

Full Length Research Paper

Adaptation study and genotype by environment interaction of bread wheat genotypes in Tigray, North, Ethiopia

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ABSTRACT

In selecting and recommending a cultivar to growing environment understanding the selection environment and tackling the underlying factor is vital. Sixteen bread wheat genotypes were tested across six environments with the objective of selecting bread wheat genotype with less genotype by environment interaction and higher yield. The experiment was conducted in randomized complete block design using three replication. The classical analysis of variance were significant ($P < 0.01$) for environment genotype and genotype by environment interaction. The magnitude of the environmental variance explained was 27 times larger than the genotype and 10 times larger than the genotype by environment interaction. Using the Additive Main effects and Multiplicative Interaction (AMMI) the two principal components was significant and cumulatively explained 78.6%. The AMMI1 biplot indicated that the genotypes ETBW-6463 was higher yielder and with low contribution to the genotype by environment interaction which was stable genotype. The testing environment E1, E2 and E3 was favorable while, E4, E5 and E6 were less favorable. The genotypes ETBW-6170, Danda'a, ETBW-6463 and ETBW-6295 were near to the origin of the biplot in the AMMI2 and with wider adaption across the growing environment while, the genotype ETBW-6765, ETBW-6754, ETBW-6434 and ETBW-6801 were specifically adapted to E4, E3, E5 and E1 respectively.

Keywords: AMMI, biplot, Bread wheat, stability

INTRODUCTION

Bread Wheat (*Triticum*spp) in Ethiopia, one of the major crops that are central to achieving development in agriculture and the fourth most important cereal crop after tef (*Eragrostis*tef), maize (*Zea mays* L.) and sorghum (*Sorghum bicolor* L.) in area coverage and production wheat occupies an area of about 1.69 million ha with total production of more than 4.53 million tons per year (CSA, 2016). The crop is not only critical to smallholder incomes but the food and nutrition security of tens of millions of Ethiopians.

Despite the availability of wheat varieties with a yield

potential of 6-7ton/ha, the actual average yield is not more than 2.67ton/ha (CSA, 2016), which is 3ton /ha lower than the global average. The low production and productivity of the crop is attributed to diverse and enigmatic constraint like, soil degradation from erosion and soil compaction (Hamza and Anderson 2005), Stripe rust (*Pucciniastriformis*) and stem rust (*P. graminis* f. sp. tritici) (Bekele and Tanner, 1995). Furthermore, uncertain rainfall and very low levels of irrigation make intensive cultivation with improved seeds and fertilizer risky (McCann, 1995).

The low correlation between the potential yield of bread wheat in the country and the actual average yield obtained by farmers even could be worst in areas like Tigray where, the study was conducted by which the rainfall distribution is low and erratic. The low correlation between the genetic and non genetic component is named as genotype by environment interaction and it is higher where the variation between genotypes for morph-physiological characters conferring resistance or avoidance. There is also wider variation between environments for incidence of the same stress such as climatic, soil, biotic and management factors (Bänziger *et al.*, 2001).

Genotype by environment interaction is lack of association between the genetic and the non- genetic factor by which one genotype tend to give good yield in one environment and low yielder in the other environment and it a common phenomenon in agriculture by which difference between genotypic values may increase or decrease from one environment to another which might cause genotypes to even rank differently between environments. Genotype by environment interaction is a major concern in plant breeding by which it reduces progress from selection and it is difficult for cultivar recommendation to target environment Kang and Pham (1991).

Genotype by environment interaction may offer opportunity for selection and adaptation of genotypes that show positive interaction with the specific location which help in the effective utilization of specifically adapted genotypes and prevent loss of yields by selecting broadly adapted genotypes (Ceccarelli *et al.*, 2007). The method of analysis used to quantify genotype by environment interaction and the model accuracy and separation of the useful patten and noise is important in interpreting and utilization of the significant genotype by environment interaction.

The Additive Main effects and Multiplicative Interaction (AMMI) is commonly used method in plant breeding for the analysis of genotype by environment interaction. 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 it is useful for understanding complex genotype by environment interactions. The results can be graphed in a very informative biplot that shows both main and interaction effects for both genotypes and environments (Gauch and Zobel, 1990). Hence, the main objective of this research is to quantify the magnitude of genotype by environment interaction and facilitate cultivar recommendation using the additive Main effects and Multiplicative Interaction model.

