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Genotype by Environment Interactions and Yield of Sesame (*Sesamum indicum* L.) Varieties Across the Diverse Agro-ecologies of Ethiopia

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Abstract

Sesame is an important oil crop both in area coverage and production in Ethiopia, serving one of the major export crops. However, productivity is low because of a lack of detailed information about genotypes, environment, and their interaction. Sixteen sesame varieties were evaluated at nineteen environments and grain yield and yield components were analyzed. Analysis of variance was computed and GGE-biplot and AMMI approaches were used. Environments were divided into six groups. E7, E13, and E14 were highly discriminating and representative in the first, second and third groups, respectively, and identified as a core test site in that group, which would be used to facilitate the identification of superior sesame varieties and reduce testing costs While E1, E18, and E19 were identified as the only test site in groups four, five, and six. Among all Ethiopian representative sesame sites, E16 and E17 were close to the ideal environment, which is suitable to select widely adapted genotypes. Setit-1 as the ideal variety in terms of yield and stability across variable environments, which could serve the most desirable

genotype to be directly recommended for farmers' use and to be used as source material for breeding that targets high-yielding and stable genotypes.

Keywords: genotype × environment interactions, GGE-biplot, ideal genotype, ideal Environments

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, which grow in pods (Weiss, 1983). It requires 25^{o}C to 27°C for rapid germination, initial growth, and flower formation while temperature below 18^{o}C after germination restricts growth and extreme temperature (>40^{o}C) during flowering reduces fertilization. Sesame is very 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 (Ashri, 1998).

In Ethiopia, Sesame is a very important oil crop in terms of both area coverage and production (CSA, 2019). The target of sesame breeding in Ethiopia is to develop varieties that meet the demands of sesame growers, processors, and consumers. Over twenty varieties were released by research centers.

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 environments. However, the selection of superior genotypes in METs usually leads to in genotype-by-environment interactions that always complicate the interpretation of results obtained and reduce efficiency in selecting the best genotypes (Annicchiarico, 1994). This interaction is because of the changes within the genotype's relative performance across environments, as a results of differential responses of the genotypes to varied abiotic and biotic factors (Dixon and Nukenine, 1997). Hence, a significant Genotype by Environment interaction (GEI) for a quantitative trait like grain yield can complicate the identification of superior genotypes for both improved and new crop introduction. Analyzing the magnitude of GEI helps exploiting the opportunities of adaptability. The two most used statistical analyses in use are the additive main effects and multiplicative interaction (AMMI) model, the genotype main effect, and also the genotype x environment interaction effect (GGE) model (Gauch, 2006).

As sesame could be a short-day plant and sensitive to light, heat, and moisture stress the yield isn't stable (Abate 2015) and no detailed multi-environment evaluation of Ethiopian sesame has been undertaken thus far. The objectives of

this study were to see yield performance, stability, and adaptability of varieties; to determine the representativeness and discriminating ability of the test locations; and to identify core testing sites for the selection of superior varieties.

Materials and Methods

The Research trial was conducted at 19 environments (Table 1) for two cropping seasons. A total of sixteen sesame varieties were evaluated (Table 2). The varieties were planted in each environments during the 2017/18 and 2018/19 cropping seasons. The environment by year combinations would have been twenty-four environments, but the second-year data of five environments were lost because of security, forcing the analysis to be made for data of nineteen environments. The experiment was laid out in a randomized complete block design with three replications.

Data were recorded for plant height, primary branch, days to 50% flowering, number of capsules per plant, seeds per capsule, 1000-seed weight, days to physiological maturity, pod bearing zone, seed yield, bacterial blight were recorded according to the sesame descriptors list of International Plant Genetic Resources Institute and National Bureau of Plant Genetic Resources (IPGRI and NBPGR, 2004). After harvesting manually, yield-related traits were measured in the laboratory. Seed yield was collected per plot and later converted into tons per hectare.

