*American Journal of Biological and Environmental Statistics*
2025, Vol. 11, No. 1, pp. 9-16
https://doi.org/10.11648/j.ajbes.20251101.12

Research Article

# Genotype by Environment Interaction and Grain Yield Stability of Sesame (*Sesamum indicum* L.) Genotypes in Hararghe Zones, Eastern Oromia

**Shanene Haile[1, *], Ahmed Muhamad[2], Firaol Adugna[2]**

[1]Mechara Agricultural Research Center, Mechara, West Hararghe, Ethiopia
[2]Oromia Agricultural Research Institute, Addis Ababa, Ethiopia

## Abstract

Sesame is one of the oldest and most significant oilseed crops widely grown in tropical and subtropical regions around the world and is cultivated for its oil-rich seeds. Multi-environment yield trials are widely used for selecting superior sesame advanced lines to be released as a new variety for target environments in Ethiopia sesame breeding programs. The study was conducted for two years at Mechara, Milkaye, Ibsa and Fadis in 2021, 2022 cropping season. Total of 18 sesame genotypes including standard checks were planted in Randomized Complete Block Design with three replications. The objective of the experiment to estimate the magnitude of GEI and to select stable and adaptable genotypes for the target environment(s). AMMI analysis of variance revealed that, there were highly significant ($p< 0.001$) differences among environments, genotypes and genotype by environment interaction for grain yield. Genotype G15 (972kgha$^{-1}$) was showed the mean yield performance across the test environment with 46.67% yield advantage over average yield, the most stable. Milkaye was identified as high yielding and best desirable testing environment for sesame production. Therefore, genotype G15 was proposed as candidate variety for verification trial and possible release and it can be used as parent material in the future breeding program.

## Keywords

Sesame (*Sesamum indicum* L.), Genotype, AMMI, GGE Bi-plot, GEI, Seed Yield

## 1. Introduction

Sesame (*Sesamum indicum* L.) is one of the oldest and most significant oilseed crops widely grown in tropical and subtropical regions around the world and is cultivated for its oil-rich seeds. Sesame is drought-tolerant, due to an extensive root system but it requires adequate moisture for germination and early growth. It is extensively susceptible to waterlogging and heavy rains at all stages of development [3]. In Ethiopia, Sesame is important oil crop in terms of both area coverage and production [6] the target of sesame breeding in Ethiopia is to develop varieties that meet the demands of sesame growers, processors, and consumers.

In plant breeding programs, genotypes are evaluated in multi-environment trials (METs) by testing their performance across environments and selecting the best genotypes in specific and stable environments. Multi-environment yield trials are widely used for selecting superior sesame advanced

*Corresponding author: haileshanne@gmail.com (Shanene Hail)

**Received:** 25 February 2025; **Accepted:** 17 April 2025; **Published:** 22 May 2025

lines to be released as a new variety for target environments in Ethiopia sesame breeding programs. Information on the adaptation and stability of the genotypes over seasons and over sites is useful for recommending the varieties that should be grown under particular production environments and predicting the yield expectations of the test genotypes. A Genotype is considered to be the most adaptive or stable one if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments [2]. A significant portion of the resources of crop breeding is devoted determining GEI through replicated multiplication trial.

Multi environment yield trial can be analyzed to extract more information on stability, adaptability and yield performance using various statistical methods and software used by different investigators [9, 17]. AMMI model and GGE bi plot analysis are shows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions [7]. Therefore; the objectives of this study was to estimate the magnitude of GEI and to select stable and adaptable sesame genotype/s for the target environment(s).

## 2. Materials and Methods

### 2.1. Study Site

The experiment was conducted at three locations; Milkaye and Mechara on station, (Daro labu district), Ibsa (Hawi Gudina district) and East Hararghe Fedis on station during 2021 and 2022 main cropping season.

### 2.2. Treatments and Experimental Design

Total of sixteen genotypes including two standard checks tested using Randomized Complete Block design (RCBD) with three replications. A plot size of 6 rows with row spacing of 1.8meter and row length of 2.5m was used and the four middle rows were used for data collection. For statistical analysis, yield from net plot area of $2m^2$ was harvested and converted into $tonha^{-1}$ base at 10% grain moisture content. Seed rate of 5 $kgha^{-1}$ was used and planted by drilling. Fertilizer was applied at 100 kg ha-1of NPS and 50 kg ha-1 urea at planting.

