# Identification of Adaptable Improved Bread Wheat (Triticum Aestivum L.) Genotypes in North Western Ethiopia

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**Abstract**

The experiment was conducted at experimental sites of Adet Agricultural Research Center namely Finoteselam, Adet, Simada, Injibara and Debretabor in 2014 cropping season under rain fed condition in North Western Ethiopia. In Ethiopia, although there are recently released and better performing bread wheat varieties, Western Amhara Region farmers grow relatively older varieties. Therefore genotype by environment interaction study is the substantial way to evaluate the performance of genotypes across environments. The objectives of the experiment were to evaluate the extent of genotype by environment interaction in grain yield; to examine adaptability and yield stability, and to differentiate the yield advantage of improved bread wheat genotypes over the standard check and local genotypes at five environments. Twelve bread wheat genotypes were used as experimental treatments. The genotypes were laid out in randomized complete block design with three replications per site. The AMMI and GGE biplot analysis of variance showed significant differences among genotypes across environments (P≤ 0.05). Even if G5, G9, G2, G4 and G11 showed higher mean grain yield than G7 (standard check) and G12 (local check), based on AMMI and GGE biplot analysis G9, G2, G4 and G11 were wide adapted genotypes across the test environments. Among these widely adapted genotypes G4 and G11 were relatively stable. In case of grain yield stability coefficient analysis G4 was highest performed genotype while G11 was higher static stable genotype all over the test environments. Therefore uses of different statistical analysis techniques are vital to overcome wrong conclusions of the studies. Promising genotypes like Gambo(G4), Ogolcho (G2) and Tsehay (G9) could be used as alternative varieties at test environments. Shorima (G11) in all environments except Finoteselam, and Tay (G7) in all environments except Simada could be recommended for production where as Kubsa(G12), Hidase(G1), Huluka(G3) and Gassay(G6) should not be used for production over the tested environments. However, it's better to repeat the experiment to know the effect of seasonal variation on yield stability of promising genotypes.

**Keywords:** Adaptability, AMMI, GEI, GGE, Yield stability

## 1. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the world's leading cereal grains and most important food crops. It has versatile uses for making various human foods and alcoholic beverages, such as bread, biscuits, cakes, sandwich, etc. Additionally, wheat straw is commonly used as a roof thatching material and animal feed (Poehlman and Sleper, 1995).

Wheat is one of the most important small cereal crops in Ethiopia, which is ranked fourth in terms of area coverage (1663845.63 hectares) after teff, maize and sorghum (CSA, 2014/15). It is also ranked fourth in terms of total annual production (42315887.16 quintals) after maize, sorghum and teff with productivity of 2.54 t/ha (CSA, 2014/15). In particular wheat productivity in Western Amhara is 2.25 t/ha (CSA, 2014/15). This is lower compaired to world average wheat productivity which is about 3.3 t/ha. Hence, wheat production and productivity in Ethiopia are low due to the influence of diseases such as rust and lack and suboptimal use of production inputs (e.g. improved seeds, fertilizers), and breakdown of disease resistance of released varieties after few years of production (Zerihun, 2014).

Even if wheat production and productivity in the country has been increasing, it is still insufficient to meet the increasing food demand for the ever-increasing population. Ethiopia's wheat production is not self-sufficient and it covers only 75% of the national demand, while the remaining 25% of the wheat is imported from abroad mainly as food aid (Eyob *et al.*, 2014). Therefore wheat production must be boost up to cut down the demand deficiency and import currency.

In Ethiopia, although there are recently released and better performing bread wheat varieties, Western Amhara Region farmers commonly used relatively older bread wheat varieties such as Kubsa and Tay which were released in 1995 and 2005, respectively. Therefore, evaluation of recently released improved bread wheat varieties with relatively older bread wheat varieties using genotype by environment interaction study through different statistical analysis methods like AMMI biplot analysis and GGE biplot analysis enables quantification of not only the average performance of crop genotypes across environments, but it is also used for assessing the

extent of genotypes performance across a range of environments (Yasin *et al*., 2013).

The process of variety development in the country is continuing year after year through various research centers/institutes, universities and different organizations. However, once the varieties are released for production, they are used for a long period of time continuously without considering their adaptation domain and testing whether they are losing their potential or not. It is vital, therefore, to evaluate the genetic by environmental interaction of bread wheat varieties used in the region with the following objectives: to evaluate the extent of genotype by environment interaction on grain yield, and to differentiate the grain yield advantage of recently released varieties over farmers commonly used varieties.

