Evaluation and Selection of Ethiopian Bread Wheat Varieties Using Linear Mixed Model

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Abstract

Ethiopia is a country with diverse agro ecological settings which make the yield of crop variety fluctuate and make selection of best variety difficult. This study was conducted to select best bread wheat variety, variety that has higher performance with relatively stable performance across varying environments, by evaluating the varieties in terms their average performance and stability across the test environments. The yield and stability of the performance of 17 bread wheat genotypes across 18 test environments was evaluated using linear mixed model. The yield performance of genotypes was evaluated using different types of BLUPs. The stability of genotypes was evaluated using different methods under mixed model assumption. Genotypes such as ETBW5798, ETBW5800 and ETBW5879 were generally identified to have higher average yield with relatively stable performance across the test environments whereas Digelu, ETBW5875 and ETBW5899 were generally found to have poor performance in terms of average yield and stability as well. Currently very efficient experimental designs for agricultural experiment such as IBD, Alpha − lattice and Lattice designs have been introduced and such designs are not suitable for analysis using the usual

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fixed effect model and are better fitted using linear mixed model. So, a future multi environmental trial study that uses such designs must use the linear mixed model.

Keywords: BLUP-Best Linear Unbiased Predictor, ETBW-Ethiopian Bread Wheat, Genotype

1. Introduction

1.1. Background of the Study

Wheat (*Triticumaestivum L.*) is one of the first domesticated food crops and has been used as staple food for the major civilizations of Europe, West Asia and North Africa for the last 8000 years (FAO, 2002).

It is a major diet component because of its agronomic adaptability, ease of grain storage and ease of converting grain into flour for making edible, interesting and satisfying foods (FAO, 2002). In Ethiopia, wheat is the third most important cereal crop based on total annual production, contributing, 15.60% of total country's annual crop production (CSA, 2013/2014). Meanwhile the productivity of this crop is only 8.4qt ha^{-1}, which is below the national average of 14.4 qt ha^{-1} (Zelalem, 2011). This low yield is attributed to the use of traditional production system, the influence of biotic factors such as diseases and unavailability of production inputs such as improved varieties. So, the yield of this crop must be improved by selecting best hybrid (variety) that has low response to these environmental stress and have relatively better yield across these environments (Ferraudo and Percin, 2014).

Ethiopia is a country with wide agro-climatic conditions together with diverse soil and other physical surroundings (Kassa*et al.*, 2006). It has been found that this varying environment results in inconsistent performance of crop

varieties (Asnake *et al.*, 2013). The aim of breeders and agronomists is, therefore, to identify wheat variety that has relatively better yield performance with small fluctuations over these diverse environments. Such variety is obtained after rigorous breeding and selection procedures that involve testing of large collection of genotypes across diverse environments and use of efficient statistical model for the selection (Asfaw*et al.*, 2013).

Several statistical methods are available for examining the GEI and evaluation of the yield performance and stability of genotypes evaluated in MET. The linear regression of genotype values on site mean yield (Finlay & Wilkinson, 1963) is the most popular method due to its simplicity (Kassa*et al.*, 2006). But, this method is not efficient since,it does not take into account the multivariate nature of data from MET. It has also been found that this model expresses only small portion of GEI and large amount of GEI remains unexplained (Piepho, 1997; Crossa*et al.*, 2010). The AMMI model has also been used for studying the GEI of data from MET. But this method is efficient for data that has no missing values only and result in large experimental error for data with missing values.

Recently, very efficient experimental designs for field trial such as Incomplete Block Design, Lattice Design, Alpha-Lattice has been developed and used in field experiments. These designs are not suitable for statistical analysis under fixed effect models such as AMMI and Regression. Hence it is impossible to handle data from such designs, whereas, the mixed effect model can efficiently handle such data. Further, the mixed effect model can efficiently handle data that has missing values and MET data that has error variance heterogeneity across trials. Hence the use of mixed effect model over

fixed effect model for recent time analysis of data from MET is quite appealing.

The mixed model approach to analysis of MET data has several advantages as compared to the fixed effect models. This is due to the fact that mixed model can be applied to data with missing values as well as unbalanced data (Kassa*et al.*, 2006; Filho*et al.*, 2014). The method can also accommodate the heterogeneity of error variance among trials. This model can even accommodate the fixed effect model such as Finlay and Wilkinson's (1963) method as discussed by Kassa*et al.* (2006).

1.2. Objectives of the Study

The general objective of this study was to examine the genotype by environment interaction and yield stability of Ethiopian bread wheat (*Triticumaestivum L.*) using linear mixed model.

Specific Objectives

1. To evaluate the yield performance of Ethiopian bread wheat genotypes using different methods under mixed model assumptions
2. To evaluate the stability of the genotypes using different stability measures

2. Methodology

2.1. The Data

The data used in this study was obtained from Ethiopian Institute of Agricultural Research (EIAR), Kulumsa Agricultural Research Center. Accordingly, a two-year wheat yield trial data of (2011 and 2012) main cropping season that involves the evaluation of 17 bread wheat genotypes

across 9 locations was used. The specific year-location combination is considered as environment and these location-year combinations and the assigned environment code was given in Table 1.Seventeen bread wheat genotypes were used in this study among which Danda'a and Digeluwere released earlier and were given local names while the other genotypes were not given local names yet.