***Table 1.*** *List of Genotypes tested.*

| SN. | Genotype code | Genotype name | Source |
|---|---|---|---|
| 1 | G1 | BKC 104-1 | BARC |
| 2 | G2 | BKC 138-1 | BARC |
| 3 | G4 | ACC-EW-023 (2) | BARC |
| 4 | G6 | EW006*BG006-2-1-1 | BARC |
| 5 | G7 | BKC 010-2 | BARC |
| 6 | G8 | EW002 * Wama-10-2-1 | BARC |
| 7 | G9 | BKC 102-1 | BARC |
| 8 | G10 | MTM-12 13 23 (2) | IEB |
| 9 | G11 | EW002 * Dicho -5-3 | BARC |
| 10 | G12 | BKC 010-2 | BARC |
| 11 | G13 | Dicho *EW006-9-1 | BARC |
| 12 | G14 | MTM-23 13 12 (3) | IEB |
| 13 | G15 | BG006 * 010-1-2-2-1 | BARC |
| 14 | G16 | Obsa*EW023(2)-2-1-1 | BARC |
| 15 | G18 | BKC 112-1 | BARC |
| 16 | G3 | EW002 *Obsa 21-1 | BARC |
| 17 | G5 | Bha Zeyit | HU(Standard check) |
| 18 | G1 | Bha Necho | HU(Standard check) |

## 2.3. Data Collected

### 2.3.1. Phenological Parameters

Days to flowering was recorded by counting the number of days after emergence when 50% of the plants per plot had the first open flower. Days to maturity was recorded when 90% of capsule matured per plot.

### 2.3.2. Grain Yield and Yield Components

Four central rows were harvested for determination of grain yield. Grain yield was adjusted to 8% moisture content. Five plants were randomly selected from the four central rows to determine yield and yield components, which consisted of number of capsule per plant and number of branch plant. Capsules number per plant was determined by counting capsules of the five randomly selected plants. While number of primary branch was recorded by counting the total of number of branch per plant from five randomly selected plants.

## 2.4. Data Analysis

Different statistical software packages were used to analyses the data. [12] Was used for analysis of variance of the individual environments and the combined data over locations. Gen Stat 18th edition AMMI and GGE bi-plot analysis.

AMMI Stability Value (ASV) was calculated for each genotype according to the relative contribution of the principal component axis score (IPCA 1 and IPCA 2) to the interaction sum of squares [11].

Genotype Selection Index (GSI) was calculated based on the rank of mean grain yield of genotypes (rYLD) across environments and the rank of AMMI stability value (rASV) a selection index (GSI) was calculated for each genotype in which it incorporates both mean grain yield and stability index in a single criterion (as GSI= rASV + rYLD).

The combined analysis of variance across environments was done in order to determine differences between sesame genotypes data of each trait was subjected to combined analysis of variance to estimate the effect of environmental, genotype and genotype x environment interaction by using the following statistical model:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + e_{ijk}$$

Where Yijk = observed value of genotype i in block k of environment (location) j, $\mu$ = grand mean, $G_i$ = $i^{th}$ genotype effect, $E_j$= $j^{th}$ environment or location effect, $GE_{ij}$ = the interaction effect between $i^{th}$ genotype and $j^{th}$ environment, $B_{k(j)}$= the effect of block k in location (environment) j, $e_{ijk}$ = error (residual) effect of genotype i in block k of environment j.

# 3. Result and Discussion

The combined analysis of variance revealed that high significant (P<0.001) variation among genotypes, locations and GE interaction for mean grain yield of sesame genotypes (Table 2). The significance of GEI for grain yield indicates that genotypes responded differently to the tested environments. Furthermore, they have explained that the significances variation among the environments indicate that these locations can be used as testing stations for different environments while significant differences among genotypes reveals the differential response of genotypes to different environments.

