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# Genotype X Environment Interaction and Yield Stabliity of Breade Wheat (Triticum Eastivum L.) Genotype in Ethiopia using the Ammi Analisis

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**Abstract**
The G x E interaction makes it difficult to select the best performing as well as the most stable genotypes and so its efficient interpretation is important issue in plant improvement in Ethiopia. The study cried out with objectives of to estimate the effect of genotype x environment interaction on the grain yield and stability and estimate magnitude of Genotype x Environment interaction of bread wheat genotypes in Ethiopia. Thirty Bread wheat genotypes were evaluated by Alpha lattice design using three replications at eight locations in Ethiopia during 2014/2015 cropping season. The genotypes performed best at Asassa with mean grain yield of 5.71 tons/ha. Most genotypes had however, low yield at Holleta with mean gain yield of 3.05tons/ha. AMMI analysis for the additive main effect and multiplicative interaction effect revealed significant difference for genotype, testing location and genotype by testing location interaction. The first interaction principal component (IPCA 1) captured the most of interaction 39.56% and the second interaction principal component explains additional 27%. Totally the tow interaction principal component captured 66.56% of the genotype by location interaction. According to ASV Genotype ETBW8515 (20) and ETBW8513 (16) were high yielding and stable. Using AMMI analysis Asassa (As), Debre Tabor (D), Segure (Se), Adet (Ad) and Bekoji (Be) testing locations were favorable locations while testing location Holetta (Ho), Kulumsa (Ku) and Areka (Ar) were unfavorable.
**Keywords**: AMMI, ASV, Genotype x Environment Interaction.

## 1. INTRODUCTION

Wheat (*Triticum* L.) is an annual plant that belongs to the grass family Poaceae, tribe Triticeae, and sub tribe Triticineae. It is thought to have originated on the Eurasian continent, a starting point from which man spread it throughout the world, including China and central Europe. Wheat is one of the earliest domesticated crop plants in the Pre-Pottery Neolithic Near East (Lev-Yadun et al. 2000). The center of its domestication is widely accepted to be somewhere in the Middle East (Anikster and Wahl 1979). It is the world's most widely cultivated food crop, followed by rice and maize (Gulbitti-Onarici et al. 2009), and one of the oldest and most important of the cereal crops (Harlan 1992), producing the highest global grain production of any crop (Lamoureux et al. 2005).

The genus *Triticum* exists as a polyploid series of diploid, tetraploid, and hexaploid species complexes (Provan et al. 2004). Of special cultural and economic importance are the tetraploid durum wheat *T. turgidum* L. and the hexaploid bread wheat (common wheat) *T. aestivum* L. (Baum et al. 2009).

Wheat produced in a wide range of climatic environments and geographic regions. Worldwide wheat can be grown successfully between the latitudes of $30^0$ and $60^0$N and $27^0$ and $40^0$S (Nuttonson, 1955), altitude from sea level to more than 3000 meter above sea level (m.a.s.l) and it has been reported at 4570 meter above sea level (m.a.s.l) in Tibet (Percival, 1921). The optimum growing temperature is about $25^0$c, with minimum and maximum growth temperatures of $3^0$C to $4^0$c and $30^0$c to $32^0$c, respectively (Briggle, 1980). Wheat is adapted to a broad range of moisture conditions with an average of between 375 and 875 mm of annual precipitation, it can grow in most locations where precipitation ranges from 250 to 1750 mm (Leonard and Martin, 1963). Wheat is one of the major cereal crops grown in the Ethiopian highlands, which lie between 6 and $16^0$ N and 35 and $42^0$ E, at altitudes ranging from 1500 to 3000 meter above sea level (m.a.s.l). The most suitable areas of wheat production however, fall between 1900 and 2700 meter above sea level (m.a.s.l) (Bekele *et al.,* 2000). In the highlands, rainfall distribution is bimodal and ranges between 600-2000 mm/ annum. Wheat does not grow well under very warm conditions with high reactive humidity, unless irrigation and nutrient availability are very

 

favorable. The soil types used for wheat production vary from well drained fertile soils to waterlogged heavy Vertisols (Hailu, 1991). Optimum soil pH ranges between 5.5 and 7.5. Wheat is sensitive to soil salinity.

Wheat is one of the most important cereal crops of the world and is a staple food for about one third of the world's population (Hussain and Shah, 2002). It is a major cereal crop in Ethiopia, which is largely grown in the highlands. At the national level, wheat is cultivated on 1.63 million ha of land with a total grain production of 3.43 million tons (CSA, 2013), and the country is considered the largest producer of the crop in sub-Saharan Africa. Bread wheat (*Triticum aestivum* L.) accounts for about 60% of the total wheat production in the country whereas durum wheat (*Triticum aestivum* L.) accounts for the remaining production (Hailu, 1991). Bread wheat is preferred to durum wheat by farmers in Ethiopia owing to its high yield potential, ease of mechanization, relatively higher economic returns, and good bread making quality relative to the other food crops (Tanner *et al.*, 1993).

However, one challenge faced in wheat production in the country is low productivity per unit area of land. The national average yield of the crop is estimated at 2.11 tones ha-1 (CSA, 2013), which is very low compared to the world's average yield of 3.09 tones ha-1 (FAOSTAT, 2012).

In Ethiopia Wheat is the third important crop after teff and maize covers an area over 1.5 million hectares. Ethiopia has attained a record of 3.78 million tons of wheat production in 2012/13 and continues to remain as the largest producer of wheat in Sub Saharan Africa (Dagiwoine and Alamerew, 2013).It is largely grown in the highlands of the country under rain fed conditions and constitutes roughly 20-30 % of the annual cereal production.(Hailegiorgis et al., 2011). Within Ethiopia, the Oromia and Amhara regions produce 59% and 27% of the country's wheat, respectively, with an additional nine percent coming from the Southern Nations, Nationalities, and Peoples Region (SNNPR) (Hailu, 2012.).

