CV=19.6				

NB: ns, *, **, *** = non-significant and significant effect at 5, 1 and 0.1% respectively.

The environmental mean grain yield varied from the lowest 1.70 t ha-1 at Mekelle in 2011 (E9) to highest 3.84 t ha-1 at Kulumsa 2011 (E8) (Table 4). The mean grain yield value of genotypes due to the mean effect of the environment ranged from 2.89 t ha-1 of Hawi (G12) to 3.38 t ha-1 of ETBW6095 (G6) (Table 4). 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 significant Genotypes x Environment interaction 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 (Heterogeneity of errors) over the Environment. Nevertheless, due to strong crossover type of interaction, grain yield of wheat genotypes varied from 1.26 t ha-1 in genotype ETBW5834 (G10) grown at Mekelle to 6.04 t ha-1 of ETBW6098 (G7) grown at Kulumsa within 2011 cropping season (Table 4). This rank change would be the source of the significant crossover GEI revealed in this data set. However, selection of best lines both for specific and wide adaptation based on the mean results would be misleading (Yan et al., 2000).

Table 4. The mean yield of 12 bread wheat genotypes tested in two years across five locations (2011-2012).

Genotype	Environment														Mean
	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	E11	E12	E13	E14	
G1	3.91	3.06	4.05	3.61	3.03	2.59	3.38	3.83	1.8	2.88	4.35	4.11	2.47	3.03	3.29
G2	3.85	2.81	3.69	3.47	2.2	2.54	3.52	3.93	1.93	2.38	3.97	3.38	2.63	2.79	3.08
G3	3.85	2.69	3.47	3.39	2.27	2.53	3.74	4.30	1.95	2.07	3.60	3.16	2.93	2.57	3.04
G4	3.41	2.73	3.61	3.42	3.75	2.23	3.39	4.82	1.34	2.36	3.89	4.12	2.7	2.51	3.16
G5	3.47	2.67	3.40	3.71	2.2	2.47	3.88	5.52	1.97	1.93	4.00	3.15	3.17	2.6	3.15
G6	3.72	3.02	3.89	3.96	2.29	2.69	3.79	5.08	2.14	2.53	4.61	3.61	2.95	3.06	3.38
G7	3.45	2.87	3.63	4.02	2.41	2.59	3.99	6.04	2.07	2.17	4.48	3.46	3.29	2.84	3.38
G8	3.15	2.83	3.75	3.85	2.9	2.29	3.39	5.43	1.57	2.48	4.69	3.97	2.64	2.84	3.27
G9	3.58	2.60	3.39	3.18	3.82	2.23	3.53	4.61	1.34	2.09	3.31	3.87	2.87	2.26	3.05
G10	2.94	2.61	3.6	3.53	2.58	2.02	2.95	4.66	1.26	2.39	4.51	3.8	2.13	2.66	2.97
G11	3.56	2.81	3.65	3.64	3.00	2.45	3.66	5.05	1.74	2.31	4.09	3.75	2.92	2.69	3.24
G12	3.03	2.48	3.38	3.38	2.57	2.02	3.13	4.74	1.3	2.09	4.05	3.52	2.37	2.43	2.89
Mean	3.49	2.76	3.63	3.6	2.75	2.39	3.53	4.84	1.7	2.31	4.13	3.66	2.76	2.69	3.16

Note: E1=Alemketema 2011; E2= Alemtena 2011; E3=Alemtena 2012; E4=Dera 2011, E5=Dera 2012; E6=Geregera 2011; E7= Geregera: 2012; E8=Kulimsa: 2011, E9=Mekelle: 2011, E10=Mekelle: 2012; E11=Melkassa: 2011; E12= Melkassa: 2012; E13=Sinana: 2011; E14=Sinana: 2012.

AMMI Model Analysis: AMMI multiplicative component further partitioned the GE interaction into thirteen interaction principal component axes (IPCAs). However, only the first three axes showed a significant contribution to the GEI in the AMMI model. The mean squares of the three interaction principal components contributed to 71.8% of the total GEI with 63 degrees of freedom. The remaining ten principal components contributed an insignificant portion of the variation. The AMMI biplot, which accounted for 64.62% of the GxE, provide the interaction principal component scores of the first and 2nd IPCA with 44 degrees of freedom. The first PC axis (PC1) score explained 32.16 % of the variation in GEI, while the second PC axes accounted for 22.46% of the variability. Many researchers witnessed that the best accurate AMMI model prediction can be made using the first two IPCA (Gauch and Zobel, 1996; Yan *et al.,* 2000 and Annicchinario, 2002). Therefore, the dataset obtained from the interaction of 12 genotypes tested at 14 environments was best predicted by the first two IPCAs. On the other hand, the IPCA scores of a genotype in the AMMI analysis are reported as an indication of the stability of a genotype across environments (Gauch and Zobel, 1996; Purchase, 1997). Accordingly, the closer the IPCA scores are to zero, the more stable the genotypes are across all their testing environments (Purchase, 1997).