***Table 2.*** *The combined ANOVA for grain yield of sesame genotypes over locations and years.*

| Source of variation | DF | SS | MS | F. Value | Pr (>F) |
|---|---|---|---|---|---|
| Replication | 1 | 65409 | 65409 | 1.455 | 0.23001 ns |
| Location | 6 | 11695900 | 1949317 | 43.357 | 0.0001*** |
| Genotype | 17 | 2453684 | 144334 | 3.21 | 0.0001*** |
| Replication (with in Location) | 6 | 8558774 | 142646 | 3.173 | 0.00622 ** |
| Location* Genotype(Interaction) | 102 | 7387124 | 72423 | 1.611 | 0.00552 ** |
| Residuals | 126 | 5664890 | 44959 | | |

Key: ** = highly significant and ns= non-significant, DF.=degree freedom, SS= Sum of square, MSS= Mean Sum of square

## 3.1. Yield Performance Across Environments

The performance of the tested sesame genotypes for grain yield across location and year presented in (Table 3). The average grain yield ranged from the lowest 240kgha-1 at McARC on station in year-2 to the highest 1152.7kgha$^{-1}$ Milkaye site in year-1, with grand mean of 722.36kgha-1. The grain yield across environments ranged from the lowest

of 589.35 kgha-1for G4 to the highest of 971.83 kgha$^{-1}$ for genotype G15. This wide variation might be due to their genetic potential of the genotypes. Genotype G15 was the top ranking genotype in all environments across the years (Table 3), The difference in yield rank of genotypes across the environments exhibited the high crossover type of genotypes x environmental interaction [4, 15].

***Table 3.*** *Combined mean yield of sesame genotypes across four locations over two years (2021 -2022).*

| Genotype | McARC year 1 | McARC year 2 | Milkaye year1 | Milkaye year 2 | Ibsa year 1 | FARC year 1 | FARC year 2 | Over all Mean | Yield Ava.% |
|---|---|---|---|---|---|---|---|---|---|
| ACC-EW-023 (2) | 538.19 | 402 | 756.94 | 548 | 723.95 | 777.76 | 396.7 | 589.35 | 0 |
| BG006 * 010-1-2-2-1 | 611.11 | 635 | 815.97 | 744 | 765.62 | 822.22 | 766.7 | 734.72 | 8 |
| Bha Necho | 434.02 | 485 | 736.11 | 738 | 683.33 | 764.81 | 912.5 | 675.37 | 0 |
| Bha Zeyit | 395.83 | 610 | 652.77 | 915 | 578.12 | 942.59 | 575 | 662.573 | 0 |
| BKC 010-2 | 625.00 | 619 | 847.22 | 475 | 781.25 | 900.00 | 488.3 | 672.42 | 0 |
| BKC 102-1 | 604.16 | 479 | 809.02 | 810 | 765.62 | 752.78 | 487.5 | 668.29 | 0 |
| BKC 104-1 | 847.22 | 615 | 1104.16 | 715 | 923.95 | 834.72 | 554.2 | 794.23 | 17 |
| BKC 112-1 | 722.22 | 638 | 947.91 | 765 | 890.62 | 796.29 | 745.8 | 781.05 | 15 |
| BKC 138-1 | 628.47 | 485 | 847.22 | 573 | 807.29 | 936.11 | 529.2 | 683.60 | 0 |
| Dicho *EW006-9-1 | 677.08 | 715 | 937.5 | 673 | 869.79 | 918.51 | 491.7 | 749.86 | 11 |
| EW002 * Dicho -5-3 | 229.16 | 983 | 392.36 | 881 | 572.91 | 636.11 | 608.3 | 610.29 | 9 |
| EW002 * Wama-10-2-1 | 631.94 | 610 | 857.63 | 742 | 828.12 | 895.83 | 704.2 | 747.46 | 10 |
| EW002 *Obsa 21-1 | 552.08 | 550 | 798.61 | 952 | 724.10 | 948.14 | 730 | 745.23 | 10 |
| EW006*BG006-2-1-1 | 555.55 | 785 | 798.61 | 825 | 734.37 | 936.11 | 704.2 | 756.93 | 12 |
| EW023(2) *BG006-13-1-1 | 427.08 | 654 | 677.08 | 931 | 609.37 | 598.14 | 708.3 | 652.88 | 3 |
| MTM-12 13 23 (2) | 781.25 | 240 | 1045.13 | 556 | 901.04 | 992.59 | 1020.8 | 786.84 | 16 |
| MTM-23 13 12 (3) | 795.14 | 710 | 1086.8 | 675 | 921.87 | 688.88 | 520.8 | 766.67 | 13 |
| Obsa*EW023(2)-2-1-1 | 1107.63 | 863 | 1152.7 | 1017 | 1057.29 | 909.25 | 741.7 | 971.83 | 43.8 |
| Mean | 620.17 | 487 | 846.64 | 898 | 785.47 | 836.16 | 836.16 | 722.36 | |
| CV% | 39.6 | 33.5 | 31.97 | 30.5 | 29.29 | 16.96 | 16.96 | | |
| LSD | 402.61** | 270.8* | 443.78** | 454.8ns | 377.16** | 235.09* | 235.09* | | |