In Ethiopia, more than 87 improved bread wheat varieties were released from 1974 to 2011; 30 varieties from 1974 to 1997 and from 1998 to 2011 fifty-seven varieties were released and some of them are in production in different agro-ecological zone of the country (Degewione and Alamerew, 2013).

The success of crop improvement activities largely genotype evaluation by eliminating unnecessary testing depends on the identification of superior genotypes for sites (Letta, 2009). Genotype × Environment (GE) interaction results in genotype rank changes from an environment to another, a difference in scale among environments, or a combination of these two situations (Aycicek and Yildirim, 2006). G × E interactions are of major importance, because they provide information about the effect of different environments on cultivar performance and have a key role for assessment of performance stability of the breeding materials (Moldovan et al. 2000). Limitation of information on GEI of bread wheat cultivars in Ethiopia becoming an important issue. Yield is a complex quantitative character and is greatly influenced by environmental fluctuations; Hence, the selection for superior genotypes based on yield per se at a single location in a year may not be very effective, Eberhart and Russell (1966). Lack of high yielding varieties adapted to diverse agro-ecological conditions is the major reason of low productivity (Seetharam, A., 1995).

The G x E interaction makes it difficult to select the best performing as well as the most stable genotypes and so its efficient interpretation is important issue in plant improvement program. The central aims of this study were, therefore, to identify stable high yielding Bread wheat genotypes (pipeline varieties) that could be adapted for wider and/or specific environments and make recommendations for possible release and production in the test environments and similar agro ecologies in Ethiopia. The study cried out with objectives of to estimate the effect of Genotype x Environment interaction on the grain yield and stability of bread wheat genotypes and to estimate magnitude of Genotype x Environment interaction of bread wheat genotypes in Ethiopia.

## 2. Materials and Methods

*2.1. Description of locations of the experimental sites.*

Thirty Bread wheat genotypes ware evaluated at Holetta, Bekoji, Kulumsa, Asassa, Adet, Segure, Debere Tabor and Areka locations, which are major wheat growing areas of Ethiopia with altitude of 2400, 2780, 2200, 2300, 2240,2230, 2706 And 1850 meter above sea level respectively. Thirty Bread wheat Genotypes were included in this study. Hidasse and Danda'a were used as standard check in this study. Full descriptions of the genotypes were given in Table 1.

 

**Table 1: Description of 30 bread wheat genotypes tested at eight locations in 2014/2015.**

| Entery | Name | Pedgree | source |
|---|---|---|---|
| 1 | Hidasse | | Breeder seed 2013 |
| 2 | ETBW6861 | WAXWING*2/HEILO | PVT-II-13 |
| 3 | ETBW8506 | AGUILAL/FLAG-3 | 1st-HRAYT-13 |
| 4 | ETBW8507 | DURRA-4 | 1st-HRAYT-13 |
| 5 | ETBW7120 | QAFZAH-23/SOMAMA-3 | PVT-III-13 |
| 6 | ETBW8508 | REYNA-8 | 1st-F/IAYT-13 |
| 7 | ETBW7213 | CHAM-4/SHUHA'S'/6/2*SAKER/5/RBS/ANZA/3/KVZ/HYS//YMH/TOB | PVT-VI-13 |
| 8 | ETBW8509 | REYNA-29 | 1st-F/IAYT-13 |
| 9 | ETBW7038 | ATTILA/3*BCN//BAV92/3/TILHI/5/BAV92/3/PRL/SARA…. | PVT-III-13 |
| 10 | ETBW8510 | HIJLEEJ-1 | 1st-F/IAYT-13 |
| 11 | ETBW7058 | ROLF07//TAM200/TUI/6/WBLL1/4/HD2281/TRAP#1/3/KAUZ*2/TRAP.. | PVT-VI-13 |
| 12 | ETBW8511 | BOW #1/FENGKANG 15/3/HYS//DRC*2/7C | 1st-F/IAYT-13 |
| 13 | ETBW7147 | CROC-1/AE.SQUARROSA(224)// OPATA/3/QAFZAH-21/4/SOMAMA-3 | PVT-VI-13 |
| 14 | ETBW8512 | BABAX/LR42//BABAX*2/3/KURUKU/4/KINGBIRD #1 | 21HRWYT |
| 15 | ETBW7871 | PAURAQ/4/PFAU/SERI.1B//AMAD/3/WAXWING | PVT-IV-13 |
| 16 | ETBW8513 | MUTUS//WBLL1*2/BRAMBLING/3/WBLL1*2/BRAMBLING | 21HRWYT |
| 17 | ETBW6940 | UTIQUE 96/FLAG-1 | PVT-III-13 |
| 18 | ETBW8514 | TUKURU//BAV92/RAYON/3/WBLL1*2/BRAMBLING/4/WBLL1*2 | 21HRWYT |
| 19 | ETBW7368 | D. 56455 | PVT-V-13 |
| 20 | ETBW8515 | BECARD/3/PASTOR//MUNIA/ALTAR 84 | 21HRWYT |
| 21 | ETBW7364 | ACSAD1115 | PVT-V-13 |
| 22 | ETBW8516 | KACHU/KIRITATI | 34ESWYT |
| 23 | ETBW7194 | VAN'S'/3/CNDR'S'/ANA//CNDR'S'/MUS'S'/4/TEVEE-5 | PVT-V-13 |
| 24 | ETBW8517 | FRNCLN*2/TECUE #1 | 34ESWYT |
| 25 | ETBW7101 | KAMB2/PANDION | PVT-VI-13 |
| 26 | ETBW8518 | SUP152/AKURI//SUP152 | 34ESWYT |
| 27 | ETBW7872 | QUAIU/5/FRET2*2/4/SNI/TRAP#1/3/KAUZ*2/TRAP//KAUZ | PVT-IV-13 |
| 28 | ETBW8519 | ATTILA/3*BCN*2//BAV92/3/KIRITATI/WBLL1/4/DANPHE | 34ESWYT |
| 29 | ETBW6937 | AGUILAL/FLAG-3 | PVT-II-13 |
| 30 | Danda'a | | Breeder seed 2013 |