Table 1. Brief Summary of Environments that were used in the Study

Location(Year)	Environment Code	Location(Year)	Environment Code
Adet (2011)	E1	Adet (2012)	E10
Arsi Negelle (2011)	E2	Arsi Negelle	E11
Arsi Robe (2011)	E3	(2012)	E12
Assasa (2011)	E4	Arsi Robe (2012)	E13
Dembi (2011)	E5	Assasa (2012)	E14
Holeta (2011)	E6	Dembi (2012)	E15
Kulumsa (2011)	E7	Holeta (2012)	E16
Meraro (2011)	E8	Kulumsa (2012)	E17
Shambu (2011)	E9	Meraro (2012)	E18
		Shambu (2012)	

The list of these genotypes together with the assigned genotype code in this study (for the ease of analysis) was given in Table 2.

Table 2. List of genotypes that were used in the study

Genotype Name	Genotype Code	Genotype Name	Genotype Code
Danda'a	G1	G10	ETBW5879
Digelu	G2	G11	ETBW5890
ETBW5798	G3	G12	ETBW5899
ETBW5800	G4	G13	ETBW5900
ETBW5825	G5	G14	ETBW5956

ETBW5826	G6	G15	ETBW5957
ETBW5827	G7	G16	ETBW5958
ETBW5850	G8	G17	ETBW5961
ETBW5875	G9		

2.2. Analytical Methods

The basic statistical model used in the study was given by:

$$Y_{ijk} = \mu + G_i + E_j + (GE)_{ij} + R(E)_{kj} + \varepsilon_{ijk} \qquad (1)$$

Where, Y_{ijk} is the yield response of kth replicate of ith genotype in j^{th} environment, μ is the grand mean, G_i is the main effect of ith genotype, E_j is the main effect of jth environment, $(GE)_{ij}$ is the interaction effect of ith genotype with j^{th} environment, $R(E)_{kj}$ is the effect of kth replication nested within j^{th} environment and ε_{ijk} is the random error associated with the ijk^{th} observation. The genotype, GEI and the replication within environment are assumed to have random effect and environments are assumed to have fixed effect.

2.2.1. Model Formulation and Estimation of Parameters

The mixed model permits the elements of Y to be correlated unlike the standard linear model which assumes independent and uncorrelated elements of Y. This can be handled either through the specification of covariance matrix of ε i.e, $\varepsilon \sim N(0, R)$ or permitting the random effect and random coefficient in the analysis through inclusion of $Z\gamma$ into the mixed effect model, where $\gamma \sim N(0, G)$ is random effect and Z is the associated design

matrix. The focus of this work was on the latter case where the covariance among the data is modeled through $Z\gamma$. The linear mixed model for the objective model in equation 1 was derived as follows.

The model in equation 1 was written in matrix form as

$$Y = X\beta + Z\gamma + \varepsilon \tag{2}$$

Where X is design matrix associated with the vector of fixed effect β. γ contains the coefficients of random effects and Z is the corresponding design matrix of random effects and ε is matrix of model error. The random components were assumed to have joint distribution with mean zero and uncorrelated covariance matrix. i.e.

$$\begin{pmatrix} \gamma \\ \varepsilon \end{pmatrix} \sim N\left[\begin{pmatrix} 0 \\ 0 \end{pmatrix} ; \begin{pmatrix} G & 0 \\ 0 & R \end{pmatrix} \right] \tag{3}$$

Where, G is the covariance matrix of random effects. Under this assumption, the model in equation (1) and (2) is called the linear mixed model and the statistical analyses in this study were based on this model.

2.2.2. Estimation of parameters and the BLUP procedure

The estimation of the parameters was done as follows.

1st, the covariance parameters G and R were assumed to be known and the Best Linear Unbiased Estimators (BLUEs) of β and the Best Linear Unbiased Predictors (BLUPs) of γ were obtained using the Henderson's (1984) method and then the estimates of the covariance matrices G and R, $\underline{\theta}$, were obtained and substituted into the solution for BLUEs and BLUPs of β and γ. The estimator and predictor of β and γ were obtained as follows

The joint distribution of the random effects is given by:

$$f(\gamma, \varepsilon) = \frac{1}{(2\pi)^{(n+g)/2}} \left| \begin{matrix} G & 0 \\ 0 & R \end{matrix} \right|^{-1/2} \exp\left\{ -\frac{1}{2}\left[Y - X\beta - \frac{\gamma}{Z\gamma} \right]^T \left[\begin{matrix} G^{-1} & 0 \\ 0 & R^{-1} \end{matrix} \right] \left[Y - X\beta - \frac{\gamma}{Z\gamma} \right] \right\}$$

(4)

Where g is number of elements in γ and the superscript T denotes the transpose operator to the matrix.