Key: McARC= Mechara Agricultural Research Center, Fedis= Agricultural Research Center, CV= coefficient of variation in percentage, LSD= least Signiant difference at 5 percent

## 3.2. AMMI Analysis

The AMMI model analysis of variance for grain yield showed highly significant differences ($P \leq 0.01$) for genotypes, environments and genotypes by environments interactions. Partitioning of the variance components indicated that 34.09% was due to environment, 5% due to replication, 7.15% due to genotype, and 21.5% due to GEI (Table 4). The large proportion of variance due to environment and low contributions of variance due to genotype and medium due to GEI. Great variation indicates the significant influence of environment in evaluation of sesame genotypes for yield performance. The present finding line is with [6], who found similar results in sesame.

The first IPCA captured 45.57%of the interaction sum of squares; similarly, the second IPCA explained 30.19% of the GEI sum of squares. The sum of squares for the first two IPCAs cumulatively contributed to 75.76 % of the total GEI.

*Table 4. AMMI analysis of variance for grain yield tested at seven environments.*

| Source variation | DF | SS | MSS | % Explained SS |
|---|---|---|---|---|
| Total | 377 | 34299202 | 90979 | |
| Treatments | 125 | 21536708 | 172294*** | 62.79. |
| Genotypes | 17 | 2453684 | 144334*** | 7.15 |
| Environments | 6 | 11695900 | 1949317*** | 34.09 |
| Replication | 14 | 1737221 | 124087*** | 5 |
| Interactions | 102 | 7387124 | 72423** | 21.5 |
| IPCA1 | 22 | 3366452 | 153021** | 45.57 |
| IPCA2 | 20 | 2230268 | 111513*** | 30.19 |
| Residuals | 12 | 12871 | 1073 | |
| Error | 238 | 11025273 | 46325 | |

Note: d.f. = degree freedom, SS= Sum of square, MSS= Mean Sum of square, SS%= Percentage of sum of square, IPCA 1and 2= first and second principal component

## 3.3. AMMI Stability Value (ASV)

AMMI Stability Value (ASV): [11] indicated ASV as the distance from the coordinate point to the origin in a two dimensional scatter gram of IPCA1 scores against IPCA2 score should also see to decide the stability of genotypes. The genotypes with low stability value (ASV) is said to be stable and the breeder chose the stable genotypes, having grain yield above the grand mean yield. In this study genotype G14 showed lowest ASV followed by G16, G3, G1, G8 and G15 (Table 5) indicating these genotypes can be suitable for the studied environments. However, since stability in itself should not be the only parameter for selection, as the most stable genotype wouldn't necessarily give the best yield performance [10].

## 3.4. Genotype Stability Index (YSI)

Genotypes with the least genotype stability index (GSI) and high grain yield are considered as the most stable [8]. Genotypes with lowest estimated value are desirable and considered as the most stable. Based on genotype stability index (GSI), G15 and G16 had the lowest GSI values and high mean yield over average yield and showed stable performance over the testing sites. Therefore, these genotypes are wide adaptation.

*Table 5. AMMI stability value with IPCA 1 and IPCA 2 scores for yield and yield stability index.*

| Genotype code | Grain yield | RMYD | IPCA1 | IPCA2 | ASV | RASV | GSI | RGSI |
|---|---|---|---|---|---|---|---|---|
| G15 | 893.58 | 1 | -4.13 | -3.94 | 4.44 | 5 | 6 | 1 |
| G6 | 778.37 | 2 | -4.5 | 1.21 | 6.36 | 9 | 11 | 4 |
| G11 | 775.99 | 3 | -17.94 | -5.63 | 24.65 | 17 | 20 | 9 |
| G17 | 751.64 | 4 | 5.64 | -9.96 | 11.1 | 14 | 18 | 7 |
| G16 | 722.68 | 5 | 0.93 | 1.5 | 1.718 | 2 | 7 | 2 |
| G3 | 718.58 | 6 | 1.13 | -8.12 | 8.15 | 11 | 17 | 6 |
| G8 | 709.52 | 7 | 2.09 | 3.22 | 3.73 | 4 | 11 | 4 |
| G18 | 709.25 | 8 | -2.26 | -13.11 | 13.19 | 15 | 23 | 11 |
| G14 | 708.53 | 9 | 0.49 | -0.44 | 0.95 | 1 | 10 | 3 |
| G12 | 697.28 | 10 | -5.66 | 9.08 | 9.1 | 12 | 22 | 10 |