## 2. MATERIALS AND METHODS
### 2.1. Study Areas Description and Experimental Treatments
The experiment was conducted during 2014 cropping season under rain-fed conditions at experimental sites of Adet Agricultural Research Center namely, Finoteselam, Adet, Simada, Injibara and Debretabor. Twelve improved bread wheat varieties namely, Hidase, Ogolcho, Hulluka, Shorima, Gambo, Danda'a and Kubsa which have been released by Kulumsa Agricultural Research Center, Tsehay, Bollo and Menze which have been released by Debrebirhan Agricultural Research Center, and Tay and Gassay which have been released by Adet Agricultural Research Center were used as treatments for the study.

Table 1. Altitude, geographical location, soil type and climate data of the research sites

| Environments | Code | Altitude (masl) | Geographical location | | Soil type | Climate data | |
|---|---|---|---|---|---|---|---|
| | | | Latitude | Longitude | | RF(mm) | Temp(C$^0$) |
| Finoteselam | E1 | 1917m | $10^042'$N | $37^016'$E | Nitosol | NA | 18.76 |
| Adet | E2 | 2240m | $11^016'$N | $37^029'$E | Nitosol | 658.6 | 17.53 |
| Simada | E3 | 2460m | $11^003$N | $37^030'$E | Luvisol | 736.1 | 13.27 |
| Injibara | E4 | 2560m | $10^057'$N | $36^056'$E | Luvisol | 1562.9 | NA |
| Debretabor | E5 | 2591m | $11^051'$N | $38^001'$E | Luvisol | 1102.7 | 15.48 |

Source: AARC (2014) and ANRSMA (2015)

Table 2. Description of genotypes used for the study

| code | Genotypes name | Pedigree | Released by | Year of release | Grain yield (t/ha) during releasing time | | Adaptation Zone | |
|---|---|---|---|---|---|---|---|---|
| | | | | | On station | On farm | Altitude(masl) | RF(mm) |
| G1 | Hidase | ETBW 5795 | KARC | 2012 | 4.4-7 | 3.5-6 | 2200-2600 | >500 |
| G3 | Huluka | Flag 5 | KARC | 2012 | 4.4-7 | 3.8-6 | 2200-2600 | 500-800 |
| G2 | Ogolcho | ETBW 5520 | KARC | 2012 | 2.8-4 | 2.2-3.5 | 1600-2100 | 400-500 |
| G11 | Shorima | ETBW 5483 | KARC | 2011 | 2.9-7 | 2.3-4.4 | 2100-2700 | 700-1100 |
| G4 | Gambo | QUIAU#2 | KARC | 2011 | 3.5-5.7 | 4.5 | 750 | - |
| G9 | Tsehay | HAR 3837 | DBARC | 2011 | 3.8 | 2.8-3.5 | 2600-3100 | >900 |
| G5 | Danda'a | DANPHE#1 | KARC | 2010 | 3.5-5.5 | 2.5-5 | 2000-2600 | >600 |
| G8 | Bolo | HAR 3816 | DBARC | 2009 | 2.8-3.5 | 2.3-3.3 | 2580-3100 | >904 |
| G10 | Menze | HAR 3008 | DBARC | 2007 | 1.9-3.3 | 1.5-2.7 | 2800-3100 | >904 |
| G6 | Gassay | HAR 3730 | ADARC | 2007 | 4.4-5 | 3.5-4.7 | 1890-2800 | >700 |
| G7 | Tay(SC) | - | ADARC | 2005 | 2.5-6.1 | 3.4-5.8 | 1900-2800 | >700 |
| G12 | Kubsa(LC) | HAR 1685 | KARC | 1995 | 5.8-6.3 | 4-4.5 | 1850-2800 | 500-800 |

Source: MoA, Crop Variety Register (1995-2013)

ADARC- Adet Agricultural Research Center, DBARC- Debrebirhan Agricultural Research Center, KARC- Kulumsa Agricultural Research Center, SC-Standard Check, LC-Local Check

### 2.2. Experimental Procedures and Analysis Methods
The treatments were laid out using a randomized complete block design with three replications per site and six rows per plot. Planting was done in July with the recommended seeding rate (150 kg/ha) on the plot area of 1.2 m*2.5 m with net harvested area of 0.8m*2.5m. Urea and DAP fertilizers as source of nitrogen and phosphorous were applied as per their recommendation rate and time of application for bread wheat specified to each experimental site. All other agronomic practices were applied as per their recommendations for bread wheat in the respective experimental sites.

