

# Evaluation of the Performance of Some White Seeded Sesame (*Sesamum Indicum* L.) Genotypes Using GGE Biplot in Northern Ethiopia

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## Abstract

Sesame known as queen of oil seed crops is mainly grown for its oil of local consumption, sources of income and great contribution for the national economy of Ethiopia. However, the productivity and production is low due to environments, genotypes, Interaction and management variation. Four sesame genotypes were evaluated for their interactions with environments and seed yield stability analysis at three environments during the 2015 main cropping season. The objectives of the study were to estimate the magnitude and nature of GEI and to identify stable and/or high yielding white seeded sesame genotypes in Abergelle Agricultural Research Center mandate areas, Northern Ethiopia. The study was conducted using a randomized complete block design with three replications at each environment. The combined analysis of variance revealed highly significant ( $P \leq 0.01$ ) environment (E), genotype (G) and genotype  $\times$  environment interaction (GEI). Environment explained 79.84% of the total (G + E + GE) variation, whereas G and GE explained 17.21% and 2.95% of the total variation, respectively. The magnitude of the environment was 4.6 times greater than the genotype, implying that most of the variation in seed yield was due to the environment. The significant genotype by environment interaction effects were further partitioned in to two significant interaction principal components by using the genotype main effect plus genotype  $\times$  environment interaction (GGE) biplots model. The first two principal components for mean yield and stability of the GEI explained 96.81% with PC1 = 90.88 and PC2 = 5.93 of the GGE sum of squares, respectively, while 3.19% was attributed to noise. Thus, model diagnosis (fitting) showed that the first two PCs were significant and can be taken to interpret this data. The which-won-where biplot identified one winning genotype in one mega environment. The winning genotype across locations was Humera-1. Thus, the GGE (genotype and genotype by environment interaction) biplot analysis indicating that Humera-1 was considered as the most desirable and stable one's, therefore can be recommended for wider cultivation due to better seed yield and stability performance across the test environments in the dry lowland areas of Southeast and Central zones of Tigray region, Northern Ethiopia.

**Keywords:** Dry lowland, GEI, GGE biplot, Mega environment, *Sesamum Indicum* L.

## INTRODUCTION

Sesame (*Sesamum indicum* L.) belongs to the order Tubiflorae, family Pedaliaceae, is an important and ancient oil-yielding crop. It has an edible seed and has high quality oil (Pathak *et al.*, 2014). It is cultivated in tropical and subtropical regions of Asia, Africa and South America (Zhang *et al.*, 2013). It is warm-season annual crop primarily adapted to areas with long growing seasons and well-drained soils (Hansen, 2011). Sesame is the oldest self-pollinating annual oil seed originated in Africa, Ethiopia domesticated over 5000 years ago. Although originated in Africa, it was spread early through West Asia to India, China and Japan which became secondary distribution centers and it is now cultivated in many parts of the world (Yamanura, 2008). The average world sesame seed yield productivity was about 0.51 ton/ha (FAOSTAT, 2014).

Ethiopian sesame is among the highest quality in the world, as seeds are naturally produced at near-organic levels. Sesame seed is branded as the Humera, Gonder and Welega types which are well known in the world market by their white color, sweet taste and aroma. The Humera and Gondar sesame seeds are suitable for bakery and confectionary purposes; on the other hand, the high oil content of the Welega sesame seed gives a major advantage for edible oil production (Yamanura, 2008). It is an important agribusiness sector in Ethiopia and is one of the six priority crops of the Agricultural Growth Programme (AGP) (USAID, 2012). It accounts for 90% of the value of exported oil seeds, estimated at 379 million USD (FAOSTAT, 2012). It is 2<sup>nd</sup> only to coffee in foreign exchange earnings in Ethiopia (USIAD, 2014). It is the 2<sup>nd</sup> oil seed oil crop in terms of area coverage of 420,494.87 ha and the total production 288770 ton/ha next to noug (*Guizotia abyssinica* Cass.) (CSA, 2015).

The major sesame regions in Ethiopia are, Tigray (western and north western 36%), Oromia (East Welega 17%) Benishangul Gumuz (Belles valley 15%), Amhara (Metema 31%) are the most sesame producing regions in the country (Adefris *et al.*, 2011). Even though sesame is source of income for many small scale farmers, investors, traders, exporters and for Ethiopia economic growth, the industrial processing and utilization of

sesame have not been fully developed in the country. Despite the fact, sesame is highly marketable oil crop and superior sources of income in many sesame growing areas of Ethiopia; its productivity is low and unstable across locations and years due to biotic (weeds, insects and diseases etc.), abiotic factors (soil type, altitude, rainfall distribution and intensity etc. Seed shattering at maturity, lack of uniform maturity of capsules, lack of wider adapting cultivars, non-synchronous maturity, poor stand establishment, lack of fertilizer responses and low harvest index etc. (Ashri, 1994).