| Genotype code | Grain yield | RMYD | IPCA1 | IPCA2 | ASV | RASV | GSI | RGSI |
|---|---|---|---|---|---|---|---|---|
| G13 | 697.28 | 11 | -7.6 | 4.54 | 4.9 | 8 | 19 | 8 |
| G1 | 668.05 | 12 | -2.1 | 2.01 | 2.92 | 3 | 15 | 5 |
| G5 | 667.11 | 13 | 8.09 | -3.14 | 10.66 | 13 | 26 | 13 |
| G9 | 633.13 | 14 | 3.17 | -5.58 | 6.22 | 10 | 24 | 12 |
| G10 | 617.98 | 15 | 21.26 | 4.57 | 31.61 | 18 | 34 | 15 |
| G2 | 603.9 | 16 | 3.33 | 3.48 | 4.8 | 7 | 23 | 11 |
| G7 | 600.11 | 17 | -4.19 | 16.3 | 16.56 | 16 | 33 | 14 |
| G4 | 521.94 | 18 | 2.22 | 4.02 | 4.45 | 6 | 24 | 12 |

Key: ASV= AMMI stability value, RASV=Rank of AMMI stability value, RMYD=Rank of mean yield, GSI=Genotypic selection index, RGSI= Rank of Genotypic selection index

## 3.5. GGE-Biplot

GGE bi-plot analysis is a multivariate analytical technique that graphically displays a two way table and allows visualizing the relation among genotypes, environments and their interactions. It is necessary to construct GGE bi-plot for visual observation in order to understand which genotypes best performed in which environment, or which genotypes were stable and unstable as well as to visualize the discriminating ability and representativeness of the environments.

According to [16], discriminating ability and representativeness view of the GGE- biplot is the important measure of test environments, which provide valuable and unbiased information about the tested genotypes. Environments with longer vectors had the more discriminating ability of the genotypes, whereas environments with very short vectors had little or no information on the genotype difference.

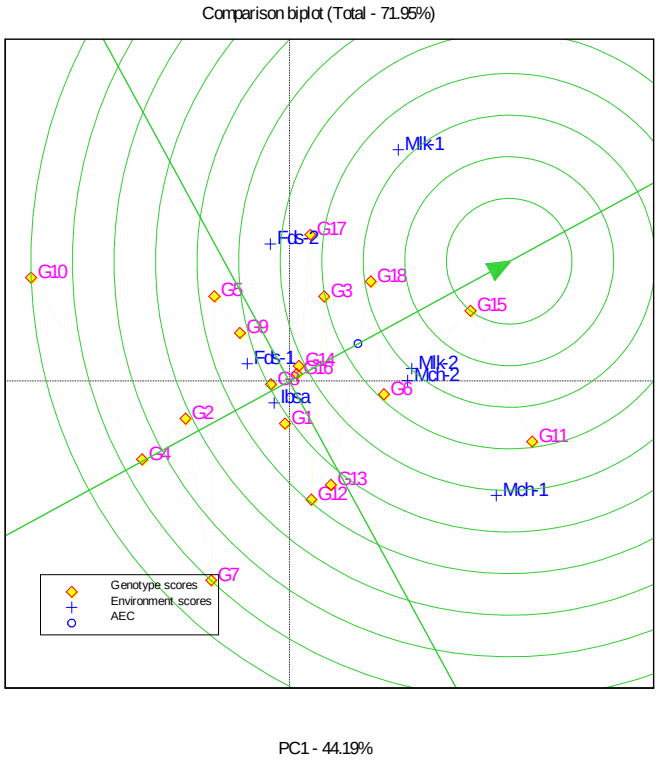


***Figure 1.*** *GGE-bi-plot showing a comparison of all sesame genotypes with in good performing ideal genotypes for grain yields.*

Key: Environments (Milk-1=Milkaye year -1, Milk-2=Milkaye year -2, Mch-1=Mechara year-1, Mch-2=Mechara year-2, Fds-1=Fedis year-1, Fds-2=Fedis year-2 and Ibsa-1=Ibsa year-1

An ideal genotype is defined as a genotype with the greatest PC1 score (mean performance) and with zero GEI, as represented by an arrow pointing to it. Genotype is located closer to the ideal genotype; it becomes more desirable than other genotypes which are located far away from the ideal genotype. Therefore, concentric circles were drawn around the central circle which contains the ideal genotype in order to visualize the distance between each genotype and the ideal genotype. From the present investigation (Figure 1) G15 was laid on small concentric circle so it is "ideal" genotype, with the highest mean grain yield, followed by G18 located closer to the ideal genotype and was considered as desirable genotype. Similar result was reported by [13, 1].