Maximization of $f(\gamma, \varepsilon)$ with respect to β and γ requires minimization of P, where

$$P = \left[y - x\beta - \frac{\gamma}{z\gamma} \right]^T \left[\begin{matrix} G^{-1} & 0 \\ 0 & R^{-1} \end{matrix} \right] \left[y - x\beta - \frac{\gamma}{z\gamma} \right]$$

(5)

Differentiating this equation (5) with respect to β and γ and rewriting it will give

$$\left[\begin{matrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \end{matrix} \right] \left[\begin{matrix} \tilde{\beta} \\ \tilde{\gamma} \end{matrix} \right] = \left[\begin{matrix} X'R^{-1}Y \\ Z'R^{-1}Y \end{matrix} \right]$$

(6)

Which is the popular Henderson's mixed model equation (MME), and the solutions were given as follow.

$$\left[\begin{matrix} \tilde{\beta} \\ \tilde{\gamma} \end{matrix} \right] = \left[\begin{matrix} (X'V^{-1}X)^{-1}X'V^{-1}Y \\ GZ'V^{-1}(Y - X(X'V^{-1}X)^{-1}X'V^{-1}Y) \end{matrix} \right]$$

(7)

2.3. Test for the Overall Significance of the Model

Combined ANOVA was performed over the entire environment to test the significance of effects using the Generalized Linear Model (GLM). The type-III Sum of Square (SS), usually called corrected SS was used to construct the table, since the usual type-I SS is biased due to imbalance in the data set due to the presence of missing values (Milliken and Johnson, 1984, as cited in Little *et al.*, 2006). In Type-III (Corrected SS) elements of the analyzed

genotype by environment data matrix were derived from LSE and imbalance was eliminated by estimation of missing plots based on experimental design of the study. The SS were computed from linear hypothesis: H0: Lβ=0, where L is the matrix of coefficient corresponding to the effect being tested.

Further intervention was made to the data using the method proposed by Zobel *et al.* (1988) to separate the pattern and noise in the GEI. The authors had shown that the SS for interaction (SS_{G*E}) can be further partitioned in multiplicative components related to Eigen values of matrix of GEI. Such method of analysis that links the analysis of variance with the principal component analysis is called Additive Main effects and Multiplicative Interaction (AMMI) and was done as follows.

2.4. The Additive Main Effect and Multiplicative Interaction Effect (AMMI) and ASV

The Additive Main effect and Multiplicative Interaction effect (AMMI) model as proposed by Zobel *et al.*, (1988), involves the application of the conventional analysis of variance to the environment and genotype main effect and principal component analysis to the GEI. Accordingly, the AMMI model for the evaluation of I genotypes tested in J environment was given as:

$$y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{r} \lambda_k \, \alpha_{ik} \gamma_{jk} + \varepsilon_{ij} \qquad (8)$$

where, y_{ij} is the mean of ith genotype evaluated in jth test environment obtained from predicted yield response, $\hat{y}_{ijk}$, μ, g_i and e_j are the overall mean (grand mean), the main effect of the ith genotype and the jth environment respectively; λ_k is the singular value for the kth principal component axis (PCA); interaction parameters α_{ik} and γ_{jk} are elements of the kth singular

vector for genotypes and environments, respectively; ε_{ij} is the residual and $r \leq \min(I - 1, J - 1)$. The procedure of AMMI analysis was done as follows.

Suppose that W is G by E matrix of I genotypes evaluated in J environments. From this, G by E matrix of cell mean the environment and the genotype main effect has been removed to establish matrix Z. This was done as follows.

$$Z = Z_{ij} = \bar{y}_{ij} - \hat{\mu} - \hat{\alpha}_i - \hat{\beta}_j \tag{9}$$

Where, $\bar{y}_{ij}$ is the predicted mean of ith genotype in the jth environment, $\hat{\mu}$ is the grand, $\hat{\alpha}_i$ is the estimated effect of ith genotype and $\hat{\beta}_j$ is the estimated effect of jth environment.

This matrix, Z was then partitioned into three matrices, U, Λ, and V, using the Singular Value Decomposition (SVD) procedure as follows.

$$Z_{IJ} = U_{I,r}\Lambda_{r,r}U'_{J,r}(r \leq \min(I - 1, J - 1)) \tag{10}$$

The AMMI model obtained from this SVD procedure was given as:

$$y_{ij} = \mu + g_i + e_j + \sum_{k=1}^{s} \alpha_{ik}^* \gamma_{jk}^* + \theta_{ij} + \varepsilon_{ij} \tag{11}$$

Where, $\alpha_{ik}^* = \alpha_{ik}\lambda_k^{0.5}$ is the genotype score obtained by SVD of GEI and $\gamma_{jk}^* = \lambda_k^{1-0.5}\gamma_{1j}$ is the corresponding environment score, and θ_{ij} is the noise or part of GEI that remains unexplained by rank s truncated AMMI model. The full AMMI (saturated) model contains s=r IPCAs and is denoted as AMMI-r, but the value of s is usually less than r *i.e*, smaller number of IPCAs are needed to sufficiently explain the pattern in GEI and the remaining information is contained in the AMMI noise, θ_{ij}. Such AMMI model (AMMI model with fewer IPCAs) is called truncated AMMI model.

