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ARTICLE

Full Length Research Paper

Evaluation of the performance of some white seeded sesame (*Sesamum Indicum* L.) genotypes using GGE biplot analysis in Northern Ethiopia

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Sesame (*Sesamum indicum* L.) 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, there is a low productivity and production 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≤0.01) environment (E), genotype (G) and genotype × 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 into two significant interaction principal components using the genotype main effect plus genotype x environment interaction (GGE) biplots model. The first two principal components for seed yield stability of the GGE biplot analysis explained 96.81% of the total variation caused by G+GE of PC1 and PC2 accounted for 90.88 and 5.93% 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 indicated 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.

Key words: Dry lowland, GEI, GGE biplot, mega environment, *S. 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 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 remains 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 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 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 one of the six priority crops of Agricultural Growth Programme (AGP) (USAID, 2012). It accounts 90% of the value of exported oil seeds, estimated at 379 million USD (FAOSTAT, 2012). It is the 2nd to coffee in foreign exchange earnings in Ethiopia (USIAD, 2014) and 2nd to 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%) and 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 a source of income for many small scale farmers, investors, traders, exporters and 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.) and abiotic factors (soil type, altitude, rail fall distribution and intensity etc.). Seed shattering at maturity is due to, 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 increase yields

through growing genotypes specifically adapted to a given area. The main features of quantitative traits are they are highly influenced by the environment and 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 production yield potential and export demanded 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 there is no information available on globally demanded white seeded sesame genotypes. Therefore, study on GEI and due attention for such white seeded sesame genotypes is essential in Ethiopia.

Therefore, the objectives of the study were to:

1. Estimate the magnitude and nature of GEI for seed yield and
2. Identify stable and/or high yielding white seeded sesame genotypes and assess their performance across locations using GGE biplot analysis in Northern Ethiopia.

MATERIALS AND METHODS

Description of the study areas

Field experiment was conducted under rain-fed condition at Abergelle Agricultural Research Center mandate areas (Table 1) during the 2015 main cropping season at three environments, namely; Agbe, Dabanu and Finaruwa. They are found in Tanqau Abergelle district (Central zone), Kola Temben district (Central zone) and Seharti Samre district, Southeast zone of Tigray regional state, respectively. They are representing the dry low land moisture stress areas of Abergelle Agricultural Research Center, Northern Ethiopia.

The distribution of rainfall at the mandate area 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.,

Table 1. Description of the study locations in 2015 main cropping season.

| Location | Geographic position | | | Soil properties | | T (°C) | | RF |
	Altitude	Latitude (N)	Longitude (E)	Texture	pH	Max	Min	mm
Agbe	1450	13°37' 53''	39°01'29''	Sandy clay	7.33	36	19	450
Dabanu	1510	13°46' 40''	38°59'30''	Sandy clay	7.53	33	16	515
Finaruwa	1300	13°21' 08''	38°59'54''	Sandy clay	7.16	41	24	301

Source: Abergelle Agricultural Research Center, 2015.

Table 2. Description of genotypes used in the study.

Genotype	Status	Sources	Color	Remark
Humera-1	Released variety	HuARC	White	Through selection
Setit-1	Released variety	HuARC	White	Through selection
Hirhir	Advance line	HuARC	White	Collection
Local	Local check	Abergelle area	White	Farmer cultivar

Source: Humera Agricultural Research Center Annual report, 2015.

2017).

Experimental genotypes

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

Experimental design and crop management

The trial was carried out in randomized complete block design (RCBD) with three replications across locations employed with experimental plot size of 2 m x 5 m with 1m between plots and 1.5 m between blocks keeping inter and intra row spacing of 40 and 10 cm, respectively. Each plot had a total area of 10 m^2 and total of five rows and 6m^2 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. Seed was manually drilled in the rows at a seed rate of 8 kg ha^{-1} and thinned after 25 days of sowing. 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

The total seed yield harvested from the net plot area was weighed using a sensitive balance, adjusted to standard moisture level at 10% and weighted to get the seed yield per plot in grams, which was converted to kg ha^{-1} for analysis.

Data analysis

Homogeneity of residual variances was tested prior to a combined analysis using Bartlett's test (Steel and Torrie, 1980). Analysis of variance for each environment, combined analysis of variance over environments and GGE biplot analysis was computed using General Statistics (GenStat) 16th edition (2010).

