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# Genotype by environment interaction and stability study in bread wheat (*Triticum aestivum* L.) genotypes in Guji Zone, Southern Ethiopia

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# Abstract

Today, wheat is among the most important crops grown in Ethiopia, both as a source of food for consumers and source of cash for our country. Ethiopia has a diversified agro-ecology and enormous potential for wheat production, spanning from low land to high land. In this study, 17 bread wheat genotypes were evaluated at six environments to investigate genotype-environment (G E) interactions and yield performance stability across environments. The field experiment was set up in three replications using a randomized complete block design at mid-land areas of Guji Zone of Southern Ethiopia. The combined analysis of variance revealed that, there were highly significant differences among main effects and interactions for grain yield and yield components, indicating that the presence of diversity in genotypes and environments. The highest grain yield were recorded from BWRVT/76(44.62kgha-1) followed bv BWRVT/54(44.58kgha-1) .According to AMMI ANOVA, Environments explained 33% of the total variation , genotypes 28.24% and GxE 22.28% explained of the total variation, respectively . IPCA1 and IPCA2 accounted for 52.24% and 22.65% of the GE interactions SS, respectively. According to GGE biplot model analysis, genotype BWRVT/76 and BWRVT/40 are ideal genotypes, because both are located at the center of the concentric circle. Thus, these two genotypes, BWRVT/76 and BWRVT/40, were identified as candidate genotypes to be verified for potential release for the highlands of Guji, Southern Ethiopia, and similar agro-ecologies. Also, genotypes BWRVT/75 and BWRVT/54 are high yielder but not stable. As a result, genotypes BWRVT/75 and BWRVT/54 may be used in the future for wheat breeding program, crossing.

Keywords: GGE Bi-plot; Stable; Grain Yield; Bread wheat; Guji Zone

# 1. Introduction

Bread wheat is one of the most significant cereal crops that can grow in a wide range of agro-ecologies in Ethiopia. It grows well in a range of lowland to high elevation. Wheat provides for around 17% of total grain production in Ethiopia, making it the third most important cereal crop after maize and tef <sup>[1]</sup>. Although wheat yields in Ethiopia in general and the Oromia area in particular are remain low, the national average productivity is expected to be 3.4 tons/ha <sup>[1]</sup>, which is lower than the research average yield of 4-6 tones ha<sup>-1</sup>. Several factors influence wheat production and productivity in Ethiopia. The key issues contributing to Ethiopia's low production and productivity are the lack of access to a stable and adaptable to current climate change. Ethiopia is noted for its various agro-ecologies for wheat production; however, most of the released varieties may not perform well in Ethiopia's diverse agro-ecologies and respond differently to different conditions.

The primary source of variances between genotypes in yield stability is the wide occurrence of genotype-environment interactions (GE-interactions), i.e. the ranking of genotypes depends on the particular environmental conditions where

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they are produced. These interactions of genotypes with environments can be as a result of a differential reaction to environmental stress factors like drought, fluctuation of rain fall, diseases and soil acidity, and therefore, climate change focusing breeding strategy is one of significance approach in improving yield stability <sup>[2]</sup>. Assessment of different genotypes across sites and over time is now not only necessary for selecting and recommending high-yielding cultivars, but also for identifying suitable places that represent the optimal environment <sup>[3]</sup>.

GxE is an important tool used by plant breeders, agronomists, and farmers all over the world to determine the best genotypes and acceptable environments. Several statistical methods for examining genotype-environment interactions and finding genotypes for particular and wide adaptation have been created using data on G by E interdependence. GGE biplots show genotype plus genotype by environment, whereas AMMI biplots represent additive main effects and multiplicative interaction. Therefore, the study aimed to identify high-yielding bread wheat genotypes that perform consistently across testing sites in midland Guji, Southern Oromia.