Table 1. Description of nineteen environments used for evaluation of sesame varieties

Environments	Env. Code	Soil type	Temperature (°C)	Rainfall (mm)	Latitude	Longitude	Altitude a. m. s. l
Bable 2017/18	E1	Sandy loam	20- 90	671	09^0 13'N	042^0 19'E	1669
Gofa 2017/18	E2	Sandy-clay loam	17.9 -30.9	1116	06^0 20'N	36^0 56'E	1305
Gofa 2018/19	E3						
Assosa 2017/18	E4	Loams and black clay		900 -1300	10^0 02'N	34^0 33.8'E	1650
Banat 2017/18	E5				13^0 49'N	36^0 30'E	635
Banat 2018/2019	E6						
Humera 2017/18	E7		18.8-37.6	576.4	14^0 15'N	36^0 37'E	609
Humera 2018/19	E8						
Kebebew 2017/18	E9				13^0 36"N	36^0 41"E	689
Kebebew 2018/19	E10						
Metema 2017/18	E11			1030.2	12^0 39'N	36^0 17'E	760
Metema 2018/19	E12						
Pawe 2017/18	E13	Nitisol		1586	11^0 18'N	36^0 24'E	1100
Shiraro 2017/18	E14		18.8-34.9	676.7	14^0 24'N	37^0 45'E	1018
Shiraro 2018/19	E15						
Tach Armacho 2017/18	E16			970.88	13^0 88'N	37^0 43'E	1022
Tach Armacho 2018/19	E17						
Worer 2017/18	E18	Fluvisol and Vertisol soil	19.5- 32.5	450	90^0 60' N	40^0 9'E	740
Mender67 2017/18	E19	Clay loam			$12^0$57'N	36^0 15'E	690

Table 2. Description of 16 released sesame varieties evaluated in 12 locations during the 2017/18 and 2018/19 cropping season

Genotype	Genotype code	Source of seed	Year of Release	Seed color	Oil (%)	Maturity date
HUMERA-1	G1	HUMERA ARC	2011	White	54-56	90-110
SETIT-1	G2	HUMERA ARC	2011	White	52-54	80-90
SETIT-2	G3	HUMERA ARC	2016	White	53.77	80-87
HUARC-4	G4	HUMERA ARC	2017			
ABASENA	G5	WORER ARC	1990	White	40.6-48.7	103-120
ADI	G6	WORER ARC	1993	White	40.20-57.7	85-91
TATI	G7	WORER ARC	2000	Light grey	47.48- 48.71	111-115
Acc-051-02-sel 1(2)	G8	WORER ARC	2017			
OBSA	G9	BAKO ARC	2010	White – tan	51.55	120-137
CHALESA	G10	BAKO ARC	2013			
DANGUR	G11	PAWE ARC	2015	Grey	56.7	124
GONDAR-1	G12	GONDAR ARC	2016	White	50	101
MECHAL	G13	SIRINKA ARC	2013	White	50.4	105-120
BENSHANGUL-1	G14	ASSOSA ARC	2016	White	54	90-115
BAHA NECHO	G15	ALEMAYA ARC	2016	White	52	114-129
BAHA ZEYT	G16	ALEMAYA ARC	2016	Light grey	56	113-134

Data analysis

Analysis of variance (ANOVA) was made first for each environment and once homogeneity of residual variances was tested, combined analysis using Bartlett's test (Steel and Torrie, 1980) was done. The combined ANOVA of the environments was performed, to identify the possible interactions of genotypes with environments. ANOVA for each environment, combined ANOVA over environments, and GGE-biplot analysis were computed using GenStat and SAS software. Stability and adaptability analyses were done using the AMMI, and multivariate GGE-biplot methods after the significance of the G x E interaction was determined.

AMMI and GGE-biplot analysis

The AMMI's stability value (ASV) was calculated using the formula suggested by Purchase et al. (2000) as

$$ASV = \sqrt{\left[\left[\frac{SSIPCA1}{SSIPC2}\right] * [IPCA1score]\right]^2 + (IPCA2score)^2}$$

Where: IPCA1= Interaction principal component analysis axis one, IPCA2= Interaction principal component analysis axis two, SS= sum of squares.

The seed yield biplots of the first two principal components were constructed using GenStat and GEA-R software.

Results and Discussion

Anlysis of variance and mean values

Data obtained from the different environments were analyzed separately, and thereafter combined for after the error homogeneity test, conducted between testing environments. The combined ANOVA across different locations showed that mean squares for the environment were significant ($p < 0.01$) for all measured traits of the varieties studied. Genotype (G) mean squares were significant ($p < 0.05$) for all traits measured except for pod per plant. Genotype by environment interaction was significant for most traits measured except for pod per plant and pod length (Table 3). Genotypes were significant for most traits, except for pod per plants, indicating that the genotypes responded differently to the test environments and thus, call for the need to identify high-yielding and stable genotypes across the locations. The highly significant GEI for grain yield of the released sesame varieties seeks to justify the need for the testing of the genotypes in multiple locations over years before recommendation.