The essential feature of AMMI model is that optimal truncated AMMI model can be determined using well defined statistical procedure. This procedure is called the test for the significance of IPCAs and has been achieved using the (Gollob's, 1968) method. Therefore, selection of the optimal model was based on F tests for the successive terms of the interaction, the number of included terms corresponding to the number of significant IPCAs.

2.4.2. The AMMI Stability Value (ASV)

The AMMI model proposed by (Zobel *et al.*, 1988) does not provide quantitative measure for evaluating genotype in terms of stability in their yield performance across test environments. The AMMI Stability Value (ASV) was proposed by Purchase *et al.* (2000) in order to fill this gap. The ASV value for the ith genotype was computed as follows:

$$ASV_i = \sqrt{\left[\frac{IPCA1\ ss(IPCA1\ score)}{IPCA2\ ss}\right]^2 + (IPCA2\ score)^2} \qquad (12)$$

Where; IPCA1 ss is the sum of squares of the first IPCA and IPCA2 ss is the corresponding SS for the second IPCA. The genotypes were then compared based on this stability measure such that genotype with the lowest ASV value got rank 1 and genotype with higher ASV are less stable and had specific adaptation.

2.5. Evaluation of Genotypes Using Mixed effect Model

The performance of genotypes has been evaluated using different methods under the mixed model methods. This was mainly done through different types of BLUPs. These procedures contain the fixed environment effect and the random genotypic effects.

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2.5.1. The Broad and Narrow BLUPs of Genotypes

The BLUP is also known as a shrinkage estimator because the estimate of a random effect

shrunk to adjust for uncertainty arising from its probability distribution and hence it is devised to maximize the correlation between estimates of the realized values of the random effects and the "true" values of the random effects. Accordingly, the broad BLUP of genotype i was computed as:

$$G_{i\ BROAD} = \hat{\mu} + \hat{g}_i + \frac{\sum_{j=1}^{E} \hat{e}_j}{E} \tag{13}$$

The narrow BLUP of genotypes was computed as

$$G_{i\ NARROW} = \hat{\mu} + \hat{g}_i + \frac{\sum_{j=1}^{E} \hat{e}_j}{E} + \frac{\sum_{j=1}^{E} (\widehat{ge})_{ij}}{E} \tag{14}$$

Where, $\hat{\mu}$ is the estimated grand mean, $\hat{g}_i$ is the predicted effect of the ith random genotype effect, $\hat{e}_j$ is the estimated effect of jth environment and E is the number of environments.

2.5.2. The Superiority Measure of Genotypes

This method has been proposed by Lin and Binns (1988) for evaluation of genotype with respect best genotype in given test environment. This procedure was proposed for the fixed effect methodology where the environment speific means were obtained using LSmean procedure in GLM. But, in this study the environment specific BLUPs of genotypes were used for computing the statistics. Accordingly, the superiority measure for the ith genotype, Pi was computed as follows:

$$P_i = \sum_j \frac{(x_{ij} - m_j)^2}{2n} \tag{15}$$

Where, x_{ij} is the environment specific predictor of ith genotype evaluated in j^{th} environment, m_j the maximum of jth environment and n is the total number of environments. The measure indicates how often a genotype is close to being the best in the given test environments and hence genotype with Pi value close to zero is considered as best compared to other genotypes.

2.6. Stability Analysis

The stability analyses were done under the mixed model methodologies and different stability measures were used. These stability measures were discussed below.

2.6.1. The Difference between the Broad BLUP and Narrow BLUP

This method was proposed by (Reano, 2010) and had been called Reano's Stability Value (RSV) and under this method; stable genotypes are defined as those genotypes with estimates of broad BLUP closer to estimates of narrow BLUP. Accordingly, the stability measure of ith genotype was computed as

$$SG_i = \text{BROAD BLUP}(G_i) - \text{NARROW BLUP}(G_i) \tag{16}$$

The genotypes were then ranked based the numerical value of this stability measure. Accordingly genotype with very small SGi value was identified as the most stable genotype whereas genotypes with higher value of SG_i are genotypes that were susceptible to GEI and hence identified to have unstable performance across test environments.

2.6.2. The Harmonic Mean of the Relative Performance of Genotypic Value

The harmonic mean of relative performance of genotypic value (MHPRVG) has been proposed by (Mendes *et al.*, 2012), and used for simultaneous evaluation stability and adaptability of genotype under evaluation. Accordingly, the MHRPVG of the ith genotype was given as follows.

$$MHRPVGi = \frac{n_i}{\sum_{j=1}^{n} \overline{GV}_{.j}/GV_{ij}} \tag{17}$$

Where: n_i = number of environments where genotype i was evaluated and $\overline{GV}_{.j}$ is the average of GV_{ij} in environment j and GV_{ij} are the environment specific BLUP of genotypes.