# 2. Material and methods

The experiment was undertaken over the last two years (2021 and 2022) in three locations, for a total of six locations. The experiment was arranged in randomized completed block design with three replications. Materials were planted on a plot size of, 1.2mx2.5m having six rows with 20 cm between rows. In both years, 17 advanced genotypes were tested in a regional variety trial alongside newly released varieties (Adola 1 and Deka) at Adola, K/Sorsa and Derartu locations. Seed rate of 150kgha<sup>-1</sup> and fertilizer rate of NPS 121kgh<sup>-1</sup> and urea 50kgha<sup>-1</sup> were utilized. All the agronomic managements and practices were adopted as per recommendation for each location. Yield data was taken per plot basis and converted to kgha<sup>-1</sup> for each plot. The lists of the genotypes are located in Table 1

| S.N | Genotype | Gen.Code | Category               | S.N | Environments | Env. code |
|-----|----------|----------|------------------------|-----|--------------|-----------|
| 1   | Adola 1  | G1       | Std.Check              | 1   | Adola2021    | 1         |
| 2   | BWRVT/27 | G2       | Advanced breeding line | 2   | Adola2022    | 1'        |
| 3   | BWRVT/40 | G3       | Advanced breeding line | 3   | K/Sorsa2021  | 2         |
| 4   | BWRVT/42 | G4       | Advanced breeding line | 4   | K/Sorsa2022  | 2'        |
| 5   | BWRVT/44 | G5       | Advanced breeding line | 5   | Derartu2021  | 3         |
| 6   | BWRVT/46 | G6       | Advanced breeding line | 6   | Derartu 2022 | 3'        |
| 7   | BWRVT/49 | G7       | Advanced breeding line |     |              |           |
| 8   | BWRVT/51 | G8       | Advanced breeding line |     |              |           |
| 9   | BWRVT/52 | G9       | Advanced breeding line |     |              |           |
| 10  | BWRVT/53 | G10      | Advanced breeding line |     |              |           |
| 11  | BWRVT/54 | G11      | Advanced breeding line |     |              |           |
| 12  | BWRVT/55 | G12      | Advanced breeding line |     |              |           |
| 13  | BWRVT/56 | G13      | Advanced breeding line |     |              |           |
| 14  | BWRVT/60 | G14      | Advanced breeding line |     |              |           |
| 15  | BWRVT/75 | G15      | Advanced breeding line |     |              |           |
| 16  | BWRVT/76 | G16      | Advanced breeding line |     |              |           |
| 17  | Deka     | G17      | Std.Check              |     |              |           |

Table 1 Lists of Bread wheat genotypes and environments included in the study

# 2.1. Data Analysis

All collected raw data were subjected GenStat 18<sup>th</sup> edition and analyzed.

# 3. Results and discussion

The combined analysis of variance (Table 1) revealed that, there were very highly significant differences (p<0.001) among environments, genotypes and their interactions for grain yield (table 1). This significance difference indicates the presence of variability in genotypes as well as diversity of growing conditions at different locations and reflects the differential response of genotypes in various environments<sup>[4]</sup>.

| S.V           | D.F | S.S       | M.S         | F pr. |
|---------------|-----|-----------|-------------|-------|
| Rep           | 2   | 3.998     | 1.999ns     |       |
| Genotypes     | 16  | 2142.097  | 133.881***  | <.001 |
| Loc           | 5   | 5905.921  | 1181.184*** | <.001 |
| Genotypes.loc | 80  | 3362.227  | 42.028***   | <.001 |
| Residual      | 202 | 1283.531  | 6.354       |       |
| Total         | 305 | 12697.774 |             |       |

**Table 2** Combined ANOVA for grain yield of bread wheat tested across mid land of Guji Zone, 2021/22

#### 3.1. Mean Comparison in Grain Yield and Yield Components

**Table 3** Combined means of grain yield (qtha-1), yield components, some agronomic and quality traits of bread wheatgenotypes tested across three locations for consecutive two years, 2021 and 2022