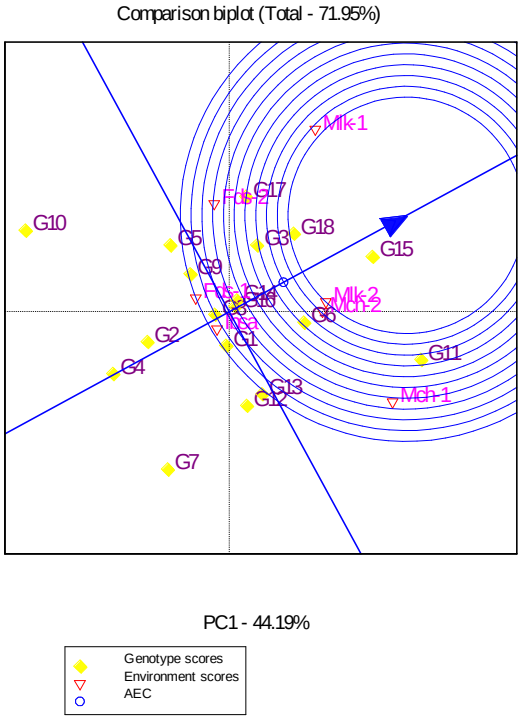


***Figure 2.*** *GGE-bi-plot based on environment-focused scaling for comparison of the environments with the ideal environment.*

Key: Environments (Milk-1=Milkaye year -1, Milk-2=Milkaye year -2, Mch-1=Mechara year-1, Mch-2=Mechara year-2, Fds-1=Fedis year-1, Fds-2=Fedis year-2 and Ibsa-1=Ibsa year-1

The ideal test environment should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments). Such an ideal environment was represented by an arrow pointing to it (Figure 2). Actually, such an ideal environment may not exist, but it can be used as an indication for genotype selection in the METs. An environment is more desirable if it is located closer to the ideal environment. Therefore, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and the ideal environment [16]. Accordingly, Milk year -2, which fell on concentric circle, followed by Milk year -1 and Mch year -2 near to concentric circle an ideal test environment in terms of being the most representative of the overall environments and powerful to discriminate genotypes (Figure 2). Similar result was reported by [14] on common bean have used GGE bi-plot to identify the best desirable testing environment.

## 4. Conclusion and Recommendation

AMMI analysis of variance result showed 75.67% of the total variation accounted due to environment (34.09%), genotype (7.15%) and G x E interaction (21.5%) contributed to the observed variations among genotypes for yield. Genotype G15(972kgha$^{-1}$) showed the best yield performance across the test environment with 46.67% yield advantage over average yield, the most stable among tested genotypes across environments. Milkaye site was identified as high yielding and best desirable testing environment for sesame production. Therefore, genotype G15 was proposed as candidate variety for verification trial and possible release and it can be used as parent material in the future breeding program.

## Abbreviations

| | |
|---|---|
| AMMI | Additive Main Effects and Multiplicative Interaction |
| AEC | Average Environment Coordinate |
| ANOVA | Analysis of Variance |
| ASV | Ammi Stability Value |
| CSA | Central Statistical Authority |
| G | Genotype |
| GEI | Genotype by Environmental Interaction |
| GSI | Genotype Stability Index |
| IPCA | Interaction Principal Component Axis |
| MET | Multi Environmental Trial |
| PCA | Principal Component Analysis |
| rASV | Rank of Ammi Stability Value |
| rYLD | Rank of Yield |

## Acknowledgments

The author would like to acknowledge Oromia Agricultural Research Institute for funding the research work. Grateful thanks Mechara Agricultural Research Center for facilitated vehicles and research equipment's. The author also thanks Bako Agricultural Research Center and Institute of Ethiopia Biodiversity for provided seed. Pulse and Oil Crops Research Team members in particular for the success of variety development.