2.7. The Graphical Methods

According to Yan and Tinker (2006), GGE biplot is a graphical procedure that allows the analysis of the two-way interaction in a table of I genotypes by J environments such that systematic patterns between the components of rows (genotypes), between the components of columns (environments) as well as patterns between rows and columns can readily be assessed and evaluated. The GGE biplots were produced using the R package named GGE Biplot GUI, non-commercial package created by Yan and Tinker (2006). The procedures assume that matrix of I genotypes evaluated in J environments can be sufficiently approximated by rank- two (i.e.r= 2) matrix. Hence, the biplot procedure starts with centering this G by E matrix to establish the matrix Z. then the matrix Z was decomposed into three matrices, U, Λ, and V, using the Singular Value Decomposition (SVD) as discussed in AAMI procedure whereas, centering was done as follows.

$$Z = Z_{ij} = \bar{y}_{ij} - \mu - \beta_j \qquad (18)$$

The plots were then produced by plotting the IPCA-1 score Vs IPCA-2 of this SVD procedure.

3. Results andDiscussion

3.1. Introductory Remarks

In this study, the data of 17 Ethiopian bread wheat genotypes evaluated in 18 test environments were analyzed using linear mixed model. Most of the Statistical analyses were done using Statistical Analysis System (SAS V. 9.2). The codes that have been used were given in the data can be obtained from the authors upon request. The environments and genotypes were coded for the ease of analysis in this study according to Table 1 and 2 respectively. The exploratory data analysis was made prior to all statistical analysis in this study. Further, different numerical and graphical methods for test for the model adequacy checking were made. The results of this procedure have not been revealed but the SAS codes for this procedures can also been obtained from the author upon request. Separate analysis of variance was conducted for the individual environments under evaluation using the usual fixed effect ANOVA model for Randomized Complete Block Design in order to check for the significance of the genotype and replication effects. Then, the data have been combined over environments and the combined analysis of variance was then made as follows.

3.2. Test for the Overall Significance of the Model

The test for the overall significance of the model was done using the combined analysis of variance (ANOVA). The result of the combined

ANOVA over the test environments was given in the upper panel of Table 3. It has been found that all effects are highly significant (P-value<0.001). The environmental effect was highly significant, indicating that there are significant differences/ variation among environment for grain yield, which may attributed to temperature, soil type rainfall and other environmental factors that vary across the environments. The genotype effect was also highly significant indicating that there is difference among genotypes in their yield performance in a given environment and hence difficult to select single genotype that better performs across the test environments.

3.3. Interpretation of the Additive Main Effect and Multiplicative Interaction Effect (AMMI)

The AMMI procedure has been used in order to further investigate the nature of GEI and explore the information contained in it. The result of this procedure was presented in the lower panel of Table 3 and the corresponding interpretations were given as follows. It has been found that 17.61% of total variation was attributed to the GEI and only 13.31% of total variation in the data has remained unexplained (as error). Further intervention was made to this interaction to using the AMMI model to identify the information contained in it.

Table 3. The combined analysis of variance and Gollob's test for the significance of IPCAs in AMMI for grain yield of bread wheat genotypes.

Source	DF	SS	MS	% GEI var. exp	cumm. %	% of total variations
Env	17	185705.1	10923.83**			60.55
Rep(env)	54	10306.68	190.86**			3.96
Gen	16	15833.05	989.57**			5.16
env*Gen	272	54006.76	198.55**			17.61
IPCA1	32	24820.05	775.623**	44.67	44.67	
IPCA2	30	11614.92	387.16**	20.91	65.58	
IPCA3	28	5913.93	211.21**	10.64	76.22	
IPCA4	26	3932.57	151.25**	7.08	83.30	
IPCA5	24	2822.36	117.60*	5.08	88.38	
IPCA6	22	1862.49	84.66*	3.35	91.73	
Residual (noise)	110	4592.62	302.38ns	8.27	100	
Error	847	40821.1	48.195	0.13311		13.31
Total	1206	306672.7				

**P-value<0.001, *P-value<0.01, IPCA-interaction principal component axis, SS-sum of squares, MS- Mean Square

3.4. Evaluation of Genotypes

The genotypes were evaluated using different Types of BLUPs purely under mixed model and the enhanced fixed effect methods. These methods were discussed as follows.

3.4.1. The Broad BLUP and Narrow BLUP of Genotypes

The result for the evaluation of genotypes using different types of BLUP procedures was presented in Table 4. The first panel of this table contains the broad BLUP of genotypes together with their rank, based on the magnitude of the estimate given in bracket and the standard error of the estimates. The BLUP procedure had generally revealed that, ETBW5798 has the highest average followed by ETBW5800, ETBW5879 and ETBW5890, respectively. The procedure had also identified ETBW5899, G2, ETBW5875 and ETBW5850 as bread wheat genotypes with relatively lower performance.