| Genotypes   | GY    | DH    | DM     | GP    | РН    | SL   | TKW   | GLN   | РС    | ZI    | SR   | Y.adv |
|-------------|-------|-------|--------|-------|-------|------|-------|-------|-------|-------|------|-------|
| Adola 1     | 34.77 | 53.61 | 96.78  | 43.17 | 77.85 | 7.11 | 29.34 | 26.50 | 13.45 | 38.15 | 10MS |       |
| BWRVT/27    | 37.80 | 56.61 | 100.72 | 44.11 | 71.15 | 7.76 | 33.81 | 30.65 | 14.43 | 45.70 | 20MS |       |
| BWRVT/40    | 44.58 | 49.22 | 95.72  | 46.50 | 75.29 | 7.57 | 37.59 | 30.10 | 14.96 | 43.93 | Т    | 22.91 |
| BWRVT/42    | 33.96 | 56.72 | 99.39  | 42.67 | 70.63 | 7.79 | 35.84 | 29.85 | 14.30 | 48.73 | 10MS |       |
| BWRVT/44    | 35.52 | 51.83 | 93.22  | 41.39 | 71.01 | 7.07 | 32.67 | 28.87 | 14.30 | 43.58 | 10MS |       |
| BWRVT/46    | 32.64 | 56.61 | 99.56  | 42.94 | 72.13 | 7.96 | 33.29 | 31.92 | 14.60 | 51.60 | Т    |       |
| BWRVT/49    | 36.32 | 50.89 | 93.83  | 42.94 | 71.02 | 7.33 | 35.77 | 30.07 | 14.38 | 46.88 | 20S  |       |
| BWRVT/51    | 32.62 | 52.83 | 97.28  | 44.44 | 74.13 | 7.58 | 39.46 | 31.42 | 14.38 | 50.58 | Т    |       |
| BWRVT/52    | 37.02 | 52.56 | 94.89  | 42.33 | 79.29 | 8.87 | 33.13 | 28.60 | 13.75 | 42.90 | 10R  |       |
| BWRVT/53    | 37.27 | 52.61 | 99.00  | 46.39 | 74.61 | 8.09 | 35.96 | 29.87 | 14.23 | 45.38 | 10MR |       |
| BWRVT/54    | 43.39 | 54.44 | 100.06 | 45.61 | 68.59 | 7.44 | 36.06 | 28.30 | 13.20 | 42.08 | Т    |       |
| BWRVT/55    | 32.63 | 57.61 | 104.00 | 46.39 | 75.89 | 8.31 | 35.74 | 35.12 | 15.90 | 58.45 | 5R   |       |
| BWRVT/56    | 34.27 | 55.61 | 103.33 | 47.72 | 70.94 | 8.68 | 38.06 | 33.30 | 15.28 | 55.15 | Т    |       |
| BWRVT/60    | 34.01 | 56.83 | 101.50 | 44.67 | 67.50 | 7.48 | 31.91 | 30.42 | 14.70 | 49.50 | 20S  |       |
| BWRVT/75    | 42.14 | 56.33 | 98.72  | 42.39 | 74.74 | 7.52 | 31.49 | 27.72 | 13.45 | 39.98 | 10MS |       |
| BWRVT/76    | 44.62 | 55.67 | 98.06  | 42.39 | 79.22 | 8.13 | 35.42 | 27.00 | 13.13 | 38.10 | 5MS  | 23.01 |
| Deka        | 36.27 | 55.39 | 101.89 | 46.50 | 76.89 | 7.68 | 35.38 | 30.55 | 14.58 | 48.35 | Т    |       |
| G. Means    | 35.8  | 54.43 | 98.70  | 44.27 | 73.35 | 7.79 | 34.76 | 29.95 | 14.24 | 46.36 |      |       |
| CV%         | 7.16  | 2.22  | 2.65   | 6.05  | 6.91  | 6.55 | 13.4  | 7.23  | 4.94  | 10.04 |      |       |
| LSD (at 5%) | 4.06  | 1.95  | 4.22   | 4.31  | 8.16  | 0.82 | 7.50  | 3.081 | 1.001 | 6.614 |      |       |

Key: DH = days for heading, DM = days to maturity, GP=Grain filling period, PH = plant height (cm), SL = Spike length, TKW = thousand kernel weight (cm), GY = grain yield (q/ha), GLN = gluten, PC = protein content, ZI = Zeleny index, SR= stem rust, CV (%) = Coefficient of variations, LSD = Least significant differences The combined data analysis revealed that the highest mean of yield was recorded from genotype BWRVT/76 (44.62Qt/ha) followed BWRVT/40 (44.58 qtha<sup>-1</sup>) and BWRVT/54 (39.6 qtha<sup>-1</sup>). Standard check/Deka produced the lowest yield (31.2 qtha<sup>-1</sup>). The second standard check (Adola 01) produced 34 qtha<sup>-1</sup> of grain yields, ranking 11th out of the 17 genotypes used in the trial (Table3). (Table3). Both BWRVT/40 and BWRVT/76 had yield advantages of 23.01 and 22.1%, respectively, and preceded the VVT stage for further study (table 2).

# 3.2. Mean of Genotypes for Grain Yield Across Locations

The ranking of genotypes according to their yield performance indicated that there were varied across environments (table 4). For example, advanced genotype BWRVT/40 ranked 1<sup>st</sup> at Adola 2<sup>nd</sup> year and Derartu 2<sup>nd</sup> year. However it ranked differently at remaining environments. This indicates that, the type of GxE interaction is cross-over interaction. Cross-over GxE interaction is the case when significant change in rank occurs from one environment to another <sup>[5]</sup>.