Source: Kulumsa Agricultural Research Center

### 2.2. Experimental Design, Management and season

Thirty Bread wheat Genotypes were planted at each location in Alpha lattice design (6x5) with three replications in the 2014/2015 cropping season. There were 6 blocks in each replication and each block had 5 Genotypes. Each plot was consisted of 6 rows with spacing of 20cm, 2.5m length and 1.2m width. Therefore, the area of each experimental plot was 3 m2 (1.2m x 2.5 m). The spacing between plots and replications was 0.4 m and 1.5 m, respectively. The sowing dates were at the onset of the main rainy season. Seed rate of 150 kg ha and fertilizer rate of 41/ 46 N/ P O kg ha was utilized. The experiment was conducted in the main season under rain fed condition. All the agronomic managements and practices were adopted as per recommendation for each location. Yield data was taken per plot basis and converted to ton/ha for carrying out subsequent statistical analysis.

### 2.3. Data collected

*2.3.1. Grain yield (kg/plot):*

Total dry weight of grains harvested from all 4 rows were taken as grain yield per plot and expressed as grams per plot.

### 2.4. Statistical analysis

*2.4.1. Analysis of Variance*

The data collected to analysis of variance (ANOVA) using AGROBASE 20 (Agrobase 20, 1999) and least significant difference (LSD) was used to separate the means that showed significant difference at five percent probability levels. The data to combined analysis of variance to obtain estimates of environmental, genotype, genotype x environment interaction.

*2.4.2. Stability analysis*

*2. 4.3. Additive main effects and multiplicative interaction (AMMI) Model Analysis.*

Additive main effects and multiplicative interaction (AMMI) model Analysis was performed for grain yield using AGROBASE 20 (Agrobase 20,1999).AMMI model first applies the additive analysis of variance model to two- way data, and then applies the multiplicative principal component analysis (PCA) model to residual from the additive model, that is, to the interaction (Yau, 1999). The AMMI analysis was performed according to the

 

model suggested by crossa *et* al. (1995). In this model the first component were the main effect and the additive part of the model. Grand mean, genotype means and environmental means were analyzed by the ordinary ANOVA. The second components, the non-additive interaction combination, the additive part (main effects) of the AMMI model equals the genotype mean plus the environment mean minus the grand mean, and the interaction (multiplicative part) is the genotype scores times the environmental scores (Zobel *et* al.,1988).

The AMMI Model is:

$$Y_{ijl} = \mu + G_i + E_j + (\sum \lambda_k \alpha_{ik} \gamma_{jk}) + d_{ij} + e_{ijl}$$

Where $Y_{ij}$ is the yield of $i^{th}$ genotype in the $j^{th}$ environment; $\mu$ is the grand mean; $G_i$ and $E_j$ are the genotype and environment deviations from the grand mean, respectively; $\lambda_k$ is $k^{th}$ Eigen value; $\alpha_{ik}$ is principal component score for the $i^{th}$ genotype for the $k^{th}$ principal component axis; $\gamma_{jk}$ principal component score for the the $j^{th}$ environment for the $k^{th}$ principal component axis; $d_{ij}$ is residual G x E not explained by the model; n is the number of principal components retained in the model and $e_{ij}$ is the error term.

The combination of analysis of variance and principal components analysis in the AMMI model, along with prediction assessment, is a valuable approach for understanding GEI and obtaining better yield estimates. The interaction is explained in the form of a bi plot display where, PCA scores are plotted against each other and it provides visual inspection and interpretation of the GEI components.

## 3. Result and Discussions

### 3.1. Analysis of variance (ANOVA) for individual Environments.

Grain yield tons per hectares, showed highly significant difference at seven locations and showed significant difference only at Debre Tabor. Holetta was location where most genotypes revealed least grain yield performance as compared to other locations and Asassa was the location where most genotypes revealed higher grain yield performance as compared to other locations.

*3.1.1. Performance of genotypes*

The mean grain yield over all location and genotypes was 4.56 tons/ha, with genotypes mean grain yield performance ranging from 3.79 tons/ha by ETBW8511 to 5.60 tons/ha by ETBW7038 averaged over the eight locations and the ranking for the locations. Genotypes ETBW8513 followed by ETBW7058, ETBW8517 and ETBW7101 had highest performance with an average grain yield 6.66tons/ha, 6.57 tons/ha, 6.56tons/ha and 6.55tons/ha. At Asassa all genotypes perform highest yield than the grand mean except ETBW8511 and ETBW7147 which were less grain yield than grand mean and at Holetta all genotypes grain yield were less than grand mean except ETBW6940 and ETBW7038 genotypes. Genotype ETBW7038 at Bekoji, ETBW6940, and ETBW8506 at Segure, ETBW8513, ETBW7058 and ETBW8517 at Asassa, ETBW7038 at Adet, ETBW7213 and ETBW8509 at Debre Tabor showed higher performance in each location while ETBW8511, ETBW8507 and ETBW8508 showed low performance in most of the locations. The genotypes performed best at Asassa with mean grain yield of 5.71 tons/ha. Most genotypes had however, low yield at Holleta with mean gain yield of 3.05tons/ha.