The biplots obtained from the ICPA scores of each Genotype and Environments shows the specific GxE interactions extracted from residuals which accounts for the additive genotype and environment main effects of AMMI model analysis and genotypic performance with respect to those GE interactions. The distances from the origin (0, 0) are indicative of the amount of interaction that was exhibited by genotypes either over environments or environments over genotypes (Voltas *et al.,* 2002). IPCA-1 is characterized by a large negative score for variety Kakaba, a large positive score for variety G5 and G7. The most divergent genotypes were ETBW6098 (G9) and ETBW6093 (G4) and Kakaba.

Hence, ETBW6093 (G4) they are sensitive to environmental changes and are adapted to specific environments. Genotypes ETBW5801 (G11) and Hawi (G12), accordingly, showed similar performance. IPCA scores for lines G2, G8, G11 and G12 are close to zero. This reflects their small residuals in Figure 1 and confirms their non-specific performance across the environments.

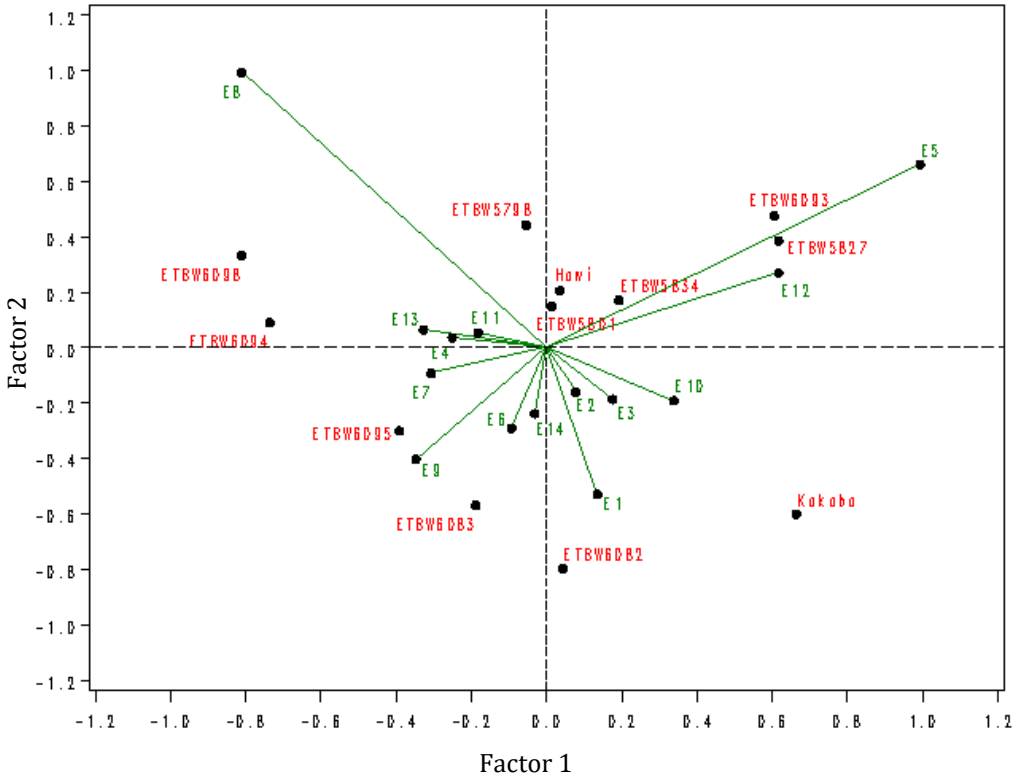

Figure 1. Biplot for 12 genotypes tested at 14 contrasting environments.

Environments with higher IPCA scores regardless of the sign discriminate among genotypes more than those with lesser IPCA scores (Kempton, 1984). Thus, discrimination among genotypes was high at environment E5, E8 and E12, while little discrimination among genotypes was observed at E11, E2, E3, and E14. The IPCA score for E6 (Mekelle 2011) and E14 (Sinana 2012) were similar in their sign, and their magnitude is close to each other relative to the remaining test locations. Therefore, the two environments could belong to the same interaction group. Positive (but low magnitude) of IPCA-score for E11 (Melkassa 2011) also indicated that there might be few similar agro-climate features of this test location with E6 and E14. However, this is due to the seasonal variation from each location. This clearly shows inefficiency of grouping environments based only on the IPCA scores.