GEI is a challenge for plant breeders and complicates cultivar recommendation because of the inconsistency of best yielding genotypes across cropping environments; however, it may also offer opportunities, of increases yields through growing genotypes specifically adapted to a given area. The main features of quantitative traits are that they are highly influenced by the environment, difficult to understand the genotype-phenotype relationship as compared to qualitative traits. Because of the genotype by environment interaction, the selection of stable genotypes that interact less with the varying environments in which they are to be grown is required (Kumaresan and Nadarajan, 2010). The effect of GEI becomes more apparent by conducting multi-location and multi-years trials, that have three main objectives: (a) to accurately estimate and predict yield based on limited experimental data; (b) to determine yield stability and the pattern of response of genotypes across environments; and (c) to provide reliable guidance for selecting the best genotypes or agronomic treatments for planting in future years at new sites (Crossa, 1990).

The current sesame production in Ethiopia has many opportunities, such as highly market demand, large area with suitable environments for production (North western and South Western Ethiopia), growing in low moisture areas, presence of genetic diversity to improve the production yield potential and export demand and very competitive world wide (Wijnands et al., 2007). However, the research attention and breeding programme which has been given to improve its yield and oil content is not comparable with its contribution to Ethiopian economy and no information available on globally demanded white seeded sesame genotypes. Therefore, study on GEI and due attention for such on the white seeded sesame genotypes will be indispensable in Ethiopia.

Therefore, the objectives of the study were to:

- (i) Estimate the magnitude and nature of GEI for seed yield and
- (ii) Identify stable and/or high yielding white seeded sesame genotypes and assess their performance across locations in Northern Ethiopia.

## Materials and Methods

### Description of the Study Areas

Field experiment was conducted under rain-fed conditions at Abergelle Agricultural Research Center mandate areas (Table 1) in three environments during the 2015 main cropping season. Abergelle is located in central zone of Tigray at about of 903 km north of Addis Ababa (Capital city of Ethiopia) and 120 km Southwest of Mekelle (Capital city of Tigray Regional State) and situated at 13°14'06" N latitude and 38°58'50" E longitude. It is agro-ecologically characterized as hot warm sub-moist lowland (SMI-4b) below 1500 m above sea level (m.a.s.l). The textural class of the soil is sandy clay. The average annual rainfall varies from 350 to 650 mm and the temperature ranges from 18 to 42°C. The distribution of rainfall is erratic and variable, which results in strong variation in crop, yields. The rainfall distribution is unimodal, concentrated during the summer (July to August) leading to one cropping season per year (Belay et al., 2017).

Table 1: The Study locations in Northern Ethiopia in 2015 cropping season

Location	Soil textural class	PH	District	Zone	Region
Agbe	Sandy clay	7.33	T/Abergelle	Central	Tigray
Dabano	Sandy clay	7.53	K/Temben	Central	Tigray
Finaruwa	Sandy clay	7.16	S/Samre	Southeast	Tigray

### Experimental Genotypes

Four white seeded sesame genotypes (two selected, one standard check and one local check) were evaluated in three locations. Description of the plant materials is presented in Table 2.

Table 2: Description of genotypes used in the study

Genotype	Status	Sources	Color	Remark
Humera-1	Advance line	HuARC	White	Collection
Setit -1	Standard check	HuARC	White	Collection
Hirhir	Localcheck	HuARC	White	Collection
Local	Local	Abergelle area	brown	Farmer cultivar

Source: Humera Agricultural research Center (HuARC) Annual report, 2015

### Experimental Design and Crop Management

The experiment was laid out in randomized complete block design (RCBD) with three replications across testing sites. Each genotype was randomly assigned and sown in a plot area of 2m x 5m with 1m between plots and 1.5

m between blocks keeping inter and intra row spacing of 40 cm and 10 cm, respectively. Each plot had a total area of 10 m<sup>2</sup> and total of five rows and 6m<sup>2</sup> net plot areas with three harvestable rows. The experimental plots were ploughed two times (first time before sowing and secondly during sowing) to maintain fine seedbed suitable for crop establishment. Each experimental plot received the same rate of DAP (100 kg/ha) and Urea (50 kg/ha) fertilizer and all field management practices were done equally and properly as per the recommendations to the dry lowland areas.

#### Data Collection

From the three experimental rows were harvested, tied in sheaves and were made to stand separately until the capsules opened. After the sheaves have dried out fully and all of the capsules opened, seeds were tipped out onto sturdy cloths or canvases and threshing was accomplished by knocking the sheaves. The total seed yield harvested from the net plot area was weighed using a sensitive balance and adjusted to standard moisture level at 10% and weighted to get the seed yield per plot in grams and converted to kg ha<sup>-1</sup> for analysis.