MATERIALS AND METHODS

Experimental layout and genetic materials

The experiments were conducted in 2014-2016 cropping season. sixteen bread wheat genotype (Danda'a, ETBW6170, ETBW6188, ETBW6189, ETBW6295, ETBW6338, ETBW6434, ETBW6463, ETBW6469, ETBW6481, ETBW6727, ETBW6754, ETBW6760, ETBW6765, ETBW6801 and ETBW6802) were incorporated. The genotypes was laid out in a randomized complete block design (RCBD) with three replication. The experimental site contained a total of 6 rows with row spacing of 0.2m and with a total plot size of 1.2 meter by 2.5 meter and spacing between plots was 0.5 meter while spacing between block was maintained at 1 meter. Seed rate was calibrated from 80kg/ha and planting was made by drilling to the six rows. Fertilizer was applied 41kg N ha⁻¹ and 46kg P₂O₅ ha⁻¹ at planting and 23kg N ha⁻¹ urea fertilizer was applied in split application during vegetative stage of the crop. Table 1

Table 1. Environment year of production and average rain fall.

Code	Environment	Year	Rainfall mm 18 years average
E1	A/gara	2014	994
E2	Mekhan	2014	704
E3	Mekhan	2015	704
E4	A/gara	2015	994
E5	A/gara	2016	994
E6	Mekhan	2016	704

Statistical analysis

Before analyzing the combining analysis the homogeneity of variance test was done using the Bartlett's (1974 using the R software using the agricolae package (Felipe de Mendiburu, 2015) and there was no violation of the analysis of variance assumption. The combined analysis for genotype environment and genotype by environment interaction was done using the R software 3.4.1 using the agricolae package. The multiplicative model of the AMMI0 AMMI1 biplot and AMMI2 plant breeding package 1.1 Umesh and Rosyara (2014) and GEA-R software was used.

AMMI combines analysis of variance (AOV) and principal component analysis (PCA) into a single model with additive and multiplicative parameters. The AMMI model equation is:

$$y_{ij} = \mu + G_i + E_j + \left(\sum_1^n K_n U_{ni} S_{nj} \right) + Q_{ij} + e_{ij}$$

Where: (i = 1, 2,.....16; j = 1,.....6); Y_{ij} = The

Table 2. Combined analysis of variance for yield of sixteen bread wheat genotypes tested over six environments.

source of variation	Df	Sum	Mean Sq	F value	Pr(>F)	% explained
ENV	5	728.76	145.752	103.2122	0.0000002843***	75.3
GEN	15	27.22	1.815	2.8411	0.0005167***	2.8
ENV:GEN	75	81.94	1.093	1.7105	0.0019985**	8.5
REP(ENV)	10	14.12	1.412	2.2109	0.0189859	
Residuals	182	116.25	0.639			

Table 3. Analysis of the multiplicative model using principal components.

	DF	sum of square	Mean of square	F value	Pr(>F)	percent	Accumulated%
PC1	19	50.9125	2.67961	4.2	0	55	55
PC2	17	21.7776	1.28103	2.01	0.0128	23.5	78.6
PC3	15	11.4331	0.76221	1.19	0.2828	12.4	90.9
PC4	13	4.8534	0.37334	0.58	0.8681	5.2	96.2
PC5	11	3.5614	0.32377	0.51	0.895	3.8	100

performance of the i^{th} genotype in the j^{th} environment; μ = The grand mean; G_i = Additive effect of the i^{th} genotype (genotype mean minus the grand mean); K_n = Eigen value of the PCA axis n ; E_j = Additive effect of the j^{th} environment (environment mean deviation); U_{ni} and S_{nj} = Scorer of genotype i and environment j for the PCA axis n ; Q_{ij} = Residual for the first n multiplicative components, and e_{ij} = error

RESULTS AND DISCUSSION

Combined analysis of variance

The main effect for environment genotype and genotype by environment interaction showed significant difference ($P < 0.01$). The explained percentage sum of square for the environment genotype and genotype by environment interaction was 75.3, 2.8 and 8.5 respectively (Table 2). 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 contributing in large to the genotype by environment interaction. The magnitude of the environmental variance was 27 times larger than the genotype and 10 times larger than the genotype by environment interaction. The low contribution of the genotype sum of square is an indication of the narrow genotypic diversity of the bread wheat genotypes.