Table 4. **The Broad BLUP, Narrow BLUP and Superiority Measure of genotypes given in qt ha^{-1}**

Genotype	Broad PGV	Std.err	Narrow PGV	Std. err	sm (Pi)
Danda'a	41.77(11)	1.6138	41.57(11)	0.9548	68.99(8)
Digelu	39.68(16)	1.6100	39.10(16)	0.9467	120.90(16)
ETBW5798	49.22(1)	1.6089	50.41(1)	0.9447	5.83(1)
ETBW5800	47.54(2)	1.6103	48.41(2)	0.9481	16.37(2)
ETBW5825	41.77(12)	1.6060	41.57(12)	0.9383	106.61(15)
ETBW5826	42.80(8)	1.6125	42.79(8)	0.9522	87.74(11)
ETBW5827	42.90(7)	1.6060	42.91(7)	0.9383	90.11(12)
ETBW5850	40.45(14)	1.6060	40.01(14)	0.9383	106.50(14)
ETBW5875	40.16(15)	1.6079	39.67(15)	0.9426	90.58(13)
ETBW5879	47.12(3)	1.6085	47.91(3)	0.9438	19.38(3)
ETBW5890	45.11(4)	1.6060	45.53(4)	0.9383	60.47(5)
ETBW5899	37.89(17)	1.6131	36.97(17)	0.9534	160.08(9)
ETBW5900	41.13(13)	1.6133	40.81(13)	0.9543	80.44(7)
ETBW5956	41.77(10)	1.6118	41.58(10)	0.9509	63.86(10)
ETBW5957	42.18(9)	1.6060	42.06(9)	0.9383	80.64(6)
ETBW5958	43.36(5)	1.6060	43.46(5)	0.9383	61.18(4)
ETBW5961	43.24(6)	1.6100	43.31(6)	0.9467	150.87(17)

**Correlation between ranking of genotype using BLUP and Superiority measure=0.647 (with P-value<0.0001),PGV-Predicted genotypic value, sm-SuperiorityMeasure,Std.err-standard error

3.4.2. The Superiority Measure

The result for genotype evaluation using the superiority measure together with rank given to the genotype relative to other genotypes under evaluation given in bracket was also presented in the last column of Table 4. Accordingly, genotype that has better performance across environment has minimum deviation from superior genotype and hence classified as better genotype. So, genotype that has the smallest value of superiority measure was given rank 1 and last rank was given to the genotype that has the largest value of superiority measure.

Accordingly, ETBW5798, ETBW5800 and ETBW5879 have got the highest rank and identified as best genotype using this procedure whereas ETBW5961, G2 and ETBW5825 were identified as genotypes with relatively poor performance across the test environments using this method.

3.5. The Stability Analyses of Genotypes

Different stability measures under the mixed model methodology were used to evaluate the genotypes under evaluation in terms of their yield stability. These stability measures have been presented with their discussion as follows.

3.5.1. The Difference between the Broad and Narrow BLUPs

The result for stability analysis of genotype using the difference between the broad and narrow BLUP of genotype together with the corresponding rank

given to genotype using the method has been presented in column 2 of Table 5 (labeled as RSV). According to this stability measure, the most stable genotype is the one with negligible GEI and hence very small value of the difference between broad and narrow BLUPs (Reano, 2010).According to this method, ETBW5826 was the most stable followed by ETBW5827, ETBW5961, ETBW5958 and ETBW5957 whereas ETBW5798, ETBW5899, ETBW5800 and ETBW5879 were identified as the most unstable genotypes.

3.5.2. The Harmonic Mean of Relative Performance of Genotypic Value (MHRPVG)

The result for stability analysis of genotype usingMHRPVG together with the rank given to genotypes based on this stability measure given in bracket has been presented in the column 3 of Table 5.According to Mendes *et al.* (2012), this procedure evaluates the stability as well as the adaptability of genotype across the test environments and hence genotypes that have higher value of MHRPVG are classified as stable as well as adaptable genotype and hence get the highest rank. Using this procedure, ETBW5798, ETBW5800 and ETBW5879 were identified to have the higher rank. The procedure had also identified that ETBW5899, ETBW5850 and Digelu as genotypes with lower rank (see Table 5).