*3.1.2. Combined analysis of variance*

In order to identify genotypes that are more stabile, better understanding of contribution of genotypes, environment and their interaction as a source of variation is important (Table 2). Shows that the mean squares relevant to the study of G X E interaction from a combined analysis of variance showed that significant difference among the testing locations for grain yield. This indicating that the locations were not similar. This variation was mainly due to the variation in rain fail distribution across the location during experimental year. Similar findings were reported by Noorul Saleem., *et* al (2015), Trakanovas and Ruzagas, (2006).

Genotypes revealed highly significant ($p<0.01$) differences for Grain yield. This indicates that there was genetic difference among genotypes for this trait. Highly significant difference ($P<0.01$) G x E interaction was obtained for Grain yield. Since the interaction between genotype and environment is significant, it could be attributed to inconsistent response of genotypes to changing environments or due to genotype-environment interaction. This was similar with finding reported by Ayaleneh et al., (2013), Brandle, (1988), Mohammed, (2009), Jalata, (2007) and Sadeghi *et* al., (2007).

The combined ANOVA showed that bread wheat grain yield was significantly affected by the environment, Genotype and G x E interaction because of significant variance at 1% level (Table 2). Environment explained 45.56% of the total (G + E + GEI) variation, while G x E interaction captured 25.37% of the total sum of squares and Genotype variation accounted about 2.59% of the total sum square (Table 2). A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing variation in the bread wheat grain yields. This was with agreement of Roostaei *et* al., (2014), Mohamed (2013), Farshadfar et al., (2012), Kaya et al., (2006) and Gauch and Zobel (1996, 1997).

 

**Table 2: Combined analysis of variance for grain yield (ton/ha.) and % explained of bread wheat tested in eight environments in 2014/15 cropping seasons.**

| Source | df | SS | MS | F-value | Pr> F | Explained. |
|---|---|---|---|---|---|---|
| Total | 719 | 1090.813 | | | | |
| Locations | 7 | 508.199 | 72.600 | 41.20 | 0.0001** | 46.56% |
| Reps within locations | 16 | 28.192 | 1.762 | | | |
| Genotype | 29 | 28.192 | 5.292 | 3.88 | 0.0001** | 2.59% |
| Genotype x location | 203 | 276.733 | 1.363 | 5.09 | 0.0001** | 25.37% |
| Residual | 464 | 124.221 | 0.268 | | | |
| Grand mean = 4.559 R-squared = 0.8861 C.V. = 11.35% | | | | | | |

*, ** Significant at 0.05 and 0.01 respectively

N.B. Abbrevation: Reps=replication; Loc=location; gen.=Genotype; df=degree freedom; SS= sums quare, MS=mean square

*4.1.3. AMMI Analysis*

AMMI Analysis showed that there were significant (p=0.01) difference among the environments, G x E interaction and Genotype for grain yield (Table 3). The result showed that the Environment captured the maximum sum of square. A large sum of squares for environments indicates that the environments were diverse; with large differences among environmental means causing most of the variation in grain yield. This was similar with finding reported by Ayaleneh et al., (2013), Brandle, (1988), Mohammed, (2009), Jagatai, (2007) and Sadeghi *et* al., (2007).

From the total sum of square the largest portion was due to environments contributing 46.59% of the total variability for grain yield, Genotype contribute small portion of variation while G x E interaction was greater than the genotype contribution for yield. This is in agreement with those finding obtained by Letta, (2009) and Ayaleneh et al., (2013).

The G x E interaction component of variation was partitioned in to seven possible interaction principal component axis (IPCA) along their contribution of sum of squares (ss) with decreasing importance (Table 3). For grain yield the first five IPCA showed highly significant (P<0.01) difference and explained 94.43% of the total interaction variance. This result is with agreement of Sivapalan *et* al., (2000). Analysis of AMMI model showed that the first principal component, PCA 1 explained 39.58% of the interaction sum of squares while the second principal component, PCA 2 explained 27.01% interaction sum of square for Grain yield. The other interaction effects explained by the remaining principal components. The two principal components (PCA1 and PCA2) together captured above 50% interaction principal component. Several authors also reported for various crops that significant and greater percentage of GXE interaction was explained by the first tow IPCA score (Wonde Abera and Labuschagne, 2005, on maize, Farshadfar, (2008), on bread wheat, Abeya Temesgen *et al., (*2008), on common bean; Girma Mengistu *et al.*, (2011), on Field pea. Except the sixth and seventh IPCA-I, the remaining first five IPC axes were showed highly significant difference and contributed 39.58%, 27.01%, 13.18%, 9.91% and 4.75% Of the GXE interactions for grain yield (Table 3).

**Table 3. Analysis of variance for grain yield of thirty bread wheat genotypes tested across eight locations in 2014/15 main cropping season using Additive Mean Effect and Multiple Interactions (AMMI) model.**

| Source | df | SS | MS | F-Value | Explained. |
|---|---|---|---|---|---|
| Location | 7 | 508.199 | 72.600 | 41.20 | |
| Genotypes (G) | 29 | 153.467 | 5.292 | 3.88 | |
| G X L | 203 | 276.733 | 1.363 | 5.09 | |
| AMMI Component 1 | 35 | 109.538 | 3.130 | 11.69** | 39.58% |
| AMMI Component 2 | 33 | 74.744 | 2.265 | 8.46** | 27% |
| AMMI Component 3 | 31 | 36.461 | 1.176 | 4.39** | 13.18% |
| AMMI Component 4 | 29 | 27.412 | 0.945 | 3.53** | 9.90% |
| AMMI Component 5 | 27 | 13.148 | 0.487 | 1.82** | 4.75% |
| AMMI Component 6 | 25 | 9.042 | 0.362 | 1.35ns | 3.27% |
| AMMI Component 7 | 23 | 6.387 | 0.278 | 1.04 ns | 2.31% |
| GXE Residual | 464 | 124.221 | | | |

** =Significant at 0.01.
ns= none Significant

N.B. Abbrevation: Reps=replication; Loc=location; gen.=Genotype; df=degree freedom; SS= sums quare, MS=mean square.