#### Data Analysis

Homogeneity of residual variances was tested prior to a combined analysis using Bartlett's test (Steel and Torrie, 1998). Analysis of variance for each environment, combined analysis of variance over environments and GGE biplot analysis was computed using GenStat 16<sup>th</sup> edition (2010).

#### Separate and combined ANOVA

As the error variance were homogenous for seed yield continued to combined analysis of variance from the mean data of all environments to detect the presence of GEI and to partition the variation due to genotype, environment and GEI. The environments (locations) in the study were assumed as random effects and the genotype effects were treated as fixed. Moreover, mean comparison using Fisher's Least Significant Difference (LSD) was performed to explain the significant differences among means of genotypes, locations (environments). GenStat 16<sup>th</sup> edition (2010) statistical software was used for statistical analyses. The model employed in the analysis was;  $Y_{ijk} = \mu + G_i + E_j + B_k + GE_{ij} + \epsilon_{ijk}$  where:

$Y_{ijk}$  is the observed mean of the  $i$ th genotype ( $G_i$ ) in the  $j$ th environment ( $E_j$ ), in the  $k$ th block ( $B_k$ );  $\mu$  is the overall mean;  $G_i$  is effect of the  $i$ th genotype;  $E_j$  is effect of the  $j$ th environment;  $B_k$  is block effect of the  $i$ th genotype in the  $j$ th environment;  $GE_{ij}$  is the interaction effects of the  $i$ th genotype and the  $j$ th environment; and  $\epsilon_{ijk}$  is the error term. Seed yield data were subjected to combined analysis of variance using GenStat 16<sup>th</sup> edition to examine the main effects of the environment (E) and genotypes (G) and their interactions (GEI) variances.

#### GGE analysis

Different approaches are used to quantify the genotype-by-environment interaction and recommend the best genotypes for target environments. The GGE biplot method is based on data visualization and proved to be helpful in: (i) detection of the genotype by environment interaction pattern, (ii) classification of mega environments, (iii) simultaneous selection of genotypes based on stability and mean yield, and (iv) characterization of testing environments based on their discriminating ability and representativeness (Yan et al. 2000). We will, thus, use this method to analyze the data.

First, the combined analysis of variance was performed, with all effects fixed. The GGE biplot was built according to the formula described by Yan et al. (2000), Yan and Hunt (2001) and Yan (2002) as:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \epsilon_{ij}$$

where  $Y_{ij}$  is measured mean yield of the  $i$ <sup>th</sup> genotype ( $i=1,2,\dots,n$ ) and  $j$ <sup>th</sup> environment ( $j=1,2,\dots,m$ ),  $\mu$  is the grand mean,  $\beta_j$  is the main effect of environment  $j$ ,  $\mu + \beta_j$  being the mean yield across all genotypes in environment  $j$ ,  $\lambda_1$  and  $\lambda_2$  are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively,  $\xi_{i1}$  and  $\xi_{i2}$  are eigenvectors of genotype  $i$  for PC1 and PC2, respectively,  $\eta_{1j}$  and  $\eta_{2j}$  are eigenvectors of environment  $j$  for PC1 and PC2, respectively,  $\epsilon_{ij}$  is the residual is the residual error term. The analysis was performed by using Genstat software 16<sup>th</sup> ed.

## RESULTS AND DISCUSSION

### Combined ANOVA and Estimation of Variances Components

Variances of homogeneity from results of the Bartlett test revealed that the mean squares of individual environments were homogenous for seed yield. So, combined analysis of variance could be done. The main effects of environments and genotype and GEI were highly significant ( $p < 0.01$ ) for seed yield. The partitioning of sum of squares explained by the environment was 79.84% followed by genotype 17.21%, while the genotype x environment interaction explained least 2.95%. The magnitude of the environment was 4.6 times greater than the genotype, implying that most of the variation in seed yield was due to the environment. This indicates the large influence of environment on yield performance of sesame genotypes across all locations. Similar result was reported on sesame (Mekonnen et al. (2015), Mohammed et al. (2015) and Yirga (2016).

Table 3. Mean grain yield (kg ha<sup>-1</sup>) of four sesame genotypes evaluated at three environments at Abergelle Agricultural Research Center mandate areas during 2015 cropping season

Genotypes	Environments			GM
	Agbe	Dabano	Finaruwa	
Hirhir	242.0 <sup>b</sup>	522.0 <sup>c</sup>	430.7 <sup>ab</sup>	398.2 <sup>c</sup>
Humera-1	355.2 <sup>a</sup>	734.0 <sup>a</sup>	506.7 <sup>a</sup>	532.1 <sup>a</sup>
Local	212.0 <sup>c</sup>	522.3 <sup>c</sup>	348.7 <sup>b</sup>	362.1 <sup>c</sup>
Setit-1	245.3 <sup>b</sup>	646.7 <sup>b</sup>	489.7 <sup>a</sup>	460.6 <sup>b</sup>
EM	263.8	606.2	443.9	438.0
LSD (5%)	18	45	105	60
CV (%)	3.4	3.7	11.9	8.1

Where: GM=Genotypic means, EM=Environment means; LSD = least significance difference, CV (%) = Coefficient of variation in percent and values with the same letters in a column are not significantly different at  $P \leq 0.05$ .