The mean value of the 16 released varieties for grain yield of the genotypes ranged from 0.42 t ha^{-1} for G6 (ADI) to 0.65t ha^{-1} for G9 (Obsa).

Table 3. Mean squares for grain yield and other agronomic traits of sesame varieties evaluated across nineteen environments

		Mean squares			
Source	**Environment (E)**	**Genotype (G)**	**Rep(E)**	**G*E**	**Error**
Degree of freedom	18	15	38	270	570
Grain Yield	2384879.29**	203750.52**	49773.41**	69906.03**	25224.84
% CTV	64.31	4.58	2.83	28.28	4.58
Days to flowering	1038.05**	431.84**	11.09**	12.98**	4.74
Days to maturity	4900.32**	405.92**	26.34**	44.8**	6.98
Number of Primary branch	27.95**	15**	3.15**	1.41	1.08
Plant height	28986.25**	3404.55**	246.41**	178.25**	124.18
Pod bearing zone	8628.52**	1006.53**	255.62**	123.17**	73.06
Pod per plant	10006.96**	387.22	534.56**	244.35	206.87
Pod length	4.17**	0.85**	0.1	0.08	0.06
Seed per pod	7535.99**	420.00**	108.38	109.66**	60.56
Bacterial blight	94.54**	9.13**	0.54	0.8**	0.29
Thousand seed weight	6.19**	1.1**	0.16	0.24**	0.14
Oil content	307.47**	20.71**	5.12**	8.41**	2.15

Notes: %CTV = percentage contribution to total variation; *Significant at 0.05 probability level. **Significant at 0.01 probability level.

AMMI analysis

The AMMI analyses of variance showed that grain yield was significantly influenced by the environment, genotype, and GEI (Table 4). The significant effect of GEI on seed yield indicated differential responses of the genotypes across the environments. This result is consistent with that of Daba et al. (2015), who found similar results in sesame. Significant GEI complicates selection since the variety with the highest mean yield may not be the best genetically (Signor et al., 2001). In the present study, environment, GEI, and genotype explained 64.31%, 28.28%, and 4.58% of the total variation, respectively (Table 4). The Genotype accounted for the smallest case, whereas environment (E) and GEI explained most of the variations. This indicated that Environment and GEI are both important in governing for expression of this trait as supported by the report of Mulugeta et al. (2014).

The environment variation explained 14 times greater than the genotype, indicating that most of the variation in seed yield was due to the environment implying that the environments were diverse and causing larger influence on yield performance of sesame varieties. A similar result was reported on sesame (Abate 2015).

A highly significant GEI indicates the necessity for further analysis for yield stability and GEI must be considered in genotype evaluation and that GGE-biplot

analysis would be essential to reach meaningful conclusions about the genotypes (Yan, 2014).

The AMMI analysis partitioned the sum of squares of GEI into nine interaction principal component axes (IPCA), of which the first four IPCA were significant (Table 4). The results from the AMMI model showed that the first IPCA captured 42.16% of the interaction sum of squares. Similarly, the second (IPCA2) explained 18.25% of the GEI sum of squares. The sum of squares for the first four IPCAs cumulatively contributed to 79.2 % of the total GEI.

However in accordance with Zobel et al. (1988) proposed that two interaction principal component axes for AMMI model was sufficient for predictive model. Other interaction principal component axes captured mostly non-predictive random variation (noise) and did not fit to predict validation observations.

Table 4. Combined ANOVA for seed yield (2017/18 and 2018/19)

Sources	DF	SS	MS	Total variation explained (%)	(%) G x E Explained	Cumulative (%)
Total	911	81128268	89054			
Genotypes	15	3056256	203750***	4.58		
Environments	18	42927829	2384879***	64.31		
Reps within Env.	38	1891390	49773***	2.83		
Interactions	270	18874631	69906***	28.28		
IPCA 1	32	7958420	248701***		42.16	42.16
IPCA 2	30	3444904	114830***		18.25	60.41
IPCA 3	28	1884065	67288***		9.98	70.39
IPCA 4	26	1663195	63969***		8.81	79.2
IPCA 5	24	876788	36533		4.65	83.85
IPCA 6	22	712870	32403		3.78	87.63
IPCA 7	20	654044	32702		3.47	91.1
IPCA 8	18	562442	31247		2.98	94.08
IPCA 9	16	411881	25743		2.18	96.26
Residuals	54	706022	13074		3.74	100
Error	570	14378162	25225			

Note: Grand mean = 558.62; R-squared = 0.8228; C.V. = 28.43%; **P<0.01; *** P<0. 001; IPCA=Interaction principal component axis.