The AMMI Analysis provides graphical representation of summary information on main effects, and the first interaction axis in the form of bi-plot of IPCA1 to classify genotypes and environments. For any G x E combination, the additive part of the AMMI Model equals the genotypes mean plus the environment mean

 

minus the Garand mean, and the interaction is the genotype score times the environment score (Zoble *et* al.,1988).

The proportion of variance explained by the first tow IPCA axis was greater than 50% in all traits. Eigen values of the first tow axis were greater than the mean of all Eigen values; hence, much of the variability was accounted by the first tow IPCA components. The environment revealed a high variability in both main and interaction effects (table-). Therefore, it was necessary to classify the environments to identify and recommend target genotypes according to adaptation. Romogosa and Fox (1993), in Triticale and Eberhart and Russell (1966) in Maize, Tiruneh, (2000) in Tef, have also reported grouping of environment and genotypes based on the G x E patterns. Similarly Adugna and Labuschagne (2002) on linseed, Asfaw et al., (2009) on soya bean in Ethiopia reported fluctuation in growing environments of Ethiopia.

3.1.3.1. AMMI bi-plot Analysis

AMMI bi-plot analysis represents graphical representation (bi-plot) to summarize information on main effect and interaction effect of both genotypes and environment simultaneously. The interaction principal component 1(IPC1) represented in y-axis where as genotype and environment mean represented in x-axis (Figure. 1). Genotypes or location placed in the right side of the original (above grand mean) were high yielding genotypes or locations where as genotypes or location placed in the left side (below grand mean) were low yielding. The IPCA score of genotypes in AMMI analysis are an indication of stability of genotypes over the environments (Gouch and Zobel, 1997). The greater the IPCA score (-ve or +ve), the more specifically adapted a genotype is to a specific environment. The closer the IPCA score to zero, the more stable the genotypes over the tested locations.

Adaptability is the result of genotype by environment interaction and generally categorized in to tow classes **(l)** the ability to perform at an acceptable level in a range of environments, generally adaptability and (2) the ability to perform well only in desirable environments, specific adaptability (Farshadfar and Sutka, 2006).

Genotypes and environments showed highest variability for both main and interaction effects. Accordingly Genotypes ETBW7058 (11), ETBW7871 (15), ETBW8513 (16), ETBW7101 (25) with high yield and Genotype ETBW8516 (22), ETBW8513 (21), ETBW7213 (7) and ETBW8508 (6) with low yield exhibited score near to zero. Therefore, these genotypes were stabile genotypes or widely adapted genotypes across diverse locations and contribute less to the magnitude of G x E interaction. Similar results were reported by Mohammed *et* al., (2013) and Ferney *et al., (2006)***.**

The genotypes ETBW8511 (12) and ETBW7147 (13) were with mean yields less than the overall mean and with the negative highest IPC1 score, where as Genotype ETBW7872 (27) and ETBW8514 (18) were with mean yield less than average mean and with positive highest IPC 1 score, ETBW7038 (9) and ETBW6940 (17) with mean yield more than average mean and with negative heist IPCA 1 score tended to contribute highly to GE interaction and accordingly can be regarded as the most unstable genotypes. Similar finding was reported by Mohammadi & Amri, (2014). Similar to genotypes location Holetta (Ho) and Kulumsa (Ku) were low yielding locations during the experimental year as well as unfavorable environments and contribute highly to G x E interaction. Location Asassa (As), Adet (Ad) and Bekoji (Be) were high yielding environments and contribute to high G x E interaction since these locations had high principal component 1 axis, these were unstable locations. Debre Tabor (D) and Segure (Se) were high yielding locations and relatively contribute to low G x E interaction and located on the bi plot graph nearest to the origin relative to the other locations. Therefore these two locations were considered as favorable locations relative to the others. Similar result was reported by Purchase, (1997), Adugna and Labuschagne, (2002).

According to Anley *et* al., (2013), genotypes that are close to each other tend to have similar performance and those that are close to environment indicates their better adaptation to that particular environment similar to that genotype ETBW8511 (12) and ETBW7147 (13) had similar performance and showed better adaptation at Kulumsa (Ku) whereas, Danda'a (30) and ETBW8510 (10) had similar performance and showed better adaptation at Areka (Ar) whereas Genotype ETBW7038 (9) and ETBW6940 ( 17) had similar performance and best at Bekoji (Be) for yield.

 