Table 4. Combined analysis of variance for four sesame genotypes across three environments

Source	DF	SS	MS	% explained
Reps. within Env.	6	9861	1643	
Environment (E)	2	704474	352237**	79.84
Genotype (G)	3	151892	50631**	17.21
GxE Interaction	6	26042	4340**	2.95
Error	24	29951	1248	

\*\*Significant at  $P \leq 0.01$ , DF = degree of freedom, SS = sum of squares, MS = mean squares

#### GGE biplot analysis

Further partitioning and analysis of the GE was computed using the GGE model (Yan, 2001). The Gollob's (1968) F-test showed that the two principal components of the biplot were significant and thus, could explain much of the variation (96.81%) in the two-way data (Zobel et al. 1988; Gauch 2006). Therefore, the GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from yield data subjected to environment effects (Yan et al., 2000, Yan and Tinker 2006). The first two principal components for mean yield and stability of the GEI explained 96.81% with PC1 = 90.88 and PC2 = 5.93 of the GGE sum of squares.

#### 'Which-Won-Where' Pattern and Mega-environment Identification

GGE biplot is an effective tool for: 1) mega-environment analysis (e.g. "which-won-where" pattern), where by specific genotypes can be recommended to specific mega-environments, 2) genotype evaluation (the mean performance and stability), and 3) environmental evaluation (the power to discriminate among genotypes in target environments). GGE biplot graph (Figure 1) revealed that the testing locations (Agbe, Dabano and Finaruwa) fall into the same mega environment with winning genotype Humera-1. The equality lines divide the biplot into sectors, and the winning genotype for each sector is the one located on the respective vertex (Yan et al., 2007). Humera-1 was vertex, thus, it was the best genotype for the three environments with mean seed yield of 532.1 kg ha<sup>-1</sup> (Table 3). This pattern suggested that Humera-1 would be selected for proper exploitation of resources in the three environments. On the contrary, the result showed genotypes (setit-1, hirhir and local) which fall in sectors where there were no locations at all; these genotypes are poorly adapted to three of the testing environments.

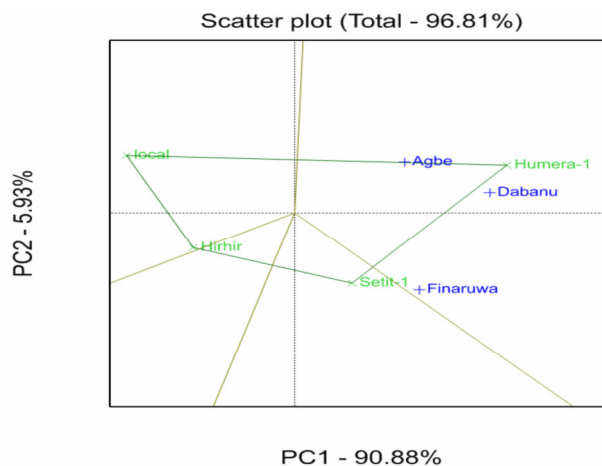


Figure 1. Polygon view of GGE biplot graph for which-won-where pattern of four sesame genotypes across three environments.

### Mean Seed Yield and Stability of Genotypes

The best genotype can be defined as the one with the highest yield and stability across environments. In the GGE biplot, genotypes with high PC1 scores have high mean yield, and those with low PC2 scores have stable yield across locations (Yan and Tinker, 2006). The average environment abscissa is represented in Figure 2 by a single head arrow pointing towards higher yield across environments. The average environment ordinate (AOE) is represented as a double-headed arrow and points towards lower stability in both directions (Yan and Hunt, 2001). Genotypes Hirhir (398.2 kg/ha) and local (361.0 kg/ha) had mean seed yield lower than the grand mean (438 kg/ha). The genotypes that yielded higher than the grand mean were Humera-1 (532.1 kg/ha) and Setit-1 (460.6 kg/ha) (Table 3). The most stable genotype was Humera-1 because it showed the shortest distance from the average environment abscissa. Hirhir and local had a large contribution to the genotype-by-environment interaction; they were unstable across environments. Considering simultaneously yield and stability, Humera-1 showed the best performance (Figure 2), suggesting its adaptation to a wide range of environments (Annicchiarico 1997). The result was in agreement with the previous findings of Yirga (2017) in sesame and Farshadfar et al. (2012), Mohamed et al. (2013), Muez et al. (2015) and Dejene (2016) the highest-yielding wheat genotypes were stable, a desirable situation for plant breeders.