Grain yield were analyzed by using GenStat (17$^{th}$ Ed) software to compute AMMI biplot analysis of genotypes and environments main and interaction effects, and GGE biplot analysis of genotypes and genotype by environment interactions. Whenever the analysis results were highly significant or significant, Fisher's LSD test at 1 % and 5% probability level, respectively, was used to separate the variable means of genotypes,

environments and genotypes by environments interaction.

The AMMI analysis of variance summarizes most of the magnitude of genotype by environment interactions into one or few interaction principal component axes (IPCA) (Zobel *et al.* 1988, Crossa, 1990). AMMI model equation is:

$$Y_{ger} - u - \alpha_g - \beta_e = \Sigma_n \Lambda_n \tau_{gn} \delta_{en} + p_{ge} + \textit{t}_{ger}$$

where $Y_{ger}$ is the grain yield of genotype (g) in environment (e) for replicate (r), $u$ is the grand mean, $\alpha_g$ are genotype mean, $\beta_e$ are the environment mean deviations, $\Lambda_n$ is the singular value for IPCA axis n, $\tau_{gn}$ are genotype eigenvector values for IPCA axis n, $\delta_{en}$ are the environment eigenvector values for (PCA) axisn, $p_{ge}$ are the residuals and $\textit{t}_{ger}$ is the error term.

GGE biplot analysis can be identified high yielding and stable varieties as well as representative and discriminating environments (Yan, 2001).

$$\text{. } Y_{ger} - \beta_e = \Sigma_n \Lambda_n \tau_{gn} \delta_{en} + p_{ge} + \textit{t}_{ger}$$

where $Y_{ger}$ is the grain yield of genotype (g) in environment (e) for replicate (r), $\beta_e$ are the environment mean deviations, $\Lambda_n$ is the singular value for IPCA axis n, $\tau_{gn}$ are genotype eigenvector values for IPCA axis n, $\delta_{en}$ are the environment eigenvector values for (PCA) axis n, $p_{ge}$ are the residuals and $\textit{t}_{ger}$ is the error term.

Lin and Binns (1988a) defined the superiority measure (Pi) of the $i^{th}$ test cultivar as the MS of distance between the $i^{th}$ test cultivar and the maximum response as:

$$P_i = [n(\overline{X}_i - \overline{M}_.)^2 + (\sum_{j=1}^{n}(X_{ij} - \overline{X}_{i.} - M_j + \overline{M}_.)^2]/2n$$

Where Xij=is the average response of the $i^{th}$ genotype in the $j^{th}$ environment, Xi=is the mean deviation of genotype i, Mj=is the genotype with maximum response among all genotypes in the $j^{th}$ location, and n is the number of locations. The first term of the equation represents the genotype sum of squares and the second part the GE sum of squares.

Becker and Leon (1988) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (Wi) or stability of the $i^{th}$ genotype is its interaction with the environments, squared and summed across environments, and express as:

$$Wi = [Yij - Yi. - Y.j - Y..]^2$$

Where, Yij is the mean performance of genotype i in the $j^{th}$ environment and Yi. And Y.j is the genotype and the environment mean deviations, respectively, and Y.. is the overall mean. For this reason, genotypes with a low Wi value have smaller deviations from the mean across environments and are thus more stable.

According to Lins et al., 1986 the variance of genotype yields recorded across the test or selection environments. For the genotype greatest stability is $S_i^2=0$. The formula is:

$$S_i^2 = \text{£}(R_{ij} - m_i)^2/(e-1)$$

Where; $S_i^2$= environmental variance, $R_{ij}$= observed genotype yield across environments; e=number of environments

## 3. RESULTS AND DISCUSSION

### 3.1. AMMI Biplot Analysis of Genotypes and Environments for Grain Yield

The AMMI Biplot analysis of variance ($P \leq 0.05$) of genotypes, environments and their interactions showed in table 3. The highest variation of genotype by environment interactions explained by PC1, the next highest variation explained by PC2 and up to PCn. In this study, PC1–PC4 showed significant variations of genotype by environment interactions. The sum square variations of grain yield accounted by genotypes, environments and their interactions were 24.45%, 54.46% and 21.29% respectively (Table 3).