Separate and combined ANOVA

As error variance were homogenous, 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 and locations (environments). GenStat 16th edition (2010) statistical software was used for statistical analyses. The model employed in the analysis was;

Yijk = μ + Gi + Ej + Bk + GEij + εijk

Where:
Yijk is the observed mean of the ith genotype, (Gi) in the jth environment (Ej), in the kth block (Bk); μ is the overall mean; Gi is effect of the ith genotype; Ej is effect of the jth environment; Bk is block effect of the ith genotype in the jth environment; GEij is the interaction effects of the ith genotype and jth environment and εijk is the error term. Yield data was subjected to combined analysis of variance using GenStat 16th edition to examine the main effects of the environment (E) and genotypes (G) and their interactions (GEI) variances.

GGE analysis

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. The GGE biplot analysis was built according to the formula described by Yan et al.

Table 3. Mean seed yield (kg ha⁻¹) of four sesame genotypes evaluated in three environments at Abergelle Agricultural Research Center mandate areas during 2015 cropping season.

Genotypes	Environments			GM
	Agbe	Dabanu	Finaruwa	
Hirhir	242.0[b]	522.0[c]	430.7[ab]	398.2[c]
Humera-1	355.2[a]	734.0[a]	506.7[a]	532.1[a]
Local	212.0[c]	522.3[c]	348.7[b]	362.1[c]
Setit-1	245.3[b]	646.7[b]	489.7[a]	460.6[b]
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≤ 0.05.

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

Source	DF	SS	MS	% explained
Replications within Environment	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≤ 0.01, DF = degree of freedom, SS = sum of squares, MS = mean squares.

(2000), Yan and Hunt (2001) and Yan (2002) as:

$$Yij - \mu - \beta j = \lambda 1 \xi i 1 \eta j 1 + \lambda 2 \xi i 2 \eta j 2 + \varepsilon ij$$

where Yij measured mean yield of the ith genotype i(=1,2,….,n) and j[th] environment j(=1,2…,m), μ is the grand mean, βj is the main effect of environment j, μ + βj being the mean yield across all genotypes in environment j, λ1 and λ2 are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, ξi1 and ξi2 are eigenvectors of genotype I for PC1 and PC2, respectively, η1j and η2j are eigenvectors of environment j for PC1 and PC2, respectively and εij is the residual in the residual error term. The analysis was performed using Genstat software 16th edition.

RESULTS AND DISCUSSION

Combined analysis of variances

Homogeneity of error variances from the results of the Bartlett test detected that, the mean square for seed yield of sesame genotypes across locations were homogenous (Table 3). The combined data across locations indicated that seed yield was highly significantly (p<0.01) influenced by environment accounted for 79.84% of the total variation while, G and GEI explained 17.21% and 2.95% of the 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. This indicated that the large influence of environment causing most of the variation in yield performance of sesame genotypes across all locations while the contribution of GEI to the total variation showed minimal role. Similar result was reported on sesame by Mekonnen et al. (2015), Mohammed (2015) and Yirga (2016) (Table 4).

GGE biplot analysis

The larger GEI relative to G confirms the possible of existence of different mega environments, thus, the current seed yield data was subjected to GGE biplot analysis. According to Gollob (1968), F-test of the two principal components (PC1 and PC2) of GGE biplot was significant (P≤ 0.01). The result was in line with the previous works of Zobel et al. (1988) and Gauch (2006), which explain much of the variation in the first two principal components for mean yield and stability of the
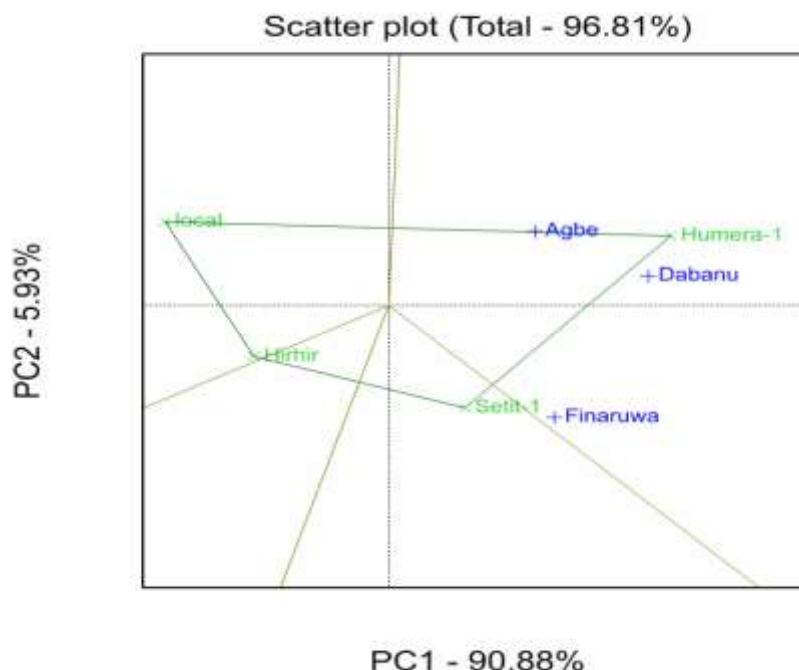
Figure 1. Polygon view of GGE biplot graph for which-won-where pattern of four sesame genotypes across three environments.