From this study, more impacting factor is the environment and this indicates that major factor that impact yield performance of genotypes in this research is the environment.

The relatively large proportion of Genotype x Environment variance, when compared to that of genotypes, is a very important consequence. The large sum of squares for environment showed that the environment was diverse with large differences among environmental means caused variation in performance of the genotypes and this could be attributed due to the unequal distribution of rain fall in the growing season, heterogeneity of locations in soil type, altitude range and diseases in discriminating the performance of genotypes across locations. Presence of significance GEI indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment.

| Genotype | 1     | R  | 1'    | R  | 2     | R  | 2'    | R  | 3     | R  | 3'    | R  |
|----------|-------|----|-------|----|-------|----|-------|----|-------|----|-------|----|
| Adola 1  | 26.40 | 15 | 31.07 | 14 | 27.67 | 16 | 30.27 | 13 | 29.73 | 16 | 45.47 | 8  |
| BWRVT/27 | 42.53 | 3  | 34.47 | 10 | 42.20 | 2  | 28.40 | 15 | 35.20 | 8  | 43.97 | 9  |
| BWRVT/40 | 41.27 | 4  | 50.01 | 1  | 38.82 | 9  | 43.53 | 3  | 42.53 | 2  | 51.31 | 1  |
| BWRVT/42 | 32.13 | 6  | 38.73 | 5  | 26.60 | 17 | 24.20 | 17 | 36.13 | 7  | 45.93 | 7  |
| BWRVT/44 | 30.60 | 9  | 35.20 | 7  | 33.20 | 12 | 37.53 | 6  | 34.40 | 10 | 42.20 | 15 |
| BWRVT/46 | 24.07 | 16 | 32.47 | 13 | 35.60 | 10 | 32.33 | 12 | 32.00 | 12 | 39.40 | 17 |
| BWRVT/49 | 29.93 | 12 | 34.67 | 8  | 41.27 | 5  | 38.60 | 5  | 30.80 | 15 | 42.67 | 12 |
| BWRVT/51 | 27.67 | 14 | 33.27 | 12 | 31.13 | 14 | 25.80 | 16 | 31.47 | 14 | 46.40 | 6  |
| BWRVT/52 | 31.67 | 7  | 34.53 | 9  | 41.87 | 3  | 33.93 | 11 | 37.87 | 5  | 42.27 | 14 |
| BWRVT/53 | 30.00 | 11 | 36.87 | 6  | 40.13 | 6  | 41.07 | 4  | 35.00 | 9  | 40.53 | 16 |
| BWRVT/54 | 48.30 | 1  | 45.00 | 2  | 39.73 | 7  | 35.53 | 8  | 40.70 | 3  | 51.07 | 3  |
| BWRVT/55 | 28.87 | 13 | 30.90 | 15 | 34.27 | 11 | 29.67 | 14 | 29.73 | 16 | 42.33 | 13 |
| BWRVT/56 | 30.40 | 10 | 33.93 | 11 | 30.93 | 15 | 35.33 | 9  | 32.00 | 12 | 43.00 | 10 |
| BWRVT/60 | 23.80 | 17 | 29.93 | 17 | 39.13 | 8  | 35.60 | 7  | 32.60 | 11 | 43.00 | 10 |
| BWRVT/75 | 31.67 | 7  | 44.40 | 3  | 44.35 | 1  | 43.77 | 2  | 39.93 | 4  | 48.75 | 4  |
| BWRVT/76 | 43.57 | 2  | 41.60 | 4  | 41.62 | 4  | 46.27 | 1  | 43.51 | 1  | 51.19 | 2  |
| Deka     | 35.40 | 5  | 30.40 | 16 | 32.40 | 13 | 34.80 | 10 | 37.60 | 6  | 47.03 | 5  |

Table 4 Combined Mean values of grain yield of bread wheat for each environments

Key: 1=environment 1, 1'=environment 2, 2=environment 3, 2'=environment 4, 3=environment 5, 3'=environment 6, R= rank

In other words, when significant GxE interactions are present, the effects of genotypes and environments are statistically non additive (or the differences between genotypes depend on the environment). The presence of a significant GxE interaction complicates interpretation of the results. That means, it is difficult to identify superior genotypes across environments when GxE interaction is highly significant. From the combined ANOVA in Table 2, GxE

interaction is highly significant and hence superiority of genotypes across environments cannot be identified by considering their mean yield performance (Table 4). Furthermore, the traditional analysis of variance determines the values of each variance source and the significance of the contribution of each component, but it does not partition the interaction in to several components and thus other types of analyses should be performed. Hence, such multi-location trial data along with a highly significant GxE interaction requires measures of stability analysis.