Purchase (1997) indicated that the IPCA scores of genotypes within the AMMI analysis are an indication of the stability of a genotype over environments. The greater the absolute value IPCA1 scores, the more specifically adapted a genotype is to a particular environment. Varieties SETIT-1 and MECHAL showed the lowest absolute scores for the IPCA1 and they were the most stable (Table 5). IPCA2 scores approximate to zero value indicate the more stable or adapted the genotype across environments conducted (Kang, M.S. and Gauch 1996, Ferney et al., 2007). When IPCA2 was considered, BAHA ZEYT was the most stable. The Stability rank of genotypes varied for IPC1 to IPC2. This means that the two

IPCA have different values and meanings. Therefore, the other option is to calculate ASV to get the estimated value between IPCA1 and IPCA2 scores as ASV was reported to produce a balance measurement between the two IPCA scores (Purchase, 1997). In the present study, Varieties MECHAL, BAHA ZEYT, BENSHANGUL- 1, and SETIT-1 were found to be stable (Table 5). As per the value of ASV, the most unstable Varieties were TATI, Acc-051-02-sel 1 (2)) and ADI. Genotype with low ASV values is considered more stable than a genotype with high ASV (Purchase 1997).

Table 5. Mean yield (kg ha^{-1}) rank, IPCA1, IPCA2 scores and ASV of the 16 sesame varieties tested across 19 environments.

No	Genotype	Yield	Rank	IPCA1	IPCA2	ASV	Rank
1	HUMERA-1	625.77	3	-7.12468	-11.0876	19.85	5
2	SETIT-1	626.2	2	-0.86882	-11.3408	11.52	4
3	SETIT-2	586.26	5	-11.2291	-12.0946	28.62	12
4	HUARC-4	566.54	8	-9.76351	-14.8257	26.99	11
5	ABASENA	554.7	11	11.0488	1.35129	25.56	9
6	ADI	418.46	16	-12.6691	9.12935	30.66	14
7	TATI	490.62	15	-16.7354	12.215	40.55	16
8	Acc-051-02-sel 1 (2)	491	14	-13.9062	11.3544	34.07	15
9	OBSA	654.66	1	12.558	-0.36402	29.01	13
10	CHALESA	559.72	9	8.2858	8.33943	20.88	6
11	DANGUR	611.72	4	10.1487	1.19988	23.48	7
12	GONDAR-1	570.17	6	10.7665	-0.2075	24.87	8
13	MECHAL	551.26	12	1.81811	3.44992	5.44	1
14	BENSHANGUL- 1	567.41	7	3.79687	2.74372	9.19	3
15	BAHA NECHO	555.17	10	11.4389	0.23806	26.43	10
16	BAHA ZEYT	508.22	13	2.43527	-0.10081	5.63	2

Where: IPCA1= Interaction principal component analysis axis one; IPCA2= Interaction principal component analysis axis two; ASV = AMMI stability value

GGE- biplot analysis of grain yield response and stability

Which Won Where/What

The principal component axis 1 (PC1) accounted for 41.56% of total variation and the principal component axis 2 (PC2) accounted for 21.76%. Cumulatively, these two PC explained 63.32% of the total variation for grain yield (Figures 1 and 2). The polygon in Figure 1 is formed by connecting the vertexes of the genotypes that are farthest away from the biplot origin, such that all other genotypes are contained in the polygon. The polygon contains a set of lines perpendicular to each side of the polygon. These lines divide the biplot into several sectors. The vertex genotype in each sector represents the highest yielding genotype (the winning genotype) in the environment that falls within that particular sector (Yan