The contribution of the growing environment as discussed by Gauch and Zobel (1989a) ranged from 80 to 90% and variation due to genotype by environment interaction and genotype is 10% to 20%. The study is in agreement with (Abay *et al.*, 2009; Bantayehu, 2009; Muez *et al.*, 2014) that had found large environmental sum of square in barley for the response variable grain yield. The result was not also in agreement for protein

content in malt barley by which the influence of the environment was lower than the genotype by environment interaction and genotype sum of square (Muez *et al.*, 2015).

AMMI analysis

Following, the output of the classical analysis of variance the genotype by environment interaction was significant with 75 degree of freedom. The multiplicative model using the Additive Main effects and Multiplicative Interaction (AMMI) was further decomposed into two significant principal components. The first principal component explained 55% of the variability in the genotype by environment interaction and the second principal component explained additional 23.5 % (Table 3). Cumulatively the two significant principal components explained 78.6% according to the Postdictive F-test of Gollob (1968) the two significant principal components are adequate for representing the variability.

The predictive accuracy is mainly based on the previous knowledge and experience using the AMMI model. Hence, the study of faba bean in Tigray was conducted and the AMMI1 showed best model fitness for the grain yield and broomrape number (Teklay *et al.*, 2015) similar result was obtained by (Hints *et al.*, 2013) in bread wheat, AMMI1 was the only significant and with the best model fitness.

AMMI biplot

The 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

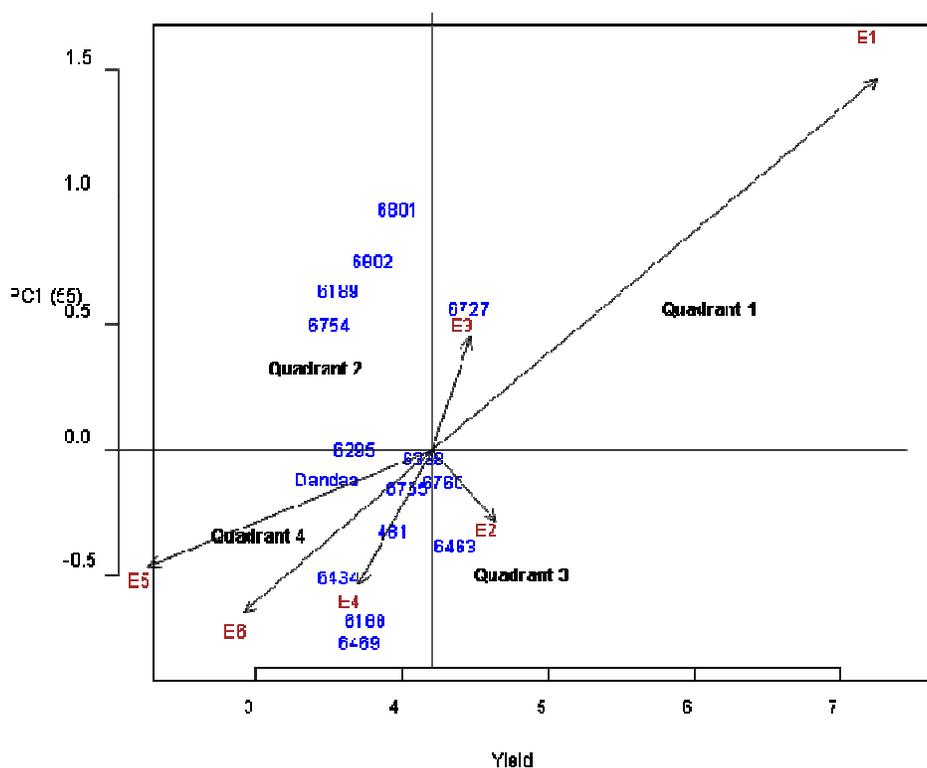


Figure 1. AMMI1 biplot for grain yield of sixteen bread wheat genotypes tested in six environment of Tigray during 2014-2016

is proportional to the response they have to the genotype by environment interaction effects (Crossa *et al.*, 1990). The interaction principal component 1 (IPCA1) represented in the y- axis where the genotypes and environments mean was plotted on the x- axis.