# 3.3. Additive Main Effects and Multiplicative Interaction (AMMI) Analysis of Variance

To identify more stable genotypes, a better outstanding of varieties, environment, and their interaction source of variation is paramount important. Table 5 displays the combined analysis of variance (ANOVA) of the 17 bread wheat genotypes over six settings using the AMMI model. The ANOVA indicated highly significant differences (p<0.001) for environments, genotypes and for the genotype environment interaction (GEI) and IPCA-1.

Out of the total variation, environment, genotypes and their interaction explained 33%, 28.24% and 22.28% respectively, and the first and second interaction principal components explained 72.89% of the total variation (IPCA1=50.24% and IPCA2=22.65%) (Table5).

| Source       | D.F. | S.S.  | M.S.    | Total variation Explained (%) | GXE Explained (%) | Cumulative(%) |
|--------------|------|-------|---------|-------------------------------|-------------------|---------------|
| Total        | 305  | 16189 | 53.1    |                               |                   |               |
| Genotypes    | 16   | 4571  | 333.8** | 28.24                         |                   |               |
| Environments | 5    | 5342  | 914.2** | 33.00                         |                   |               |
| Block        | 12   | 259   | 21.6ns  |                               |                   |               |
| Interactions | 80   | 3607  | 45.1**  | 22.28                         |                   |               |
| IPCA 1       | 20   | 1812  | 90.6**  |                               | 50.24             | 50.24         |
| IPCA 2       | 18   | 817   | 45.4*   |                               | 22.65             | 72.89         |
| Error        | 192  | 2411  | 12.6    |                               |                   |               |

#### Table 5 ANOVA table for AMMI model

\*\*\*p<0.001; IPCA=Interaction Principal Component Axis, DF=degree of freedom, SS=sum of squares, M.S=mean squares.

#### 3.4. AMMI stability value (ASV)

Purchase <sup>[6]</sup> reported that the IPCA scores of genotypes in the AMMI analysis are an indication of the stability of a genotype over environments. The greater the absolute value IPCA scores, the more specifically adapted a genotype are to a particular environment. The more IPCA2 scores approximate to zero, the more stable or adapted the genotype is over all environments sampled <sup>[7]</sup>.

In the present study, Genotypes BWRVT/55 and BWRVT/44 were found to be stable (Table 6). However, these genotypes were ranked 10<sup>th</sup> and 16<sup>th</sup> for mean grain yield. As per the value of ASV the most unstable genotypes were BWRVT/46and BWRVT/53. It is to note that a genotype with low ASV values is considered more stable than a genotype with high ASV <sup>[8]</sup>.

**Table 6** Grand mean of grain yield, IPCA1 and IPCA2 scores, ASV and GSI bread wheat genotypes across three locationsfor two years at southern Oromia in 2021 and 2022

| Genotype | Mean  | GYR | IPCA1    | IPCA2    | ASV  | ASVR | GYR+ASVR | GSI |
|----------|-------|-----|----------|----------|------|------|----------|-----|
| Adola 1  | 34.77 | 11  | 0.40989  | 1.14132  | 1.15 | 4    | 15       | 7   |
| BWRVT/27 | 37.80 | 5   | 1.29472  | -2.78522 | 2.85 | 9    | 13       | 5   |
| BWRVT/40 | 44.58 | 2   | 0.60886  | 1.34055  | 1.37 | 7    | 9        | 2   |
| BWRVT/42 | 33.96 | 14  | 2.29050  | 1.18411  | 4.59 | 12   | 26       | 15  |
| BWRVT/44 | 35.52 | 10  | -0.43089 | 0.63121  | 0.70 | 2    | 12       | 3   |