and Tinker, 2005; Yan et al., 2010). There are nine sectors in (Figure 1) with genotypes G1, G2, G3, G4, G6, G7, G9, and G10 as the vertex genotype. Environment E2 and E7 fell in the sector in which genotypes G3 and G4 were the vertices genotypes implying that genotypes G3 and G4 were the best genotypes for E2 and E7. Genotypes G1 and G2 were the highest yielding genotypes at E3, E5, and E15. Genotype G9 was the highest yielding in E4, E6, E8, E9, E10, E11, E12, E14, E16, and E17. Genotype G10 was best in E1 while genotypes G6 and G7 were the highest yielding in E19. No genotype was found as vertices and notably in the mega environment that environment 18 classified. Genotypes within the polygon of G5, G8, G11, G12, G13, G14, G15, and G16 were less responsive than the vertex genotypes. The nineteen environments fell into six sectors. This pattern suggests that the target environment may consisting cluster of six different testing environments and that different genotypes should be selected and deployed for each.

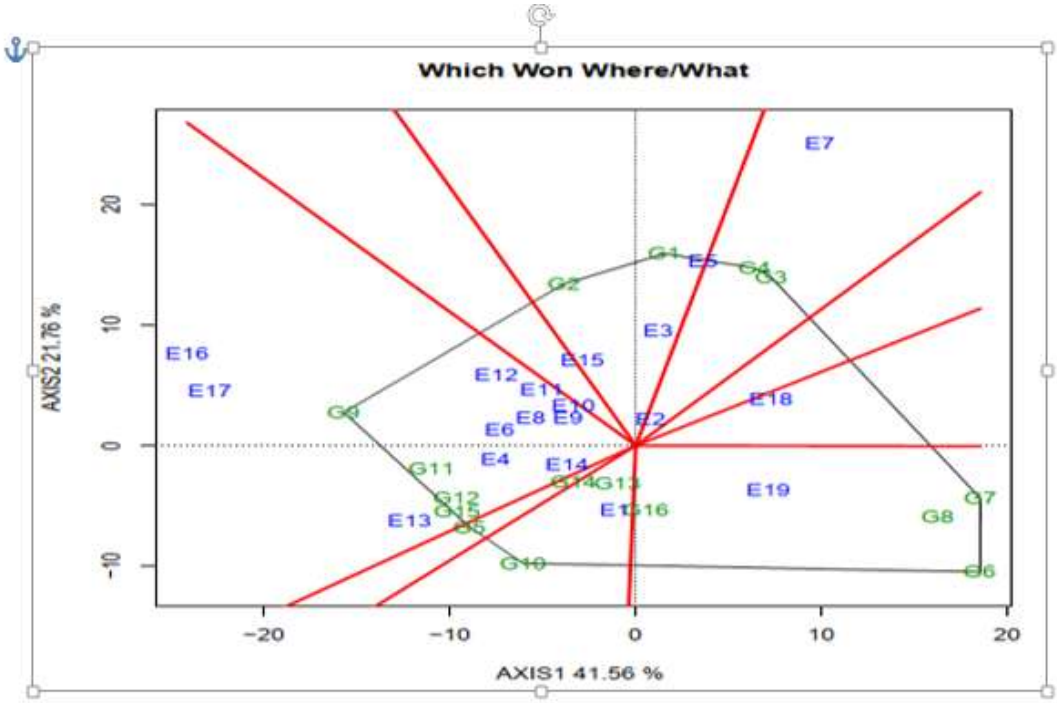

Figure 1. A "Which won where/what" of genotype × environment biplot of the 16 varieties

Mean vs. Stability

Using the stability GGE-biplot of grain yield for the 16 sesame varieties is shown in (Figure 2), the average-environment coordination (AEC) view of the GGE-biplot is depicted. The single arrowed line is the AEC abscissa (or AEA) and directs to higher mean yield across environments. The mean yield of the genotypes is estimated by the projections of their markers on the average-tester

axis. The genotypes were ranked along the average-tester axis (ATC abscissa), thus, 'G9' had the highest mean yield, followed by 'G2', 'G1', etc., whereas 'G6', 'G7' and 'G8' had the lowest mean yield. The AEC ordinate passes the plot origin and is perpendicular to the AEC abscissa and directs to greater variability (poorer stability) in either direction. The greater the absolute length of the projection of a genotype, the less stable it is. Thus, 'G3', 'G4' and 'G7' were highly unstable, whereas 'G13' 'G14', 'G16' were highly stable.