The genotypes EBW6727 was located in the first quadrant and is characterized with higher mean grain yield and with higher contribution to the genotype by environment interaction. The environments E1 and E3 were also located in the first quadrant and this environment was favorable for discriminating the genetic potential of the genotypes. In the second quadrant there was no environment and there was no correspondence with the genotypes. The genotypes ETBW-6801, ETBW-6802, ETBW-6189 and ETBW-6754 were lower yielder genotypes and with higher contribution to the increasing genotype by environment interaction. The genotypes located in the third quadrant are characterized as low yielder and stable genotypes while, ETBW-6463 was the only genotype in the fourth quadrant characterized as higher yielder and with low contribution to the genotype by environment interaction.

AMMI2 biplot

The two significant principal component interactions

explained 78.6% of the genotype by environment interaction and the second principal component further contributed additional 23.5% hence, it is important to exploit the AMMI2 model family. Genotypes which are far from the centre of biplot have high genotype by environment interaction and specifically adapted while, those genotypes nearest to centre of biplot have high stability and wider adaptation across the growing environments.

The genotype ETBW-6765 was specifically adapted to the growing environment E4, ETBW-6754, ETBW-6434 and ETBW-6801 were specifically adapted to E3, E5 and E1 respectively. The genotypes ETBW-6170, Danda'a, ETBW-6463 and ETBW-6295 were near to the origin of the biplot and with wider adaption across the growing environment. Generally there are different winning genotypes for each testing environment and this is an indication for the presence of cross over type of genotype by environment interaction (Yan *et al.*, 2007). The testing environments E1, E2, E3 and E4 with long vector length from the origin implying, the discriminating capacity for expressing the genetic potential of the genotypes. The testing environments E5 and E6 was with short vector length that indicates the less discriminating power of the genotypes. Figure 1 and 2.

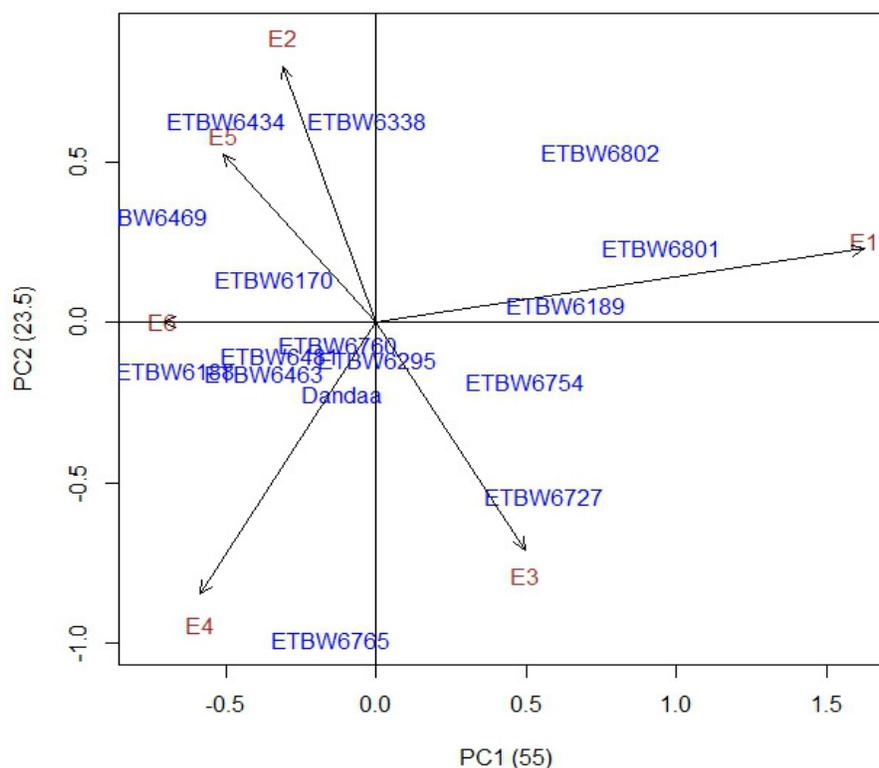


Figure 2. AMMI2 biplot for grain yield of sixteen bread wheat genotypes tested in six environment of Tigray during 2014-2016