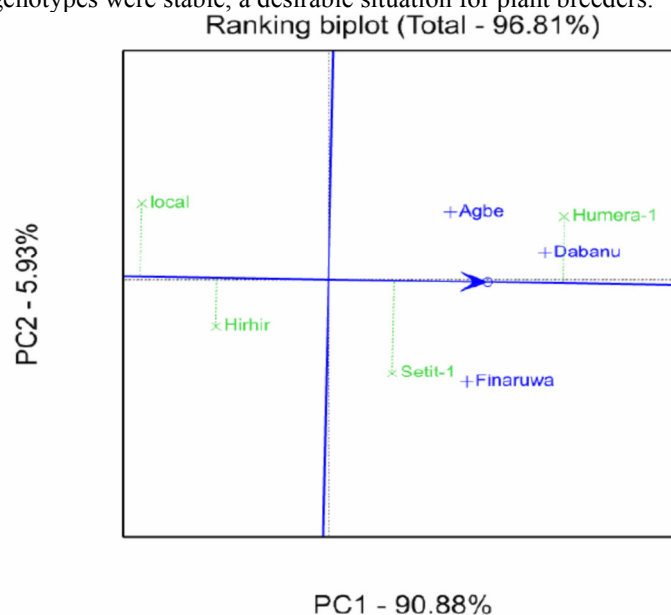


Figure 2. The mean performance and stability view of the GGE biplot with scaling focused on genotypes across environments.

### Evaluation of Genotypes Based on the Ideal Genotype

An ideal genotype has the highest mean seed yield and is stable across locations (Farshadfar et al. 2012). The ideal genotype is located in the first concentric circle in the biplot. Desirable genotypes are those located close to the ideal genotype. 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 (Yan and Tinker 2006). The ideal genotype can be used as a benchmark for selection. Genotypes that are far away from the ideal genotype can be rejected in early breeding cycles while genotypes that are close to it can be considered in further tests (Yan and Kang 2003). From this study Humera-1 was the “ideal” genotype and the highest mean seed yield. Humera-1 considered the most stable across variable environments. Genotypes closer to the ideal genotype were the stable ones, while genotypes far from the ideal genotypes were the unstable. Setit-1 was plotted to the ideal genotype considered as desirable genotype, while Hirhir and local were low yielding genotypes associated with genotypic instability (Figure 3). Genotype is more desirable if it is located closer to the ideal genotype. Similar result was reported by Farshadfar et al. (2012), Mitrovic et al. (2012) and Yirga (2016) on sesame and Muez et al. (2015) in bread wheat.

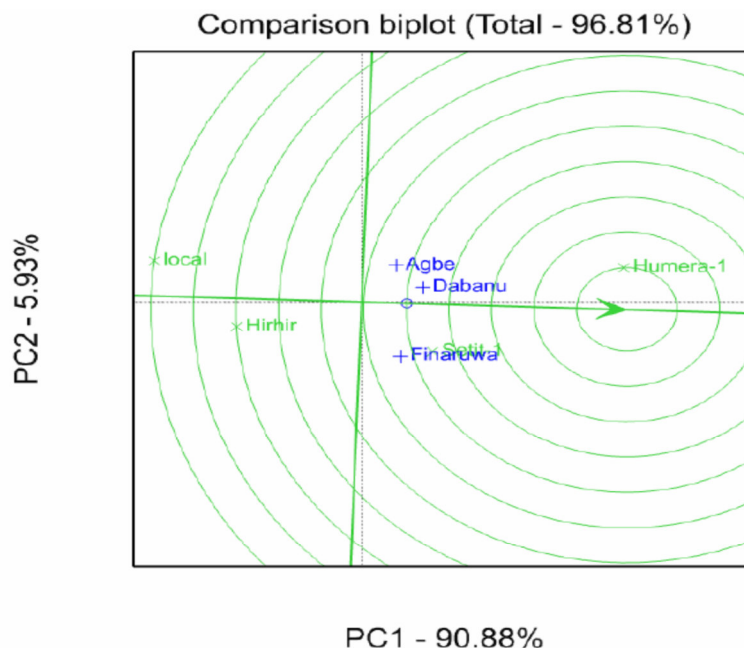


Figure 3. GGE-biplot showing the “ideal” genotype.