The adaptation of genotypes to different environments can also be explained more using the AMMI GGE biplots (Burgueno et al., 2001). The GGE biplot captures both the genotypic and GxE effects. Connecting the extreme genotypes on a GGE biplot forms a polygon and the perpendiculars to the sides of the polygon form sectors of genotypes and sites (Hernandez and Crossa, 2000). Hence, the biplot distributes all the 14 testing environments into five sectors which lie between four dotted (L1, L2, L3and L4) lines perpendicular to the horizons of a polygon drawn through the highest values of the GGE effects (Fig. 2). The genotypes at a vertex are the winners in the sites included in that sector (Vargas and Crossa, 2000). The first sector (lies in between L1and L2) consists of nine environments (E1, E2, E3, E4, E5, E6, E9, E13 and E14). In this sector, three genotypes (ETBW6095 (G6), ETBW6098 (G7) and ETBW5798 (G8)) are the winning genotypes. In the second sector (between L2and L3), where E7 (Geregera 2012) and E10 (Melkassa 2011) are inclusive, ETBW6093 (G4) and ETBW5827 (G9) are the winning genotypes. Moreover, only the standard check genotype, Kakaba (G1), is the winning genotype within the third sector under E8. In the fourth sector which is bounded by L4 and L1, ETBW6093 (G2) is the winning genotypes under environment E11and E12.

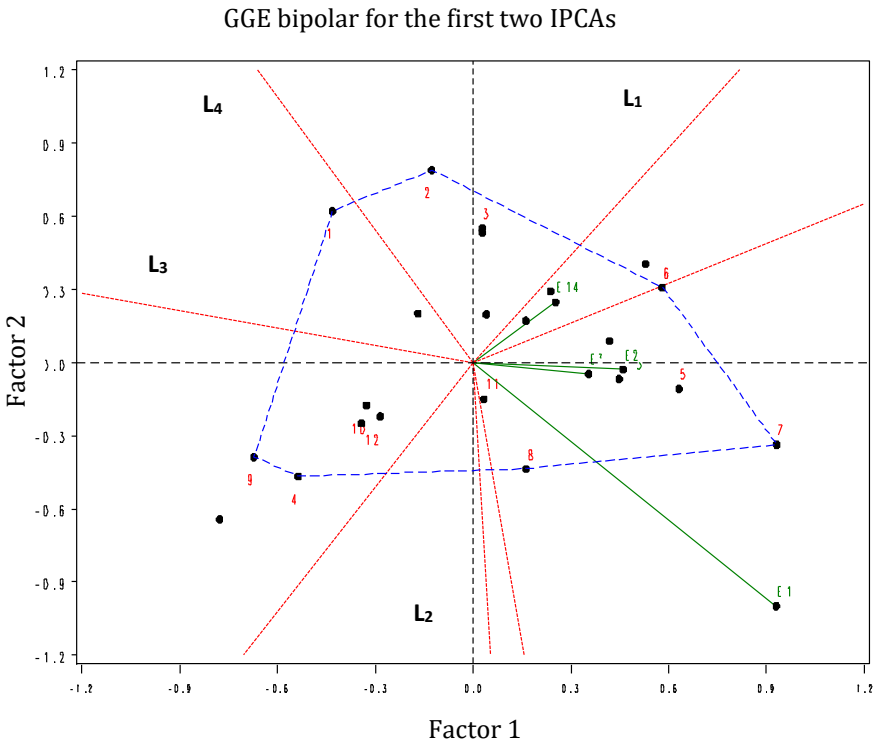

Figure 2. Biplot for the first two IPCAs to show the which-won-where pattern of 12 bread wheat genotypes evaluated across 14 environments (SREG GGE biplot).

With the present data set, the genotype G6, G7, G3, G5 and G12 expressed a highly interactive behaviour (positively or negatively), whereas environments excluding E1, E5 and E7 exhibited low interaction. The addictive behaviour of the environments which showed low interaction indicated that genotypic yield in those environments was highly correlated with the overall genotypic means across environments. Among the extreme genotypes, G4 and G9 are located in pairs indicating their similar response pattern. The genotypes located at the sector's vertex had optimum performance in their respective mega-environment.

Test locations such as Alemtena, Dera and Sinana in both years are clustered in one similar sector indicating the repeatable performance of the genotypes observed in these respective locations and they could be considered as one mega-environment for wheat variety evaluation and recommendation. Among the sites, Melkassa was relatively closer to biplot origin and hence less interactive location and could be good enough location for selection of genotypes with average adaptation. The non-repeatable performance of test genotypes for grain yield could be associated largely with the presence of prevalent diseases mainly wheat rusts and septoria leaf blotch. Hence, selection of best lines based on the analysis of GEI of grain yield data would be misleading. Wheat breeders in the national program, therefore, must speculate carefully the selection of lines for release giving due attention to the most prevalent diseases of wheat and other climatic factors.