Table 3. AMMI biplot analysis of genotypes, environments and their interactions

| Source of variation | DF | SS | MS | VR | F Pr |
|---|---|---|---|---|---|
| Genotypes | 11 | 7218 | 656.2** | 63.27 | <0.001 |
| Environments | 4 | 16222 | 4055.6** | 189.24 | <0.001 |
| Block | 10 | 214 | 21.4* | 2.07 | 0.0332 |
| Interactions | 44 | 6337 | 144.0** | 13.89 | <0.001 |
| IPCA 1 | 14 | 3320 | 237.2** | 22.87 | <0.001 |
| IPCA 2 | 12 | 1753 | 146.1** | 14.08 | <0.001 |
| IPCA 3 | 10 | 868 | 86.8** | 8.37 | <0.001 |
| IPCA 4 | 8 | 396 | 49.4** | 4.77 | <0.001 |
| IPCA 5 | 6 | 0 | 0.0 | 0.00 | 1.0000 |
| Residuals | -6 | 0 | 0.0 | 0.00 | |
| Error | 110 | 1141 | 10.4 | | |
| Total | 179 | 31132 | 173.9 | | |

DF=degree of freedom, SS=sum squares, MS=mean squares, VR=virtual reality, F Pr. =F probability

### 3.2. AMMI Biplot Analysis of Main Effects of Genotypes and Environments

The AMMI biplot analyses of the main effects of genotypes and environments depicted significant differences ($P \leq 0.05$) among genotypes and environments. Genotypes G9, G5, G11, G2 and G4 were showed above average grain yield with high main (additive) effects with the positive IPCA1 score particularly G4 being the overall best across the tested environments. Hence, G4 was identified as wide adapted to the tested environments. On the other hand, genotypes G1, G3, G7, G12, G10, G8 and G6 were depicted below average grain yield (Figure 1). Environments E2 and E3 depicted above average grain yield, while environments E1, E4 and E5 were below average grain yield (Figure 1). Therefore, E2 and E3 exerted a higher discriminating effect on the tested bread wheat genotypes.

According to Gabriel (1971), Brandu and Gabriel (1978) and Akter *et al*. (2014), genotypes that group together have similar adaptation and also environments which group together influences the genotypes in the same way. Therefore based on AMMI biplot analysis of genotypes main effects were clustered into three groups. These are G4, G2, G11, G9 and G5 in one group; G1, G10, G8 and G6 in the second group; and G12, G3 and G7 in the third group. On the base of Gauch and Zobel (1988), Zobel *et al, (*1988)*,* Crossa (1990), Misra *et al*. (2010) and Hintsa *et al*. (2013) reports a genotype or an environment with an IPCA1 score of nearly zero, has small interaction effects; and genotype and environment have the same sign on the PCA axis, their interaction is positive while different their interaction is negative. Therefore, G11 were depicted small interaction effects than other genotypes all over the test environments which mean that G11 had relatively constant grain yield response across environments. Genotypes G12, G7 and G3 with E1, E2 and E4 and the remaining genotypes with E3 and E5 were interacting positively vice versa had negative interaction effects.

The AMMI analysis selection per environment based on grain yield G4 was ranked 1st on all the tested environments, G2 (on E1, E2, E3 and E5) and G3 (on E4) were ranked 2nd, G9 (on E1, E2 and E3) and G11 (on E4 and E5) ranked 3rd. However, four different genotypes ranked 4th on the five environments (Table 4).

Table 4. The first four AMMI selections of genotypes per environment based on grain yield response

| Environment | Mean | Score | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|---|
| E3 | 39.01 | 4.417 | G4 | G2 | G9 | G11 |
| E5 | 33.21 | 0.946 | G4 | G2 | G11 | G5 |
| E2 | 56.02 | -0.950 | G4 | G2 | G9 | G11 |
| E1 | 27.88 | -1.153 | G4 | G2 | G9 | G7 |
| E4 | 36.89 | -3.261 | G4 | G3 | G11 | G5 |