**Evaluation of Environments Based on the Ideal Environment**

The ideal environment is representative and has the highest discriminating power (Yan and Tinker 2006). Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environment. Nearest to the first concentric circle, Environment Dabanu was close to the ideal environment (Figure 4), therefore, it should be regarded as the most suitable to select widely adapted genotypes. Agbe and Finaruwa were far from the ideal environment and considered as unstable. The result was in line with Yan et al. (2000), Yan and Rajcan (2002), Yan et al. (2007), Fiseha et al. (2015) and Yirga (2016) in sesame and Muez et al. (2015) in bread wheat.

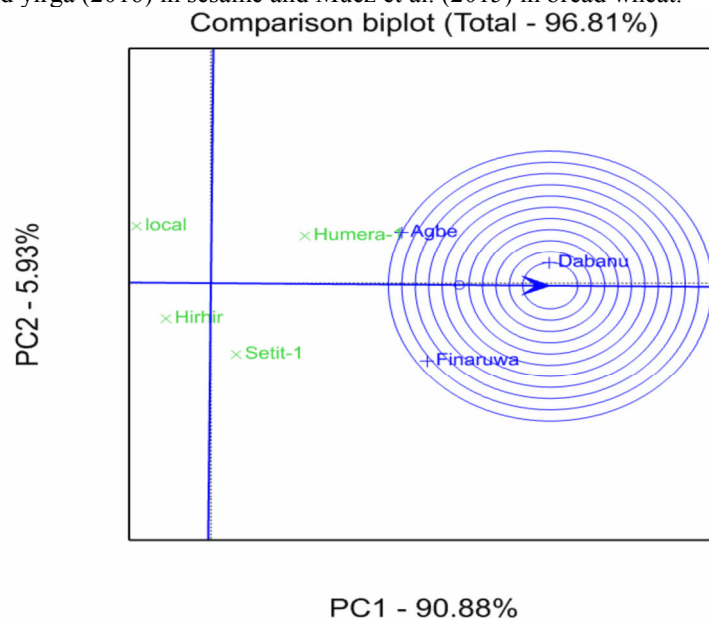


Figure 4. GGE-biplot showing the “ideal” environment.

**Relationship among Test Environments**

Further information about the discriminating power of environments, together with a representation of their mutual relationships, can be obtained by the environment-vector view of the GGE-biplot. In this case, a long environmental vector reflects a high capacity to discriminate the genotypes. Furthermore, the cosine of an angle between vectors of two environments approximates the correlation between them; a wide obtuse angle indicates a strong negative correlation, an acute angle indicates a positive correlation while a close-to- 90° angle indicates lack of correlation (Yan and Tinker 2006). With the longest vectors from the origin, environment Dabanu was the most discriminating. Finaruwa was moderately discriminating while Agbe was least discriminating.

Considering the angles between environmental vectors, yield results in Agbe and Dabano were strongly correlated (Figure 5).

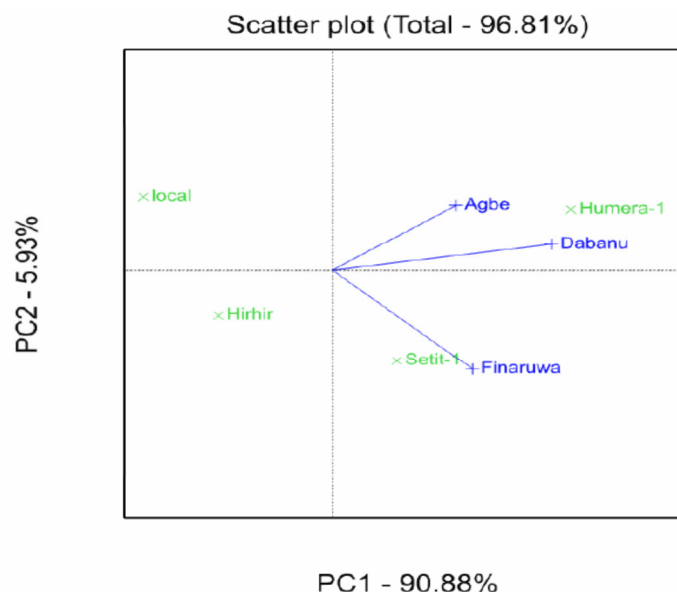


Figure 5. GGE biplot with scaling focused on genotypes, for mean seed yield and stability of four sesame genotypes across three environments.