Table 5. Summary of stability measures for genotype evaluation using different stability measures

Gen	RSV	MHRPVG	ASV
Danda'a	0.20(7)	0.9698(8)	0.854(5)
Digelu	0.58(13)	0.8850(16)	1.183(12)
ETBW5798	-1.00(17)	1.1883(1)	0.456(3)
ETBW5800	-0.88(15)	1.1292(2)	0.084(1)
ETBW5825	0.20(8)	0.9104(14)	2.139(17)
ETBW5826	0.01(1)	0.9377(13)	1.065(8)
ETBW5827	-0.01(2)	0.9455(9)	1.892(13)
ETBW5850	0.44(11)	0.8867(15)	0.915(6)
ETBW5875	0.50(12)	0.9405(11)	1.938(14)
ETBW5879	-0.80(14)	1.1212(3)	0.227(2)
ETBW5890	-0.42(10)	1.0065(4)	0.620(4)
ETBW5899	0.92(16)	0.8110(17)	1.944(15)
ETBW5900	0.32(9)	0.9439(10)	2.006(16)
ETBW5956	0.20(6)	0.9754(7)	1.078(9)
ETBW5957	0.12(5)	0.9400(12)	1.179(10)
ETBW5958	-0.10(4)	0.9914(6)	1.180(11)
ETBW5961	-0.08(3)	1.0023(5)	0.929(7)

3.5.3. The AMMI Stability Value (ASV)

The result for stability analysis using AMMI Stability Value (ASV) has been given in column 4 of Table 5. This stability measure was based on the value of the first two IPCA scores of genotype. According to this stability measure, the highest rank is given to the genotype that is close to the biplot origin, genotype that has the smallest ASV (ASV value closest to zero). Accordingly, genotypes such as ETBW5800, ETBW5879, ETBW5798 and ETBW5890 were found to be the most stable genotypes whereas, ETBW5825, ETBW5900 and ETBW5899were found to have unstable performance (genotypes with inconsistent performance) across the test environments.

In general, it has been observed that using single statistics to evaluate stability of genotype may lead to wrong conclusion and hence comparison among different stability measures must be made in order to select best genotype according to its yield stability across test environments. Accordingly, ETBW5798, ETBW5800, ETBW5879 and ETBW5890 were identified to have relatively stable performance according to these stability measures whereas genotypes such as ETBW5825, ETBW5899, ETBW5900 and ETBW5957 were identified to have relatively lower stability ranks and hence were identified as the most unstable genotypes in this typical study.

3.6. The Graphical Methods

These procedures were done to examine the pattern of GEI, the relationship between genotypes, environments and genotype environment relation and evaluate genotypes and environments in terms of their predicted average yield. Different biplots were utilized in order to achieve these objectives.

3.6.1. Ranking Genotypes Relative to the Ideal Genotype

The graphical display for the ranking of genotypes relative to ideal genotype has been given in Figure 4. It is based on genotype focused scaling (SVP=1) assuming that the mean as well as the stability are equally important in the genotype evaluation (Yan, 2001, as cited in Farshadfar*et al.*, 2011). This procedure defines an ideal genotype and compares all the remaining genotypes with it. An ideal genotype has both high mean yield and high stability across the test environments.

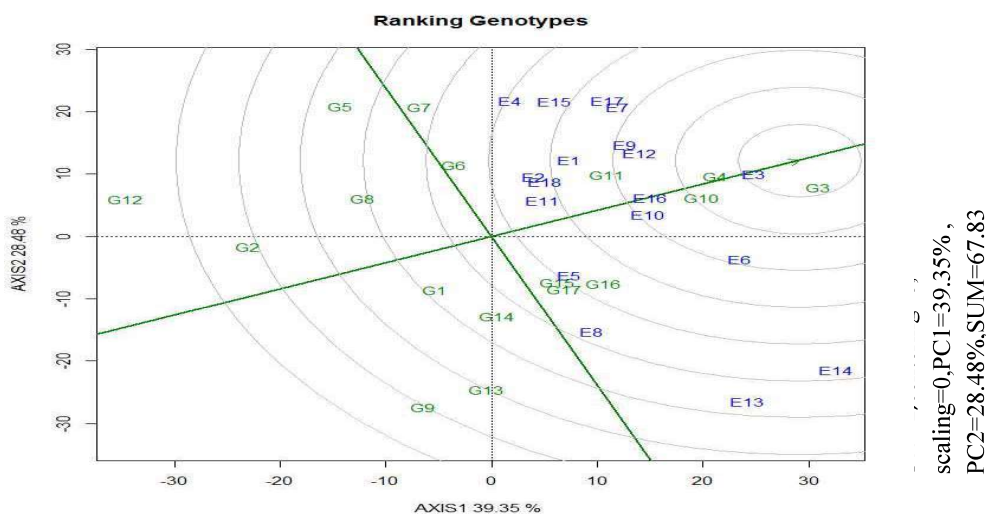**Figure 1**. The GGE biplot for ranking Genotypes relative to Ideal Genotype

Figure 1 defines an "ideal genotype" (the center of the concentric circles) to be a point on the AEA ("absolutely stable") in the positive direction and has a vector length equal to the longest vectors of the genotypes on the positive side of AEA ("highest mean performance"). Therefore, genotypes located closer to the "ideal genotype" are more desirable than others. The figure has revealed that ETBW5798, ETBW5800, ETBW5879 and ETBW5890 were identified to be desirable bread wheat genotypes using this graphical procedure. It was also found thatETBW5899, ETBW5875, ETBW5900 and Digelu have lower rank relative than the ideal genotype. In fact ETBW5899 has none of the desirable properties and is hence the poorest among all bread wheat genotypes under evaluation.