E1 = Finoteselam, E2 = Adet, E3 = Simada, E4= Injibara, E5 = Debretabor
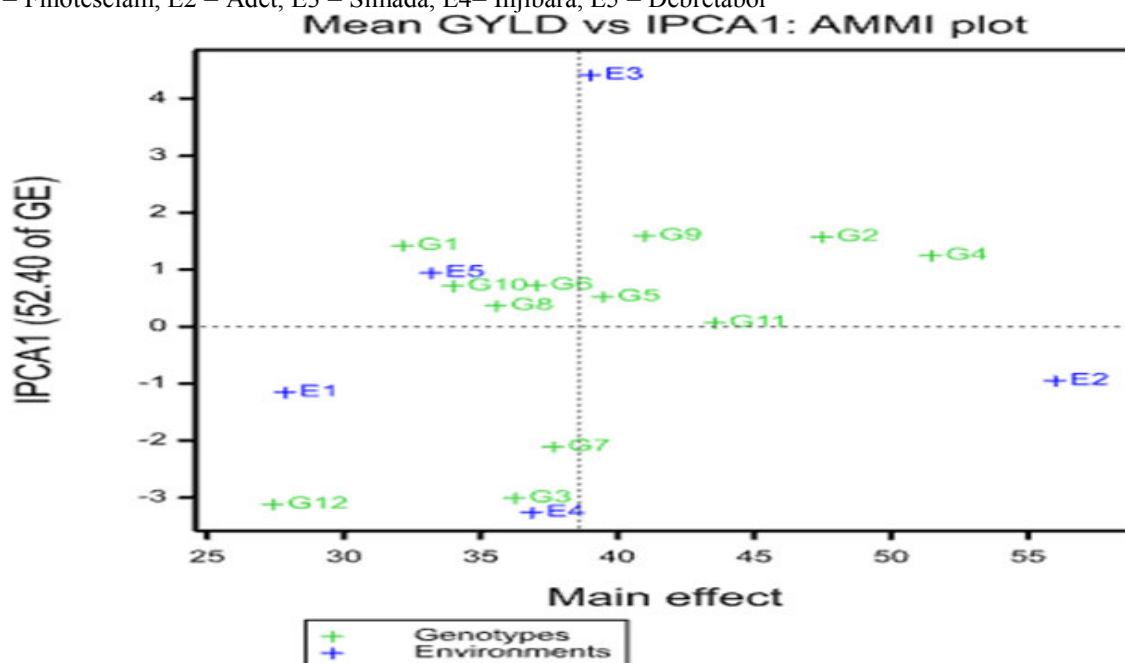


Figure 1. AMMI biplot main effects of 12 bread wheat genotypes in five environments based on mean grain yield
G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Ga'ambo, G5= Danad'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, E1= Finoteselam, E2= Adet E3= Simada, E4= Injibara, E5= Debretabor, IPCA= Interaction Principal Component Axes

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### 3.3. AMMI Biplot Analysis of Genotype by Environment Interaction Effects