## CONCLUSIONS

The combined analysis of variance result showed that sesame genotypes evaluated in the study were significantly ( $p < 0.01$ ) influenced by environment, genotype and genotype x environment interaction (GEI). The total sum of square explained by the environment was 79.84% followed by genotype 17.21%, while the genotype x environment interaction explained least 2.95%. The magnitude of the environment was 4.6 times greater than the genotype, implying that most of the variation in seed yield was due to the environment. The genotype main effect plus genotype x environment interaction (GEI) biplot was applied to analyze and visualize pattern of the interaction component. The first two principal components for mean yield and stability of the GEI explained 96.81% with PC1 = 90.88 and PC2 = 5.93 of the GGE sum of squares using environment standardized model. The GGE biplot analysis examined the nature of GE for sesame seed yield in addition to identifying best sesame genotype for tested location (Dabano) and determine the ideal of the tested locations for future sesame breeding activities. Humera-1 was close to the ideal genotype and can thus be used as benchmarks for the evaluation of sesame genotypes in the region. Considering simultaneously mean yield and stability Humera-1 followed by Setit-1 was the best genotypes while the most unstable genotypes with poor performance across locations were hirhir and local. Generally, GGE (genotype and genotype by environment interaction) biplot analysis indicating that Humera-1 was considered as the most desirable and stable one's, therefore can be recommended for wider cultivation due to better seed yield and stability performance across the test environments in the dry lowland areas of Southeast and Central zones of Tigray region, Northern Ethiopia..

## CONFLICT OF INTEREST

The authors have not declared any conflict of interest.

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## REFERENCES

- Adefris Teklewold, TadeleAmde and TesfayeBaye. 2011. Sesame cultivation and use in Ethiopia. P, 297-302
- Annicchiarico, P. and Perenzin, M. 1997. Adaptation patterns and definition of macro environments for selection and recommendation of common wheat genotypes in Italy. Plant Breed, 113, pp.197-205.
- Ashri, A. 1994. Genetic resources of sesame: Present and future perspectives. In: Arora, R.K. and Riley, K.W. (eds). Sesame Biodiversity in Asia- Conservation, Evaluation and Improvement, IPGRI Office for South

- Asia, New Delhi, India. Pp. 25-39.
- Crossa, J. 1990. Statistical analysis of multi-location trials. *Advances in Agronomy*, 44: 55-85.
- CSA (Central Statistical Agency). 2015. Agricultural Sample Survey report on Area and Production of Major Crops (Private Peasant Holdings 'Meher' Season): *Statistical Bulletin 579*. Addis Ababa, Ethiopia.
- DejeneDemisie. 2016. Genotype by Environment Interaction and Yield Stability Analysis of Ethiopian Bread Wheat Using Mixed Model. MSc Thesis, Haramaya University,
- Fantaye Belay, AtsphaGebreslasie and Hintsameresa. 2017. Agronomic Performance Evaluation of Cowpea [*Vigna unguiculata* (L.) Walp] Varieties in Abergelle District, Northern Ethiopia. *Journal of Plant Breeding and Crop Science*, 9(8): 139-143.
- FAOSTAT. 2012. Statistical Database of the Food and Agriculture of the United Nations. <http://www.fao.org> [Online]. Accessed on February 2016.
- FAOSTAT. 2014. Food and Agriculture Organization of the United Nations. <http://faostat.fao.org>. Accessed on March, 2016.
- Farshadfar E., Mohammadi R., Aghaee M., Vaisi Z. (2012). GGE biplot analysis of genotype x environment interaction in wheat-barley disomic addition lines. *Australian Journal of Crop Science* 6, 1074-1079.
- Farshadfar, E., Geravandi, M. and Vaisi, Z. 2012. Chromosomal localization of QTLs controlling genotype  $\times$  environment Interactions in barley. *International Journal of Agriculture and Crop Sciences*, 4(6): 317-324.
- Gauch H.G. 2006. Statistical analysis of yield trials by AMMI and GGE. *Crop Sci.* 46:1488-1500.
- Genstat software. 2010. Phenotypic correlation coefficient analysis using Genstat software 13th
- Gollob, H.F. 1968. A statistical model which combines features of factor analytic and analysis of variance. *Psychometrika*, 33: 73-115.
- Hansen, R. 2011. Sesame Profile. Available at <http://www.agmrc.org/>. Accessed on May 2015.
- Kumaresan, D., and Nadarajan, N. 2010. Genotype x environment interactions for seed yield and its components in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, 1(4): 1126-1132.
- Mekonnen Misganaw, Firew Mekbib and Adugna Wakjira. 2015. Genotype x environment interaction on sesame (*Sesamum indicum* L.) seed yield in Eastern Amhara Region. *African Journal of Agricultural Research*, 10 (21): 2226-2239.
- Mitrovic, B., Stanislavljevi, D., Treski, S., Stojakovic, M., Ivanovic, M., Bekavac, G., and Rajkovic, M. 2012. Evaluation of experimental Maize hybrids tested in Multi-location trials using AMMI and GGE biplot analysis. *Turkish Journal of Field Crops*, 17(1): 35-40.
- Mohamed N.E., Ahmed. A.A. 2013. Additive main effects and multiplicative interaction (AMMI) and GGE-biplot analysis of genotype  $\times$  environment interactions for grain yield in bread wheat (*Triticum aestivum* L.). *African Journal of Agricultural Research* 8, 5197-5203.
- Mohammed Abate. 2015. Genotype x Environment analysis for seed yield and its components in sesame (*Sesamum indicum* L.) evaluated across diverse agro-ecologies of the Awash valleys in Ethiopia. *Journal of Advanced Studies in Agricultural, Biological and Environmental Sciences*, 4 (2): 1-14.
- Muez Mehari, Mizan Tesfay, Haddis Yirga, Adhiena Mesele, Teklay Abebe, Assefa Workineh, Birhanu Amare. 2015. GGE biplot analysis of genotype-by-environment interaction and grain yield stability of bread wheat genotypes in South Tigray, Ethiopia. *Communications in Biometry and Crop Science*. 10, 17-26.
- Pathak, N., Rai, A.K., Kumari, R., Thapa, A. and Bhat, K.V. 2014. Sesame Crop: An Underexploited Oilseed Holds Tremendous Potential for Enhanced Food Value. *Agricultural Sciences*, 5, 519-529.
- Steel, R.G. and Torrie, J.H. 1980. *Principles and procedures of statistics*. McGraw-Hill, New York.
- USAID (United States Agency for International Development). 2014. The Business Case for Investing in a Sesame Hulling Plant in Ethiopia.
- Wijnands, J., Biersteker, J., and Hiel, R. 2007. Oilseeds Business Opportunities in Ethiopia. Survey report, Ministry of Agriculture, Nature and Food Quality, The Netherlands, The Hague. Pp. 8-20.
- Yamanura, D.M. 2008. Sesame Growing: An Idealized Overview. (In: Oil Crops: proceedings of a workshop, Cairo, Egypt, September Riley, K.W., ed.), IDRC-MR93e., IDRC-Ottawa.
- Yan W. 2001. GGE Biplot-A Windows application for graphical analysis of multi-environment trial data and other types of two way data. *Agrochimica*, 93:1111-1118
- Yan W., Hunt L.A. 2001. Interpretation of genotype  $\times$  environment interaction for winter wheat yield in Ontario. *Crop Science* 41, 19-25.
- Yan W., Tinker N.A. 2006. Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science* 86, 623-645.
- Yan, W. and Kang, M.S. 2003. GGE biplot analysis: A graphical tool for breeders, In: Kang, M. S. (ed.), *Geneticists and Agronomists*. FL: CRC Press, Boca Raton. pp. 63-88.
- Yan, W. and Rajcan, I. 2002. Biplot analysis of test sites and trait relations of soybean in Ontario, *Crop Science*, 42: 11-20
- Yan, W., Hunt, L.A. Sheng, Q. and Szlavnic, Z. 2000. Cultivar evaluation and mega-environment investigation