CONCLUSION

AMMI clearly indicated genotypes with narrow adaptability while others with superior performance in all environments. The interaction of the 12 genotypes was best predicted by the first three principal components of genotypes and environments but the first two PCs could also explain most of the variations. Thus, biplots generated using genotypic and environmental scores of the first two AMMI components can help breeders to understand the behaviour of the genotypes, environments and their interactions. Moreover, AMMI biplots have enabled identifying suitable sub-mega environments for further varietal evaluation. We identified some lines with stable performance, and genotype ETBW6095 (G6) out-yielded the average of varieties used as checks nearly by 9.0 %, thus providing useful material to the farmers in moisture-limited areas and to the wheat breeders as well. A combination of various multivariate statistics should be used to assess genotypic stability, particularly under a stressed condition.

ACKNOWLEDGEMENTS

The authors would like to acknowledge the financial support provided by East Africa Agricultural Productivity Project (EAAPP) and Ethiopian Agricultural Research Institute (EARI) for conducting the field trials. The authors also highly appreciate and acknowledge the efforts of the staffs of National Wheat Research Program collaborating centres' at Regional and Federal Research Institutes for all field management and data collection.

REFERENCES

Annicchiarico, P. 2000. Genotype X environment interactions: Challenges and opportunities for plant breeding and cultivar recommendations. FAO plant production and protection paper No. 174. FAO, Rome.

Basford, K.E., and M. Cooper. 1998. Genotype x environment interactions and some considerations of their implications for wheat breeding in Australia. Aust. J. Agric. Res. 49: 153-174.

Burgueno, J., J. Crossa and M. Vargas. 2001. SAS programs for graphing GE and GGE biplots. Biometrics and Statistics Unit, CIMMYT.

CSA. 2013. Agricultural sample survey for 2012/2013 (2005 E.C). Volume I. Report on Area and Production of major crops. Private peasant holdings, Meher season. Statistical Bulletin 532. Addis Ababa, Ethiopia.

DeLacy, I. H., K.E. Basford, M. Cooper, J.K. Bull and C.G. McLaren. 1996. Analysis of Multi-Environmental Trials, a Historical Perspective. In: Cooper, M. and G. L. Hammer (Eds.). Plant Adaptation and Crop Improvement. CABI, Wallingford, UK, PP. 39-124.

Eberhart, S., and W.A. Russell. 1966. Stability parameters for comparing varieties. Crop Sci. 6: 36-40.

Fernandez, G. C. J. 1991. Analysis of genotype X environment interaction by stability estimates. HortScience 26: 947-950.

Finlay, W., and G.N. Wilkinson. 1963. The analysis of adaptation in a plant breeding programme. Aust. J. Agric.Res. 14: 742-754.

Gauch, H.G. 1992. Statistical analysis of regional yield trials. AMMI analysis of factorial designs. Elsevier, New York, p. 278.

Gauch, H.G., and R.W. Zobel. 1996. AMMI analysis of yield trials. In Kang, M.S. and H.G. Gauch. (eds.). Genotype by environment interaction. CRC. Boca Raton. Florida, pp 85-122 pp.

Gauch, H.G, and R.W. Zobel. 1997. Identifying mega-environment and targeting genotypes. Crop Sci. 37:311-326.

Hernandez, M. V. and J. Crossa. 2000. The AMMI Analysis and Graphing the Biplot. Crop Sci. 40: 597–605.

Kempton, R.A. 1984. The use of biplots in interpreting variety by environment interaction. J Agr. Sci. 103:123-135.

Purchase, J. 1997. Parametric analysis to describe genotype x environment interaction and yield stability in winter wheat. Ph. D. University of the Free State, South Africa.

SAS Institute. 2002. The SAS system for Windows. Release 9.0. SAS. Inst., Gary, NC, USA.

Shukla, G. K. 1972. Some aspects of partitioning genotype by environmental components of variability. Heredity 28:237-245.

Tadesse, W., Y. Manes, R.P. Singh, T. Payne and H. J. Braun. 2010. Adaptation and performance of CIMMYT spring wheat genotypes targeted to high rainfall areas of the world. Crop Sci. 50:240–248.

Van Oosterom, E.J., D. Kleijn, S. Ceccarelli and M.M. Nachit. 1993. Genotype-environment interactions of barley in the Mediterranean region. Crop Sci. 33: 669-74.

Vargas, M. and J. Crossa. 2000. The AMMI analysis and graphing the biplot. Biometrics and Statistics Unit. CIMMYT.

Voltas J, E.F. Van, E. Igartua, L.F. García del Moral, J.L. Molina-Cano and I. Romagosa. 2002. Genotype by environment interaction and adaptation in barley breeding: Basic concepts and methods of analysis. In: Slafer GA, J.L. Molina-Cano, R. Savin, J. L. Araus and I. Romagosa (eds.). Barley Science: Recent Advances from Molecular Biology to Agronomy of Yield and Quality. The Harworth Press Inc., New York, pp. 205-241.

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