The AMMI biplot analysis of interaction effects of genotypes by environments depicted significant differences ($P \leq 0.05$) of genotypes and environments (Table 3). The AMMI biplot analysis of Principal Component 1 and Principal Component 2 accounted 52.66% and 27.40%, respectively, of the total genotype by environment interaction for grain yield over tested environments, totally summed up to 80.06%. Fetien *et al*. (2009), Misra *et al*. (2010) and Akter *et al*. (2014) stated that the genotypes near the origin are not sensitive to environmental interaction forces, whereas genotypes distant from the origin are sensitive and have large interaction forces. Hence from this study, genotypes G9, G12, G5, G3 and G7 were more sensitive to environmental interactive forces which were far from the origin of biplot, while genotypes G4, G2, G1, G11, G6, G8 and G10 were relatively less sensitive to environmental interactive forces. However, only G4, G2 and G11 showed above average grain yield based on AMMI biplot analysis of genotypes main effects (figure 1 and 2). On the base of Akter *et al*. (2014) conclusion environments with short spokes exert small interactive forces, whereas environments with long spokes exert strong interaction. Environment E5 had short spoke which exert small interactive forces on the genotypes than E2, E3, E4 and E1 (Figure 2). Hence genotypes grain yield response at E5 was smaller than the remaining environments.
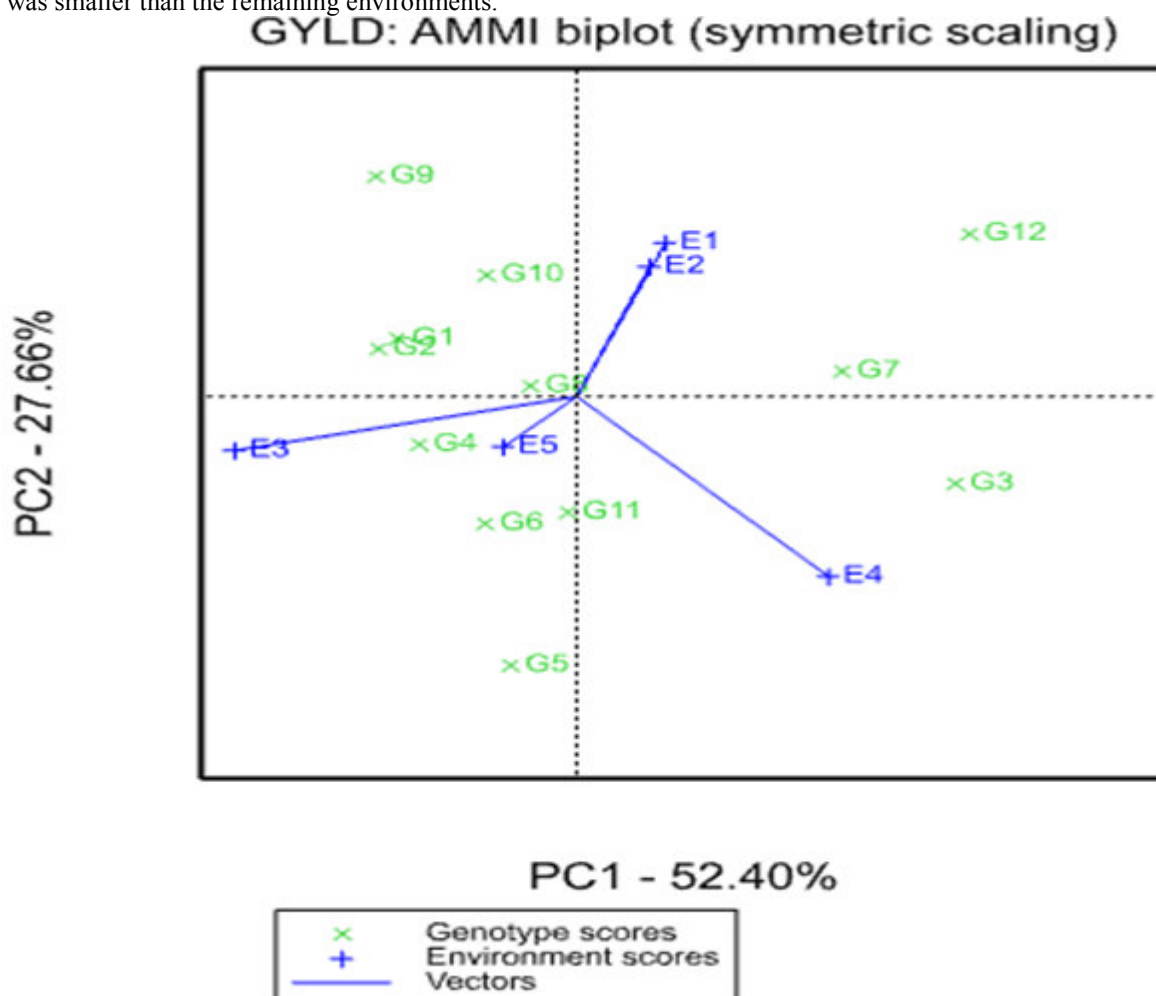