| BWRVT/46      | 32.64     | 15       | -1.06364    | 0.03897       | 29.03  | 17 | 32              | 17    |
|---------------|-----------|----------|-------------|---------------|--------|----|-----------------|-------|
| BWRVT/49      | 36.32     | 8        | -1.46296    | -0.63257      | 3.44   | 11 | 19              | 11    |
| BWRVT/51      | 32.62     | 17       | 0.91142     | 0.43085       | 1.98   | 8  | 25              | 14    |
| BWRVT/52      | 37.02     | 7        | -0.64305    | -1.14408      | 1.20   | 5  | 12              | 3     |
| BWRVT/53      | 37.27     | 6        | -1.59759    | -0.09200      | 27.74  | 16 | 22              | 12    |
| BWRVT/54      | 43.39     | 3        | 2.11122     | -0.77359      | 5.81   | 13 | 16              | 9     |
| BWRVT/55      | 32.63     | 16       | -0.00537    | -0.49078      | 0.49   | 1  | 17              | 10    |
| BWRVT/56      | 34.27     | 12       | -0.02284    | 0.72216       | 0.72   | 3  | 15              | 8     |
| BWRVT/60      | 34.01     | 13       | -1.71571    | -0.24159      | 12.19  | 15 | 28              | 16    |
| BWRVT/75      | 42.14     | 4        | -1.41139    | 0.71767       | 2.87   | 10 | 14              | 6     |
| BWRVT/76      | 44.62     | 1        | 0.04520     | -0.0015       | 1.36   | 6  | 7               | 1     |
| Deka          | 36.27     | 9        | 0.68165     | -0.04696      | 9.89   | 14 | 23              | 13    |
| Kow CVD_Croit | n Viold D | anle ACI | V_AMMI Ctob | lity Value D- | Donkon |    | notime Coletion | Indow |

Key: GYR=Grain Yield Rank, ASV=AMMI Stablity Value, R=Rank and GSI=Genotype Selction Index

#### 3.5. GGE bi-plot for Evaluation of Genotypes Relative to Ideal Genotypes

An ideal genotype has the highest mean grain yield and is stable across environments <sup>[9, 10]</sup>. Thus, starting from the middle concentric circle pointed with arrow concentric circles was drawn to help visualize the distance between genotypes and the ideal genotype <sup>[3]</sup>. The ideal genotype can be used as a benchmark for selection. A genotype is more desirable if it is closer to 'ideal' genotype <sup>[11, 12]</sup>. According to GGE biplot analysis, the optimum genotype is found in the first concentric circle in the graph. (Figure1). As a result, the biplot's first concentric circle contained the genotypes BWRVT/76 and BWRVT/40, which were considered ideal and preferred over the other genotypes. (Figure1). On the other hand, the high yielders BWRVT/54 and BWRVT/75, which are in the third circle, are not strong enough to remain stable. While the stable genotypes BWRVT/51 and Adola-1 were considered to be undesirable because they are low grain yielding and were placed far away from the concentric circle (Figure1). This result supported findings by Sharma et al. <sup>[13]</sup>, which discovered exceptional genotypes close to the ideal genotype in wheat for five years straight, Akter et al. <sup>[14]</sup>, who reported an ideal genotype of rice in the first concentric circle, and Aliyi et al. <sup>[4]</sup>, who found outstanding genotypes close to the ideal genotype in bread wheat at six environments.



Figure 1 Genotype focused GGE-bi-plot comparison

#### 4. Conclusion

The current study investigated the genotype-environment relationships and grain yield stability of 17 bread wheat genotypes grown under six regimes in southern Oromia. As a result, there were notable differences in mean grain across environments, genotypes, and the GEI interaction, suggesting that genotypes were more varied and contributed significantly to the variation. To increase crop productivity, genotypes with high yielders and stable performance across the testing location are essential. Thus, two genotypes, BWRVT/76 and BWRVT/40, were identified as candidate genotypes to be verified for potential release for the mid-lands of Guji, Southern Ethiopia, and similar agro-ecologies, based on their yield advantages over the checks, their stable performance across the testing sites, and their tolerant reaction for major diseases.

#### Recommendations

Genotypes BWRVT/54 and BWRVT/75 was high grain yielder too. But, this genotype was not selected and promoted to variety verification trail due to its poor wide adaptability across tested locations. Those genotypes gave high grain yield, but unstable may be included in other breeding program, crossing.

Another recommendation from this result output is that, further studies using more diverse locations and seasons in more number of agronomic traits yield component attributes is required to generate more reliable information on the effect of genotype, environment and GEI and identification of stable genotypes.

# **Compliance with ethical standards**

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#### Disclosure of conflict of interest

No conflict of interest to be disclosed.

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