3.6.2. The Mean Performance and Stability of Genotypes

The graphical method for mean performance and stability analysis of genotypes has been given in Figure 2. It was based on row metric preserving

where the singular values were entirely partitioned into genotype scores. For this procedure, single arrowed line that passes through the biplot origin and points to higher mean yield across environments has been drawn. This line is called the average environment coordination (AEC) abscissa and labeled as AEA. The arrow directs towards higher average yield and hence genotypes on the right most of this line have highest average yield. Double arrowed line that is perpendicular to AEC abscissa has also been drown and this line is called the AEC ordinate and is labeled as Perpendicular Line (PL). This line points towards greater variability in either direction and hence genotype that has longer vector along this line is highly unstable (Ilker*et al*., 2011).

Figure 2. The GGE biplot for mean versus stability of performance of Genotypes
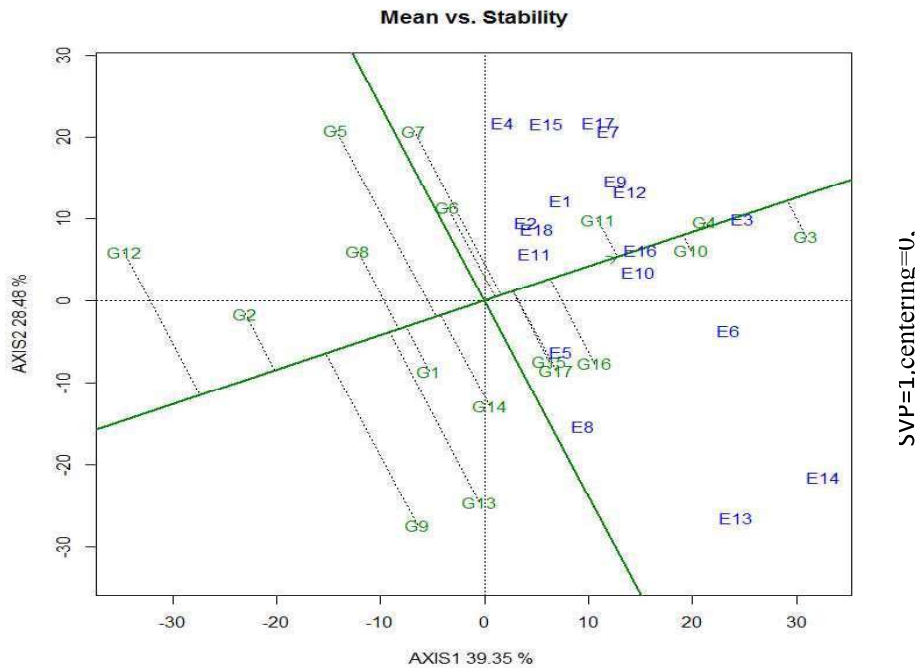
According to this procedure,ETBW5798, ETBW5800 and ETBW5879 were found to have higher average yield whereas, ETBW5899, Digelu, ETBW5875 and ETBW5900 were found to have lower average yield. The graph has also indicated that,ETBW5800, ETBW5879, ETBW5798 and ETBW5890 were the most stable genotypes whereas ETBW5825, ETBW5827, ETBW5875and ETBW5900 were identified to be the most unstable genotypes, across the test environments.

4. Conclusions and Recommendations

4.1. Conclusions

Generally, this study had identified ETBW5798, ETBW5800, ETBW5879 and ETBW5890 as genotypes with desirable property of higher average yield with relatively stable performance across the test environments using both the graphical and numerical method of genotype evaluation. Specifically, ETBW5798 was found to have consistently higher average yield with higher stability across the test environments and hence selected to be the best genotype to be released. The study had also identified that ETBW5875, ETBW5899, ETBW5900 and G2 had lower average yield with relatively unstable performance across the test environments. Hence, these genotypes are not recommended for release so that they must be dropped from further investigation in MET.

The evaluation of stability of genotypes using different quantitative stability measures under the mixed effect model has also revealed that the ranking of genotypes based on these stability measures were not all alike. Specifically genotype ranking based on RSV was different from genotype ranking based on other stability measures. So, this method must not be used alone to

evaluate the stability of genotype, rather it must be compared with other method in order to insure its reliability.

4.2. Recommendations

Based on the results of this research the following recommendations were made.

1. The study had generally identified that ETBW5798, ETBW5800 and ETBW5879 had consistently higher performance across almost all environments, so these varieties must not be discarded in future variety trial as well as variety release decision.

2. The Genotypes such as Digelu, ETBW5875 and ETBW5899 were generally found to have poor performance in terms of average yield and stability as well. So, these varieties must be dropped from further variety trial and future release objective soon.

3. Currently very efficient for agricultural experiment such as IBD, $\alpha-lattice$ and Lattice design has been introduced and such design are not suitable for analysis using the usual fixed effect model and are better fitted using linear mixed model. So future studied based on such designs must use the linear mixed model.

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