**Figure 2. AMMI biplot analysis of GEI of 12 bread wheat genotypes across five environments using symmetric scaling**
**G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Ga'ambo, G5= Danad'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, E1= Finoteselam, E2= Adet E3= Simada, E4= Injibara, E5= Debretabor and PC= Principal Component.**
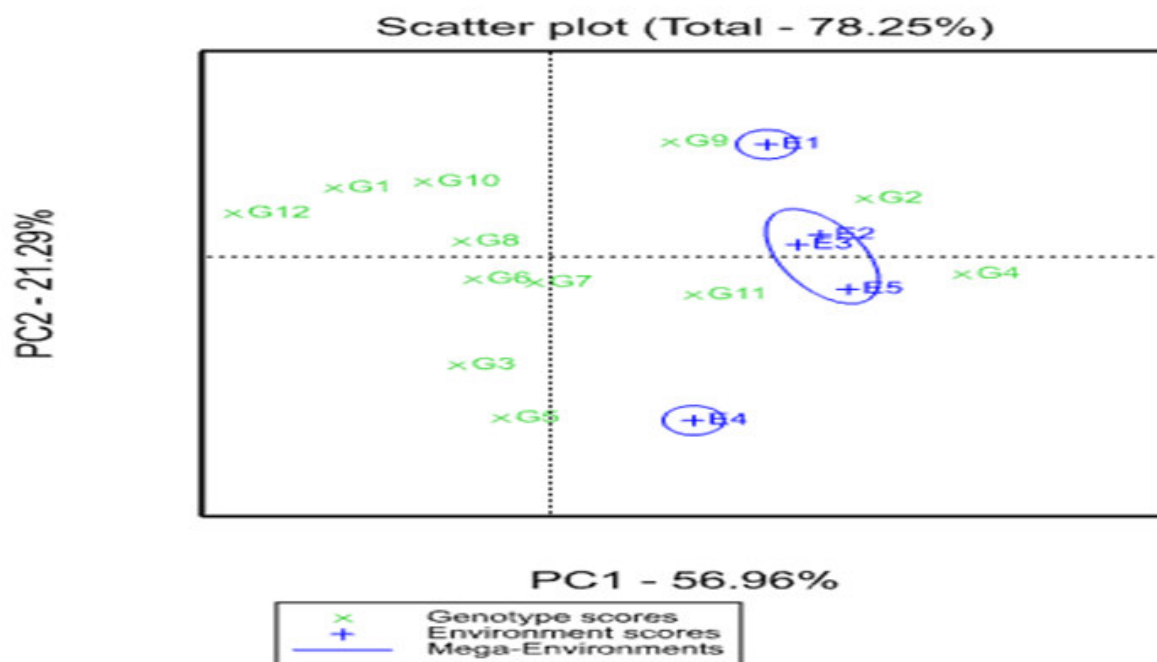
### 3.4. GGE Biplot Analysis of Genotype by Environment Interactions

GGE biplot analysis of PC1 and PC2 accounted the interaction variation of 56.96% and 21.29 %, respectively, totaling 78.25%. The 'which-won-where' pattern and sensitivity degree between the genotype and environment of a GGE biplot based on the PC1 and PC2 values was displayed in Figure 3.

According to Fetien *et al*.(2009), Mohamed (2013), and Hintsa *et al*. (2013), the genotypes that have

PC1 scores greater than zero value is identified as higher yielding, while the genotypes that have PC1 scores less than zero value is identified as lower yielding. And also, they stated that genotypes with PC2 close to zero value were stable, while genotypes with large PC2 value were unstable. Genotypes G4, G2, G11 and G9 with PC1 positive value were better adapted to the test environments. In particular, G9 was the winning genotype in E1, G4, G2 and G11 were the winning genotypes in E2, E3 and E5. Similarly G4 and G11 were the winning genotypes in E4. Therefore, based on grain yield response of better adaptable genotypes, environments are grouped in to three mega-environments E1, (E2, E3 and E5) and E4. On the other hand, genotypes G1, G3, G5, G6, G7, G8, G10 and G12 with PC1 negative value were poorly adapted to the test environments. In case of stability of genotypes across environment G6, G7, G8, G11 and G4 were relatively stable than other genotypes. Nonetheless only G11 and G4 were widely adapted genotypes all over the test environments.



**Figure 3. GGE biplot analysis of 12 bread wheat genotypes across five environments**
**G1=Hidase, G2= Ogolocho, G3=Hulluka, G4= Ga'ambo, G5= Danad'a, G6= Gassay, G7=Tay, G8= Bolo, G9= Tsehay, G10=Menze, G11=Shorima, G12=Kubsa, E1= Finoteselam, E2= Adet E3= Simada, E4= Injibara, E5= Debretabor and PC= Principal Component.**

### *4.5. Grain Yield Stability Coefficient analysis of Genotypes over Environments*

Based on cultivar superiority analysis of genotypes G4 was ranked 1st but not had a constant grain yield performance across the test environments. The smaller the value of cultivar superiority (Pi), the less is the distance to the genotype with maximum yield and the better the genotype in line with Crossa(1990). Static stability analysis of genotypes G6 was ranked 1st. Even if G6 showed a constant grain yield, but had a lower yield response. Becker and Leon (1988) stated that a genotype is static stable, it's among environmental variance is small. It would be of little use to yield when the varieties were low yielding (Kang, 1990). Wricke's ecovalence analysis of genotypes G11 was ranked 1st. According to Becker and Léon (1988) a genotype nearly zero ecovalence value is regarded as stable (Table 5).