- based on the GGE biplot. *Crop Science*, 40: 597–605.
- Yan, W., Kang, M.S., Ma, B., Woods, S. and Cornelius, P.L. 2007. GGE (Genotype and genotype by environment interaction) biplot vs. AMMI (Additive main effects and multiplicative interaction) analysis of genotype by environment data. *Crop Science*, 47(2): 643-653.
- Yan, W. 2002. Singular-value partition for biplot analysis of multi-environment trial data. *Agron. J.* 94:990–996.
- Yirga Belay. 2016. Genotype x Environment Interaction and Yield Stability of White Seeded Sesame (*Sesamum indicum* L.) Genotypes in Northern Ethiopia. MSc Thesis, Haramaya University, Haramaya, Ethiopia.
- Yirga Belay. 2017. Correlation and cluster analysis of white seeded sesame (*Sesamum indicum* L.) genotypes oil yield in northern Ethiopia. *African Journal of Agricultural Research*, 12(12): 970-978.
- Zhang, Y., Wang, L., Xin, H., Li, D., Ma, C., Ding, X., Hong, W. and Zhang, X. 2013. Construction of a High-Density Genetic Map for Sesame Based on Large Scale Marker Development by Specific Length Amplified Fragment (SLAF) Sequencing. *BMC Plant Biology*, 13, 141
- Zobel, R.W, Wright M.J, Gauch H.G, (1988): Statistical analysis of a yield trial. *Agron. J.* 80:388-39. Abay F., Bjornstad A. (2009). Specific adaptation of barley varieties in different locations in Ethiopia. *Euphytica* 167, 181–195.
- Zobel, W.R., Wright, M.J. and Gauch, H.G. 1988. Statistical analysis of a yield trial. *Agronomy Journal*, 80: 388-393. Agele, S.O: Adenawoola, A.R: Doherty M. (2004) : Growth response of soybean lines to contrasting photo thermal and soil moisture regimes in a Nigerian tropical rain forest *International journal of Biotronics* 33, 49-64.