GGE.

Therefore, the GGE biplot was constructed using the first two principal components (PC1 and PC2) derived from yield data and subjected to environment effects (Yan et al., 2000; Yan and Tinker 2006). The partitioning of the GGE through site regression model revealed that PC1 and PC2 accounted for 90.88 and 5.93% of GGE sum squares, respectively and totally explained 96.81% of the variation (Figure 1). Genotype with large PC1 scores (high mean yield) and near zero PC2 scores (high stability) is considered as high yielder and stable. Accordingly, Humera-1 with the highest mean seed yield and stability across variable environments was considered as the most desirable and stable ones.

'Which-Won-Where' pattern and mega-environment identification

The 'which-won-where' pattern (Figure 1) revealed that the testing locations (Agbe, Dabanu and Finaruwa) fall into the same mega environment with winning genotype Humera-1. GGE biplot is an effective tool for: 1) mega-environment analysis (for example, "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). 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, was the best genotype for the three environments with mean seed yield of 532.1 kg ha-1 (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.

Mean seed yield and stability of genotypes

Average tester coordinate (ATC) separates genotypes with above average mean from below average means as shown in Figure 2. 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) while genotypes Hirhir (398.2 kg/ha) and local (361.0 kg/ha) had mean seed yield lower than the grand mean (438 kg/ha). Thus, the best genotype can be defined as the one with the highest yield and stability across environments. 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
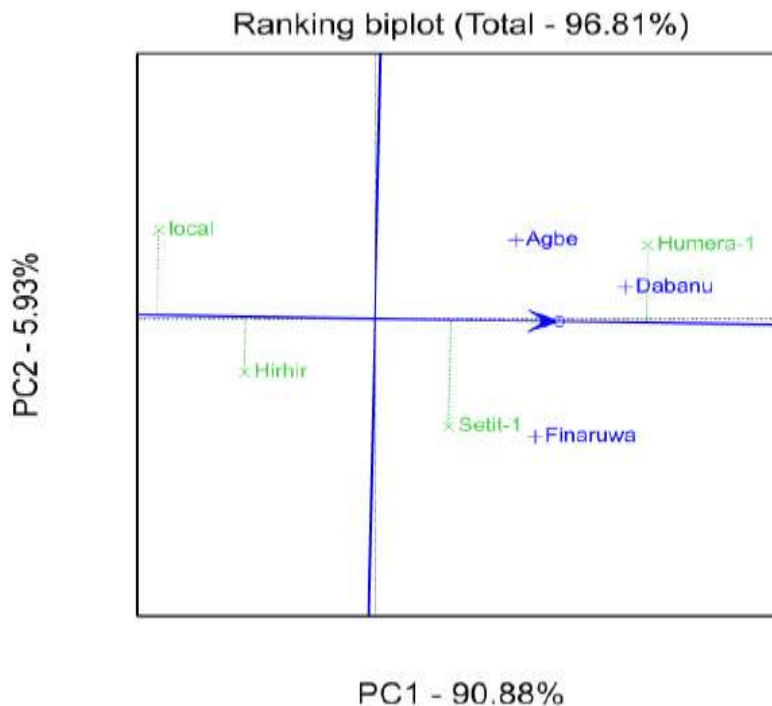
Figure 2. The mean performance and stability view of the GGE biplot with scaling focused on genotypes across environments.