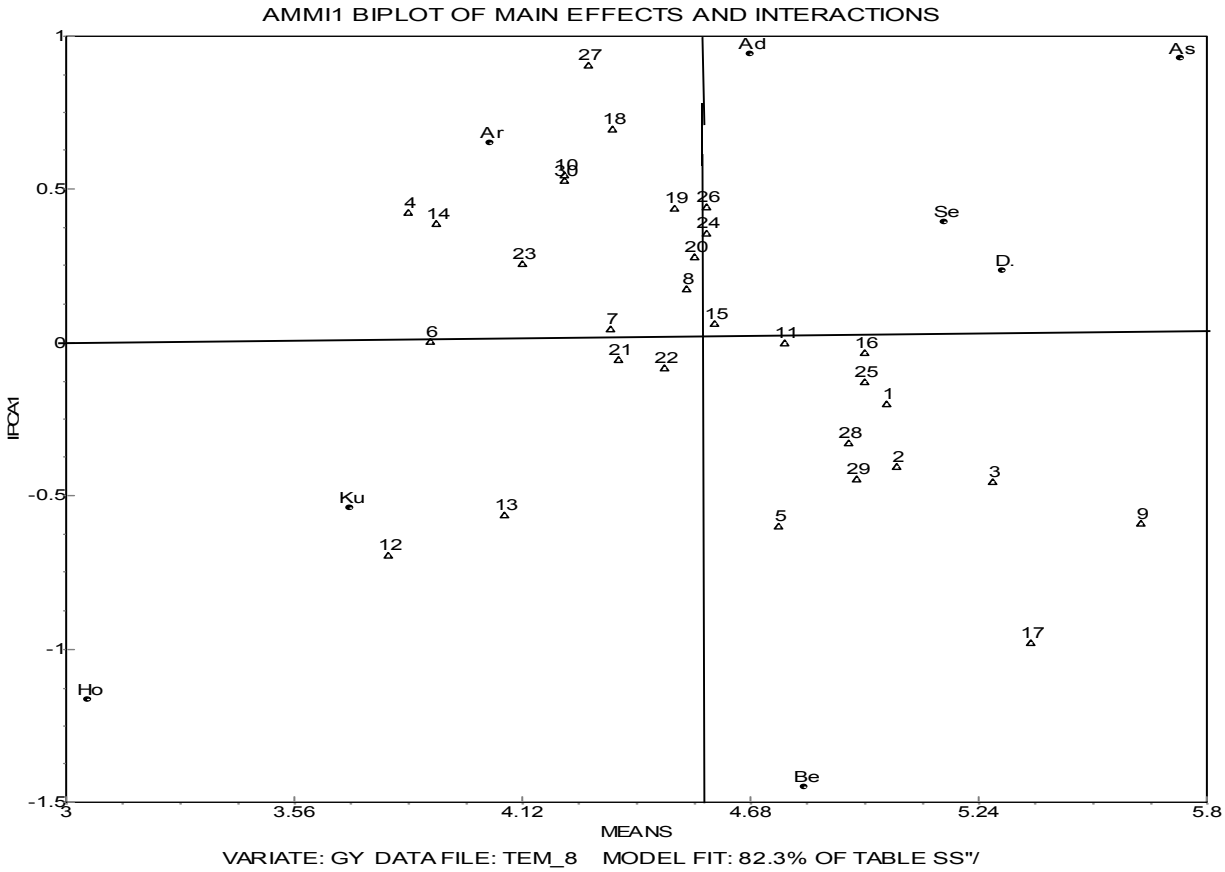


**Figure 1 AMMI Bi plot graph of Number of grains (x-axis) plotting means from 36 to 49 and with ordinate (Y-axis) plotting IPCA from,-2.7 to 2.3.**

1=Hiddase,2=ETBW6861,3=ETBW8506,4=ETBW8507,5=ETBW7120,6=ETBW8508,7=ETBW7213,8=ETBW8509,9=ETBW7038,10=ETBW8510,11=ETBW7058,12=ETBW8511,13=ETBW7147,14=ETBW8512,15=ETBW7871,16=ETBW8513,17=ETBW6940,18=ETBW8514,19=ETBW7368,20=ETBW8515,21=ETBW7364,22=ETBW8516,23=ETBW7194,24=ETBW8517,25=ETBW7101, 26=ETBW8518,27 =ETBW7872, 28=ETBW8519, 29=ETBW6937 , 30= Danda'a

Ad=Adet, Ar=Areka, As=Asassa, Be=Bekoji, D=Debre Tabor, Ho=Holetta and Se=Segure.

ETBW=Ethiopian Bread Wheat

3.1.3.2. AMMI 2 bi plot analysis

The interaction principal component analysis 1 (IPCA1) were plotted on x-axis where as interaction principal component analysis 2 (IPCA2) were plotted on y-axis for grain yield and yield components. The greater the IPCA scores, either positive or negative, as it is a relative value, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype to over all environments sampled Purchase, (1997), Adugna and Labuschagne, (2002).

AMMI2 analysis positioned the genotypes in different locations, indicating the adaptation pattern of the genotypes. Since IPCA2 scores also play a significant role (67.1%) in explaining the G X E, the first two IPCA axes were plotted against one another to investigate the G x E interactions pattern of each genotype. When looking at the environments it is clear that there is a good variation in the different environments. Debre Tabor (D) and Bekoji (Be) were the most discriminating environments as indicated by the longest distance between its marker and the origin (Figure 2). However, due to their large IPCA2 score, genotypic differences observed at these environments may not exactly show the genotypes in average yield overall locations. For the environments closer relationships were observed between Segure and Asassa. Genotypes with a smaller vector angle in between and have similar projection, designate their proximity in the grain yield performance. Those genotypes that are clustered closer to the centre tend to be stable, and those plotted far apart are unstable in performance. According, genotype ETBW8511 (12), ETBW8509 (8) and Danda'a (30), ETBW7872 (27) were unstable as they are located far apart from the other genotypes in the bi plot when plotted on the IPCA1 and IPCA2 scores. ETBW7871 (15), ETBW8508 (6), ETBW7364 (21) and Hidasse (1) were genotypes positioned closer to the origin of the bi plot which indicates their stability in performance across environments. The closer association between ETBW6861 (2) and ETBW8506 (3) indicate similar response of the genotypes to the environment. Projection of genotypes point to environmental vectors indicated specific interactions between genotype and an

 

environment. The best genotype with respect to location Adet (Ad) was ETBW8514 (18), while Danda'a (30) was the best genotype for Areka (Ar). Segure (Se) is the most favorable environment for all genotypes with nearly similar yield response for grain yield.