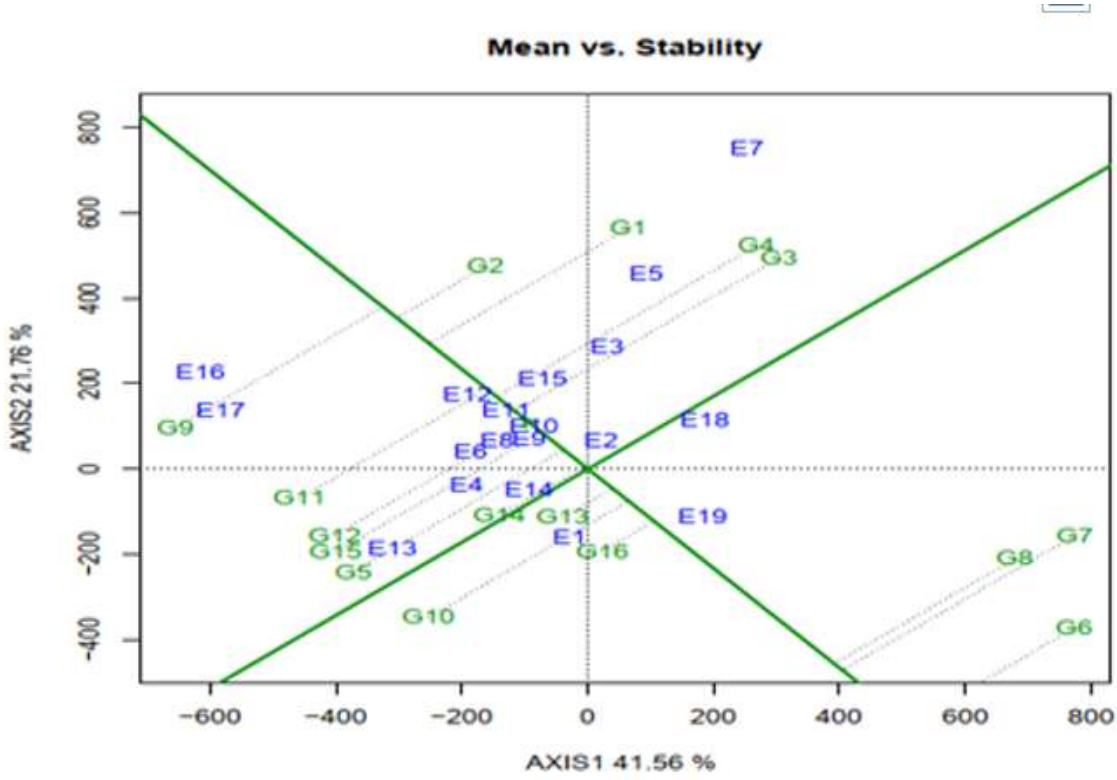

Figure 2. Average environment coordination (AEC) views of the GGE-biplot based on environment-focused scaling for the mean performance and stability of genotypes

Ranking test locations based on both discriminating ability and representativeness

Figure 3 presents the discriminating ability and representativeness of the test environment. The short-vector environments E1, E18, and E19 may be regarded as independent research environments and may be treated as unique and, therefore, essential research environments. In contrast, the long-vector test environments E5, E7, E13, E16, and E17 were more powerful in discriminating among the cultivars. Environments E5, E7, and E13 had long vectors and large angles with the AEC abscissa suggesting that they may not be used in selecting superior genotypes but may be used in culling unstable genotypes. Additionally, the distance between two

test environments measures their dissimilarity in discriminating the genotypes, and the presence of close associations among test environments recommend that the same information can be obtained from the fewer environments and this will save the testing cost. In the present study E2 and E7 and testing environment E9, E10, E11, and E12 and similarly, test environment E4, E13, and E14 as well as test environment E3 and E5 were closely associated, confirming that these environments produced similar information about the genotypes and thus implying that promising genotypes in this study selected in one of these environments will also be suitable for production in the other environment. Hence, the testing environment can be dropped in this case.