2), suggesting it's adaptation to a wide range of environments (Annicchiarico and Perenzin, 1997). This result is in agreement with the previous findings of Yirga (2017) in sesame and Farshadfar et al. (2012), Mohamed and Ahmed (2013), Muez et al. (2015) and Dejene (2016) in wheat.

Evaluation of genotypes based on the ideal genotype

The ideal genotype is located in the first concentric circle in the biplot as indicated in Figure 3. An ideal genotype should have both high mean yield performance and stable across locations. From this study, Humera-1 was the "ideal" genotype with the highest mean seed yield and stable across environments. Thus, Humera-1 is considered as the most stable across variable environments.

Starting from the middle, concentric circle pointed with arrow was drawn to help visualize the distance between genotypes and the ideal genotype (Yan and Tinker, 2006). Genotypes closer to the ideal genotype were the stable ones, while genotypes far from the ideal genotypes were the unstable. Setit-1 was plotted close to the ideal genotype considered as desirable genotype, while Hirhir and local were low yielding genotypes associated with genotypic instability (Figure 3). Therefore, desirable genotypes are those nearest to the ideal genotype (the center of concentric circle). 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.

Evaluation of environments based on the ideal environment

Similarly to the ideal genotype, the ideal environment is located in the first concentric circle in the environment-focused biplot as shown Figure 4. Desirable environments are close to the ideal environment. Accordingly, nearest to the first concentric circle, the environment Dabanu was the ideal environment to select widely adapted sesame genotypes, whereas, Agbe and Finaruwa were far from the ideal environment and considered as unstable. This 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.

Relationship among test environments

The discriminating power of environments, together with the representation of their mutual relationships, can be obtained by the environment-vector view of the GGE-biplot (Figure 5).

Furthermore, the cosine of an angle between vectors of two environments approximates the correlation between
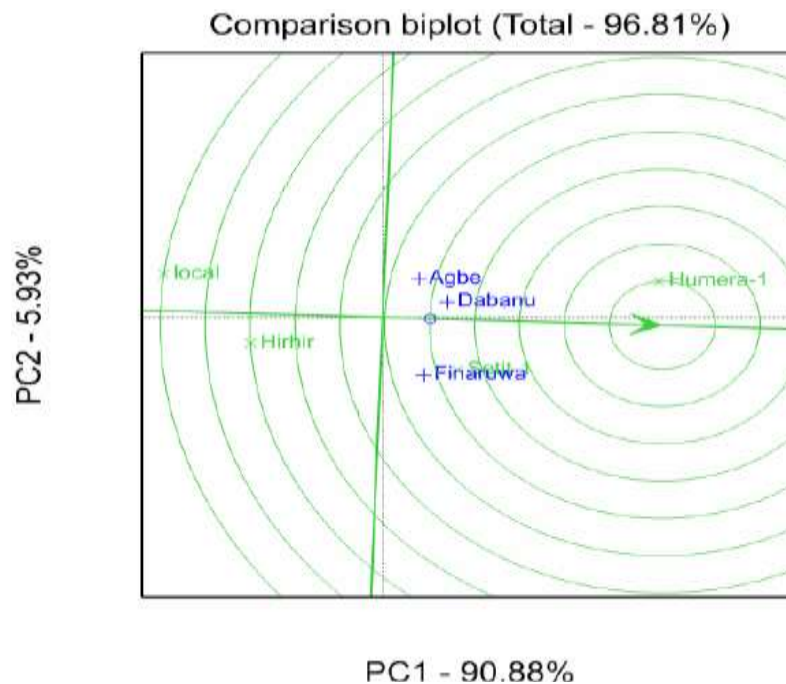
Figure 3. GGE-biplot showing the "ideal" genotype.
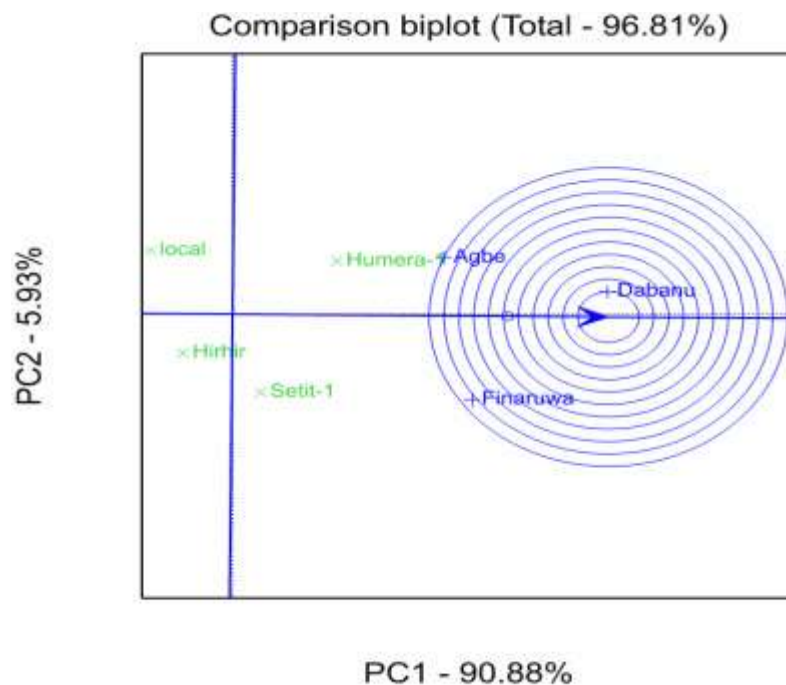
Figure 4. GGE-biplot showing the "ideal" environment.