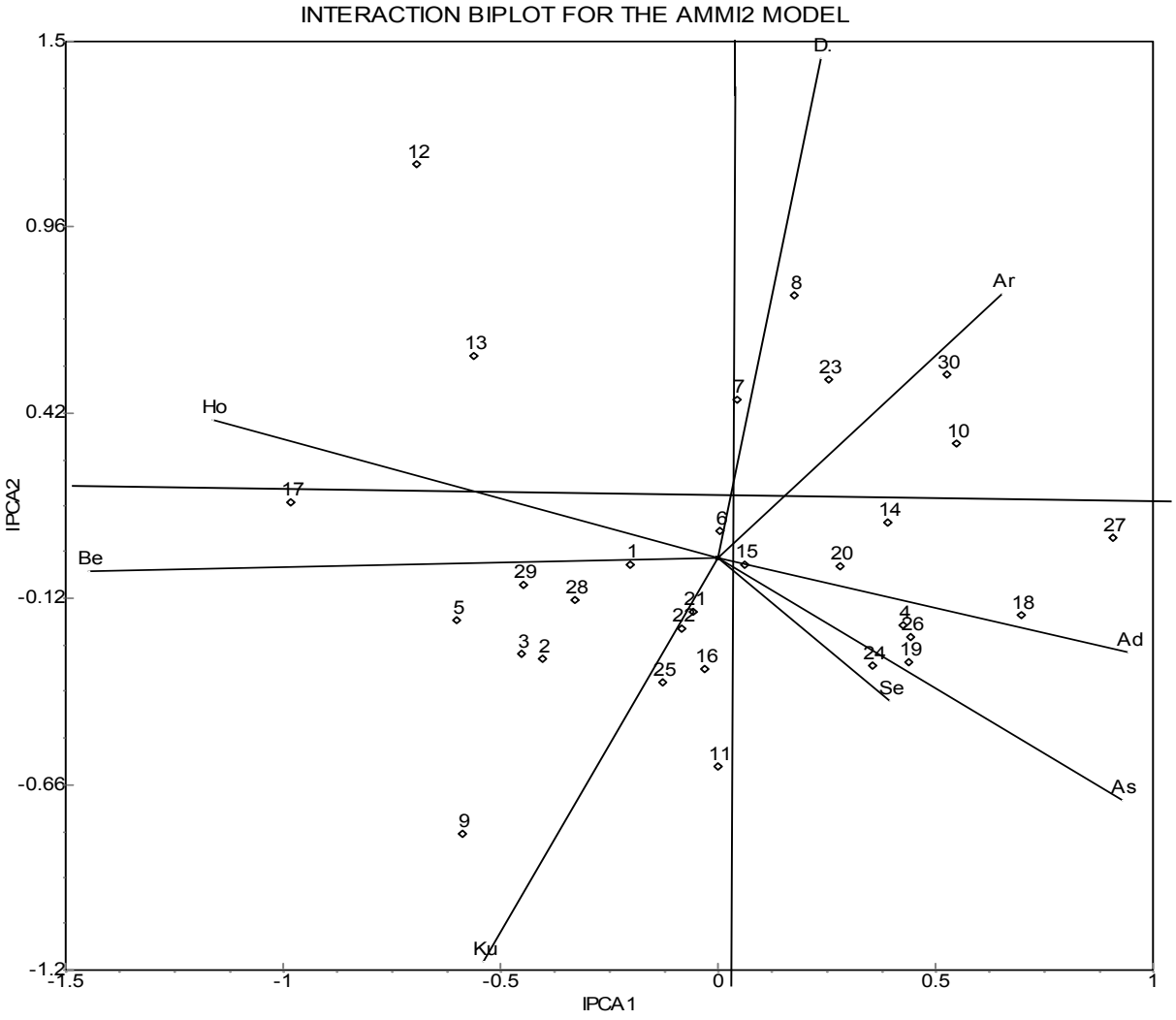


**Figure 2. AMMI 2 bi plot for grain yield of 30 Bread wheat genotypes showing the plotting of IPCA1 and IPCA2 of genotypes**.

1=Hiddase,2=ETBW6861,3=ETBW8506,4=ETBW8507,5=ETBW7120,6=ETBW8508,7=ETBW7213,8=ETBW8509,9=ETBW7038,10=ETBW8510,11=ETBW7058,12=ETBW8511,13=ETBW7147,14=ETBW8512,15=ETBW7871,16=ETBW8513,17=ETBW6940,18=ETBW8514,19=ETBW7368,20=ETBW8515,21=ETBW7364,22=ETBW8516,23=ETBW7194,24=ETBW8517,25=ETBW7101, 26=ETBW8518,27 =ETBW7872, 28=ETBW8519, 29=ETBW6937 , 30= Danda'a
Ad=Adet, Ar=Areka,As=Asassa,Be=Bekoji,D=Debre Tabor,Ho=Holetta and Se=Segure.
ETBW=Ethiopian Bread Wheat

*3.1.3.3. The AMMI stability value (ASV)*

Even if both IPCA1 and IPCA2 use for stability indication, variation was observed **in** measuring the stable genotypes between the two IPCA that means genotype which considered to be stable in IPCA1 not shown itself stable in IPCA2 as the first case Letta, (2009). The difference in stability measurement of the two principal components can be compensated by proportional difference between the IPCAs (1:2) then determined by Pythagoras theorem in effect of AMMI stability value. Purchase, (1997) noted that AMMI stability value (ASV) does not for quantitative stability measure by rather quantify and rank genotypes according to their yield stability. So based on ASV, EBWT 8515(20) rank first followed by EBWT 7364 (21), EBWT 8516 (23), EBWT8513 (16), and ETBW7213 (7) which have high stability whereas EBWT7872 (27), ETBW6937 (29) (EBWT6937), Hidasse (1), ETBW6940 (25) and ETBW7871 (15) were observed to be the most unstable genotypes in yield, respectively (Table 4).