CONCLUSION

The studied sixteen bread wheat genotype over six environments analysis of genotype by environment interaction for grain yield showed that there was significant genotype environment and genotype by environment interaction and the contribution of the environmental variance in explaining the genotype by environment interaction was 27 times higher than the genotype main effect and 10 times bigger than the genotype by environment interaction. The Additive Main effects and Multiplicative Interaction (AMMI) Further classified the significant genotype by environment interaction and the two principal component was significant and explained the overall variability with the model fitness of 78.6%.

The AMMI1 biplot indicated that the genotypes ETBW-6463 was higher yielder and with low contribution to the genotype by environment interaction considered as stable genotype. The testing environment E1, E2 and E3 was favorable while, E4, E5 and E6 were less favorable environments. Using the AMMI2 biplot analysis in each environment there is winning genotype but, of all genotypes ETBW-6170, Danda'a, ETBW-6463 and ETBW-6295 were near to the origin of the biplot and with wider adaption across the growing environment.

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REFERENCES

- Abay F, Bjørnstad A (2009). Specific adaptation of barley varieties in different locations in Ethiopia. *Euphytica*, 167(2), 181-195.
- Bänziger M, Cooper M (2001). Breeding for low input conditions and consequences for participatory plant breeding examples from tropical maize and wheat. *Euphytica*, 122(3), 503-519.
- Bekele G, Tanner DG (1995). Status of cereal production and pathology research in Ethiopia. Breeding for Disease Resistance with Emphasis on Durability. 42-50.
- Ceccarelli S, Grando S (2007). Decentralized-participatory plant breeding: an example of demand driven research. *Euphytica*, 155(3), 349-360.
- Central Statistical Agency (CSA) (2016). Agricultural sample Survey 2016 /2017 (2009.e.c.). Report on crop and livestock product utilization. Statistical bulletin 584. Addis Ababa, Ethiopia. VOLUME I. 122p.
- Crossa J, Fox PN, Pfeiffer WH, Rajaram S, Gauch Jr. HG (1991). AMMI adjustment for statistical analysis of an international wheat yield trial. *Theoretical and Applied Genetics*, 81(1), 27-37.
- Felipe de Mendiburu (2015). Statistical Procedures for Agricultural Research R package version 1.2-3(<https://CRAN.R-project.org/package=agricolae>)

- Gauch HG, Zobel RW (1988). Predictive and post dictive success of statistical analyses of yield trials. *Theoretical and Applied Genetics*76:1–10.
- Gauch HG, Zobel RW (1989a). Accuracy and selection success in yield trial analyses. *Theoretical and Applied Genetics*77:473–481.
- Gollob HF (1968). A Statistical Model Which Combines Features of Factor Analytic and Analysis of Variance Tech- niques. *Psychometrika*, 33, 73-115.
- Hamza MA, Anderson WK (2005). Soil compaction in cropping systems.A review of the nature, causes and possible solutions. *Soil Tillage Res.* 82, 121–145.
- Kang MS, Pham HN (1991). Simultaneous selection for high yielding and stable crop genotypes. *Agron. J.* 83:161–165.
- Muluken B (2009). Analysis and correlation of stability parameters in malting barley. *Afri. Crop Sci. J.* 17(3).
- R Core Team (2017). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.
- Teklay A, Yemane N, Muez M, Adhiena M, Assefa W, Hadas B (2015). "Genotype by environment interaction of some faba bean genotypes under diverse broomrape environments of Tigray, Ethiopia." *J. Plant Breeding and Crop Sci.* 7, no. 3 79-86.
- Umesh RR (2014). Analysis and visualization of data from plant breeding and genetics experiments R package version 1.1.1/r37 (<https://R-Forge.R-project.org/projects/plantbreeding>)
- Van Eeuwijk FA (1992b). Multiplicative models for genotype-environment interaction in plant breeding. *Statistica Applicata* 4:393–406.
- Yan W, Kang MS, Ma B, Woods S, Cornelius PL (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop science*, 47(2), 643-653.