Therefore static stability analysis had a drawback which implies both higher and lower grain yielding genotypes as stable. Cultivar superiority analysis only showed mean performance of genotypes across environments, nonetheless it is difficult to know whether the genotypes are stable or not.  Hence, combined use of different stability analysis methods was used to properly identify stable genotypes both in potential and consistency of grain yield over environments.

**Table 5. Stability coefficient analysis of bread wheat genotypes based on grain yield across environments**

| Genotypes | Stability coefficient | | | | | | |
|---|---|---|---|---|---|---|---|
| | Means | Cultivar superiority | Ranks | Static Stability | Ranks | Wricke's Ecovalence | Ranks |
| G4 | 51.48 | 0.3 | 1 | 187.4 | 9 | 99.3 | 4 |
| G2 | 47.5 | 16.3 | 2 | 140.8 | 5 | 122 | 5 |
| G11 | 43.58 | 47.3 | 3 | 86.7 | 2 | 47.5 | 1 |
| G9 | 41.01 | 80.2 | 4 | 260 | 12 | 257.5 | 10 |
| G5 | 39.49 | 94 | 5 | 183.7 | 8 | 230.8 | 9 |
| G6 | 37.03 | 131.3 | 6 | 53.5 | 1 | 125.8 | 6 |
| G7 | 37.67 | 138.8 | 7 | 174.4 | 7 | 155.2 | 7 |
| G8 | 35.59 | 144.2 | 8 | 87 | 3 | 50 | 2 |
| G10 | 34 | 173.8 | 9 | 127.6 | 4 | 60.8 | 3 |
| G3 | 36.26 | 181.3 | 10 | 226.3 | 11 | 334.8 | 11 |
| G1 | 32.17 | 225 | 11 | 145.6 | 6 | 221.2 | 8 |
| G12 | 27.44 | 378.9 | 12 | 206.9 | 10 | 407.2 | 12 |

**G1=Hidase, G2=Ogolocho, G3=Hulluka, G4= Ga'ambo, G5=Danad'a, G6=Gassay, G7=Tay, G8= Bolo, G9=Tsehay, G10=Menze, G11=Shorima and G12=Kubsa**

## 4. CONCLUSION AND RECOMMENDATIONS

The significant of genotypes showed differential response of grain yield across the testing environments. Therefore, it is difficult to identify one superior genotype for all the environments. According to AMMI analysis selection per environment based on grain yield G4 was ranked 1st over all the tested environments. Genotype G2 (on E1, E2, E3 and E5) and G3 (on E4) were ranked 2nd. Genotype G9 (on E1, E2 and E3) and G11 (on E4 and E5) ranked 3rd. Genotypes G11 (on E3 and E5), G5 (on E4 and E5) and G7 (on E1) ranked 4th. Hence, the rank of genotypes across environments is vital for bread wheat seed multiplication and distribution for production.

From this study, Gambo (G4) had highest mean grain yield (5.15 t/ha) whereas Kubsa (G12) had a lowest grain yield (2.74 t/ha). In addition to G4, it was also noted that G2, G11, G9 and G5 showed a higher mean grain yield than the standard check (G7) and local check (G12). Generally, G4 had 1.38 t/ha and 2.41 t/ha mean grain yield advantage over G7 and G12, respectively. Similarly, G2 had 0.98 and 2.01 t/ha mean grain yield advantage over G7 and G12, respectively

The genotypes G9, G2, G4 and G11 were hardly affected by the genotype by environment interaction and thus would perform well across a wide range of environments than the standard check (G7) and local check (G12). The genotypes that had a higher grain yield in a wide range of environments are determinant to improve production and productivity and crossing purpose because these genotypes buffering the fluctuation of environmental conditions. Among the genotypes which showed higher mean grain yield G11 and G4 was relatively stable genotype.

Therefore, based on the overall mean grain yield and stability of this study, Shorima(G11) except at Finoteselam; Tay(G7) except at Simada could be used in the Western Amhara Region. Promising genotypes like Gambo (G4), Ogolcho (G2) and Tsehay (G9) could be used as alternative varieties at test environments. Huluka(G3) and Gassay(G6) should not be used for production over the tested environments. However, it's better to repeat the experiment to know the effect of seasonal variation on yield stability and rust disease occurrence. Hence, on time adaptability and stability evaluation test should be continued to bring improved genotypes for production and to ban deteriorated genotypes out of production.

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