 

**Table 4. AMMI stability values of Grain yield for the 30 bread wheat genotypes evaluated in Ethiopia**

| Entery | Genotype | Mean | IPC1 | IPC2 | ASV | Rank |
|---|---|---|---|---|---|---|
| 1 | Hidasse | 4.98 | 0.1897 | 0.0033 | 10.904875 | 28 |
| 2 | ETBW6861 | 5.05 | 0.3948 | -0.2806 | 0.6223279 | 12 |
| 3 | ETBW8506 | 5.27 | 0.4688 | -0.2705 | 0.8563177 | 18 |
| 4 | ETBW8507 | 3.82 | -0.4013 | -0.2545 | 0.6820389 | 15 |
| 5 | ETBW7120 | 4.7 | 0.5402 | -0.1871 | 1.5708619 | 23 |
| 6 | ETBW8508 | 3.82 | -0.1033 | 0.0371 | 0.2900086 | 6 |
| 7 | ETBW7213 | 4.3 | -0.1108 | 0.4327 | 0.4336289 | 5 |
| 8 | ETBW8509 | 4.5 | -0.1875 | 0.6767 | 0.6786914 | 14 |
| 9 | ETBW7038 | 5.6 | 0.6819 | -0.8377 | 1.0049134 | 21 |
| 10 | ETBW8510 | 4.24 | -0.5285 | 0.3431 | 0.8834314 | 19 |
| 11 | ETBW7058 | 4.78 | -0.016 | -0.6042 | 0.6042003 | 11 |
| 12 | ETBW8511 | 3.79 | 0.6517 | 1.1662 | 1.2217418 | 22 |
| 13 | ETBW7147 | 4.09 | 0.5864 | 0.5948 | 0.8294625 | 17 |
| 14 | ETBW8512 | 3.93 | -0.4364 | 0.1089 | 1.7521932 | 24 |
| 15 | ETBW7871 | 4.57 | -0.1348 | -0.0056 | 3.2448328 | 26 |
| 16 | ETBW8513 | 5.02 | 0.0507 | -0.2538 | 0.254002 | 4 |
| 17 | ETBW6940 | 5.32 | 0.9405 | 0.2324 | 3.8131994 | 27 |
| 18 | ETBW8514 | 4.36 | -0.7144 | -0.1695 | 3.015784 | 25 |
| 19 | ETBW7368 | 4.54 | -0.4046 | -0.2616 | 0.6782485 | 13 |
| 20 | ETBW8515 | 4.55 | -0.2143 | -0.0105 | 0.0104881 | 1 |
| 21 | ETBW7364 | 4.4 | 0.0961 | -0.1261 | 0.1458252 | 2 |
| 22 | ETBW8516 | 4.5 | 0.049 | -0.181 | 0.1814855 | 3 |
| 23 | ETBW7194 | 4.11 | -0.2917 | 0.5097 | 0.5363422 | 9 |
| 24 | ETBW8517 | 4.54 | -0.3447 | -0.387 | 0.493996 | 8 |
| 25 | ETBW7101 | 4.95 | 0.2507 | -0.4062 | 0.4346711 | 7 |
| 26 | ETBW8518 | 4.56 | -0.3677 | -0.3037 | 0.5389109 | 10 |
| 27 | ETBW7872 | 4.3 | -0.8993 | 0.0371 | 21.798966 | 30 |
| 28 | ETBW8519 | 4.9 | 0.3171 | -0.1022 | 0.9891724 | 20 |
| 29 | ETBW6937 | 5.01 | 0.4516 | 0.01 | 20.394259 | 29 |
| 30 | Danda'a | 4.22 | -0.514 | 0.4898 | 0.7285959 | 16 |

ETBW=Ethiopian Bread Wheat

## 4. Conclusion

Yield stability is very important in bread wheat production. In Ethiopia where yield pattern of Genotypes were highly varied geographical location. Selecting genotypes in diversified testing locations and assessing yield stability of bread wheat genotypes is vital.

AMMI analysis for the additive main effect and multiplicative interaction effect revealed significant difference for genotype, testing location and genotype by testing location interaction. The first interaction principal component (IPCA 1) captured the most of interaction 39.56% and the second interaction principal component explain additional 27% totally the tow interaction principal component captured 66.56% the genotype by location interaction. The other interaction effects explained by the remaining principal components. The two principal components (PCA1 and PCA2) together captured above 50% interaction principal component. AMMI 1 model provides 82.3% model fitness and bread wheat genotype by location were well predicted by the AMMI 1 model. In multi location adaptation trial considering both stability and mean grain yield is important.

When IPCA 1 is considered Genotypes ETBW7058 (11), ETBW7871 (15), ETBW8513 (16), (25) with high yield and Genotype ETBW8516 (22), ETBW8513 (21), ETBW7213 (7) and ETBW8508 (6) with low yield were stabile genotypes. When IPCA 2 is considered Genotype ETBW7871 (15) and ETBW8515 (20) were high yielding and positioned closer to the origin of the bi plot which indicates their stability in performance across environments. According to ASV Genotype ETBW8515 (20) and ETBW8513 (16) were high yielding and stable. Using AMMI analysis Asassa (As), Debretabor (D), Segure (Se), Adet (Ad) and Bekoji (Be) testing locations were favorable locations while testing location Holetta (Ho), Kulumsa (Ku) and Areka (Ar) were unfavorable.

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