them; a wide obtuse angle indicates a strong negative correlation, while the angle between two vectors is less than 90° which indicates positive correlation or close relationship (Yan and Tinker, 2006). Considering the angles between environmental vectors, yield results in Agbe and Dabanu were strongly correlated (Figure 5). The presence of close associations between testing environments imply that similar information could be

Scatter plot (Total - 96.81%)

PC1 - 90.88%
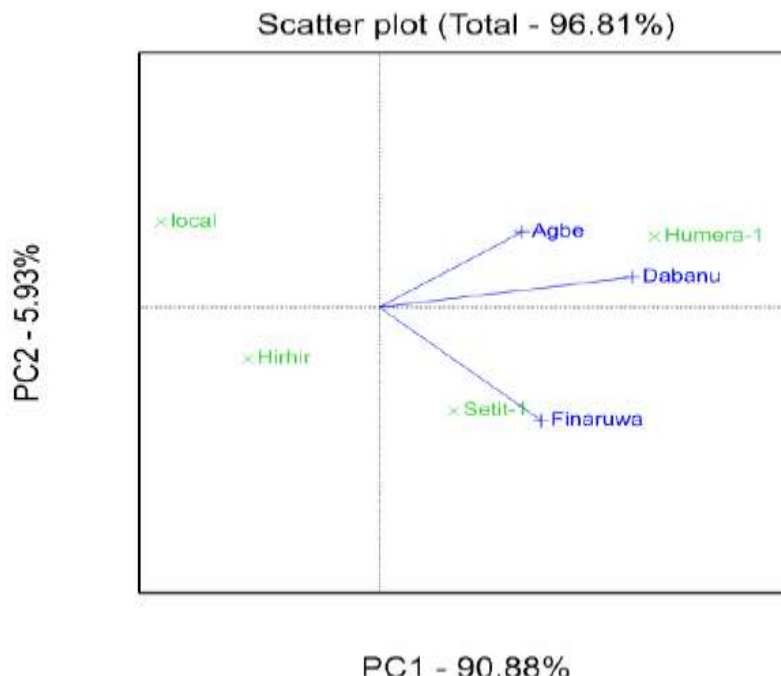
Figure 5. GGE biplot showing mean seed yield and stability of four sesame genotypes across three environments.

obtained from them.

Discriminating ability and representativeness of environments

The GGE biplot shown in Figure 5 revealed the discriminating ability and representativeness of test environments. In this case, a long environmental vector reflects a high capacity to discriminate the genotypes. Therefore, environment Dabanu with the longest vector from the origin was the most discriminating environment. Finaruwa was moderately discriminating while Agbe was least discriminating environment.

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 (GGE) biplot was applied to analyze and visualize pattern of the interaction component. The first two principal components for seed yield stability of the GGE biplot analysis explained 96.81% of the total variation caused by G+GE of PC1 and PC2 which were accounted for 90.88 and 5.93% sum of squares, respectively, while 3.19% was attributed to noise. The GGE biplot analysis examined the nature of GE for sesame seed yield in addition to identifying best sesame genotype for tested location (Dabanu) 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 plus, genotype by environment interaction) biplot analysis indicate 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 INTERESTS

The authors have not declared any conflict of interests.

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