## Author Contributions

**Shanene Hail:** Conceptualization, Data curation, Formal Analysis, Funding acquisition, Investigation, Methodology, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing

**Ahmed Muhamad:** Data curation, Investigation, Methodology, Software, Supervision

**Firaol Adugna:** Data curation, Formal Analysis, Investigation, Methodology, Supervision

## Conflicts of Interest

The authors declare no conflicts of interest.

## References

[1] Abebaw Dessie. 2020. GGE bi-plot analysis of genotype x environment interaction of cold tolerant green super rice genotypes in Ethiopia. *International Journal of Research and Review,* 7.

[2] Arshad, Muhammad. Bakhsh, Ahmad. Haggani, A. M. and Bashier, Muhammad. 2003. Genotype x Environment Interaction for grain yield in chick pea (*Cicer arietinum* L.). Pak. J. Bot., 35(22): 181-186.

[3] Ashri, A. (1998) Sesame Breeding. In: Janick, J., Ed., Plant Breeding Reviews, John Wiley & Sons, Inc., Hoboken, 179-228. https://doi.org/10.1002/9780470650110.ch5

[4] Asrat Asfaw, Fistum Alemayehu, Fekadu Gurum and Mulugeta Atnaf, 2009. AMMI and SREG GGE biplot analysis for matching varieties onto soybean production environments in Ethiopia. Scientific Research and Essay, 4(11): 1322-1330.

[5] CSA (Central Statistical Authority). (2022). Agricultural sample survey, area and production of crops (pp. 14-63). Addis Ababa: Central Statistical Authority.

[6] Daba, Chemeda, Amsalu Ayana, Habtamu Zeleke, and AW. 2015. Genotype x Environment interactions for seed yield in Sesame in western Ethiopia. East African Journal of Sciences 9: 85-96.

[7] Ding M., *et al.* "Application of the GGE biplot to evaluate genotype, environment and GxE interaction on P. radiata: a case study GGE biplot Application". AGBU, Joint venture of NSW Department of Primary Industries and the university of New England 38.1 (2007): 132-142.

[8] Farshadfar, E. 2008. Incorporation of AMMI stability value and grain yield in a single nonparametric index (GSI) in bread wheat. *Pakistan Journal of biological sciences,* 11(14): 1791-1796.

[9] Gauch, H. G. 2006. Winning the accuracy game. Am. Sci. 94: 133-141.

[10] Mohammadi, R., M. Roostaei, Y. Ansari, M. Aghaee and A. Amri. 2010. Relationships of phenotypic stability measures for genotypes of three cereal crops. Canadian Journal of Plant Science, 90: 819-30. https://doi.org/10.4141/cjps09102

[11] Purchase, J. L., Hatting, H. and Van Deventer, C. S. (2000). Genotype x environment interaction of winter wheat (T. aestivum) in South Africa: Stability analysis of yield performance. S. Afr. J. Plant Soil. 17(3): 101-107.

[12] SAS (2009). Statistical Analysis System Institute, North Carolina USA v.9.2. Gauch, H. G. 2006. Statistical Analysis of Yield Trials by AMMI and GGE. Crop Sci., 46: 1488-1500.

[13] Shanene Haile, Fantahun Adugna and Ahmed Mohamed, 2022. Proceedings of Review Workshop on Completed Research Activities of Crop Research Directorate Held at Batu Fish and other Aquatic Life Research Center, Batu, Ethiopia, 2022.

[14] Tullu, Tadessa Asefa. 2018. Genotype x Environment Interaction for Agronomic Traits and Yield Stability of Common Bean (*Phaseolus Vulgaris* L.) Varieties in Hararghe, Eastern Ethiopia. MSc. Thesis, Haramaya University, Haramaya, Ethiopia.

[15] Yan, W. and Hunt, L. A. (2001) Interpretation of Genotype x Environment Interaction for Winter Wheat Yield in Ontario. Crop-Science, 41, 19-25. https://doi.org/10.2135/cropsci2001.41119x

[16] Yan, W. and Rajcan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario, *Crop Science,* 42: 11-20.

[17] Yan, W., Kang, M. S., Ma, B., Woods, S. and Cornelius, P. L. 2007. GGE Biplot vs. AMMI analysis of genotype by environment data. *Crop Science,* 47: 643-655.