The ability of an environment to identify an ideal test environment is referred to as the discriminating power of an environment (Badu-Apraku et al., 2012) and the distance between the markers of the environment to the biplot origin, is a measure of its discriminating ability (Frutos et al., 2014). The ability of a test environment to represent the mega-environment is referred to as the representativeness (Badu-Apraku et al., 2012) and the magnitude of the projection from the marker of the environment onto the average environment coordinate (AEC) axis is the measurement of its representativeness (Frutos and Leiva, 2014). According to Yan and Tinker (2005), The small circle indicates the average-environment axis (AEA), and the arrow pointing to it is used to indicate the direction of the AEA (Yan and Tinker, 2005). Test environments having small angles with the AEA are more representative of the environment than those having large angles with it. Environments with longer vectors are more informative compared to those with shorter vectors and give more information about the genotypes. Therefore, Environments with shorter vectors could be excluded when choosing test environments since they give little information about the genotypes. Test environments with shorter environmental vectors indicate a weak correlation with test environments with longer vectors. Test environments with small angles and long vectors with the AEC abscissa are ideal for identifying the best genotypes while test environments with large angles and long vectors with the AEC abscissa are useful in culling unstable genotypes (Yan et al., 2010).

The discriminative-ness versus representativeness biplot (Figure 3) strongly suggests, E7 from E2, and E12 among environments E9, E10, and E11, and E13 from Environments E4, E13, and E14, as well as E5 from Environment E3, were better discriminating and representative environments.

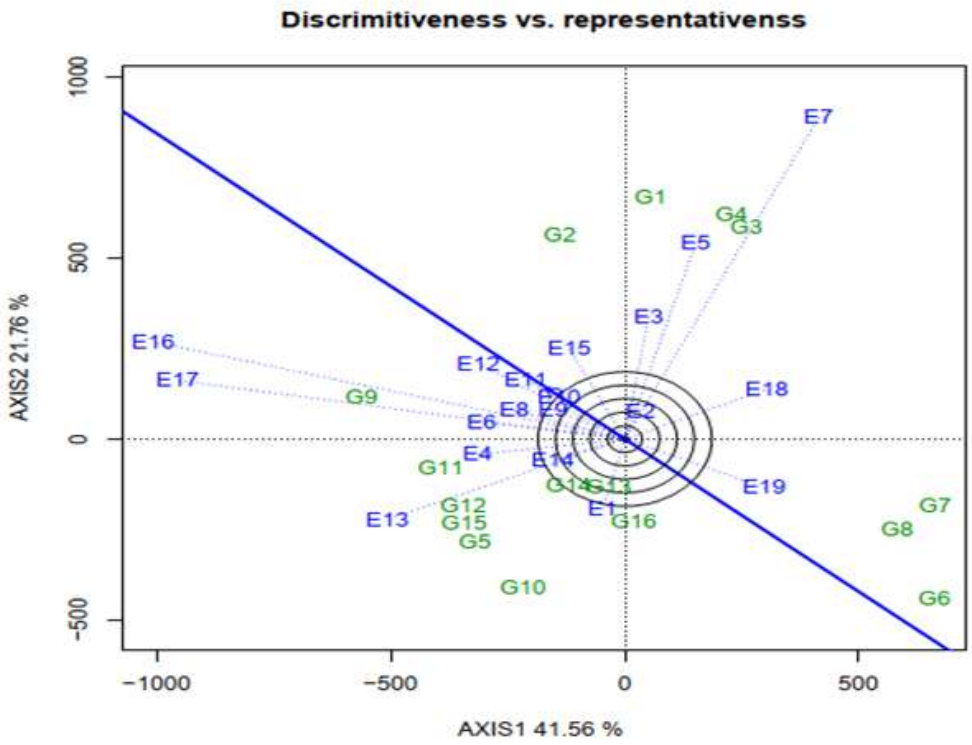

Figure 3. The discriminating ability and representativeness of the test environments

Evaluation of Varieties Based on the Ideal Genotype

In the present study G2 (setit-1) was the "ideal" genotype, since it located in the first concentric circle in the biplot. An ideal genotype has the highest mean seed yield and is stable across locations (Farshadfar et al. 2012). The ideal genotype can be used as a benchmark for selection. Desirable genotypes are those located close to the ideal genotype (Yan and Tinker, 2006), while genotypes far from the ideal genotypes were undesirable. Humera-1 was plotted to the ideal genotype considered as desirable genotype, while G6 (ADI), G7 (TATI) and G8 (Acc-051-02-sel 1 (2)) were low yielding genotypes associated with genotypic undesirable (Figure 4). 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.

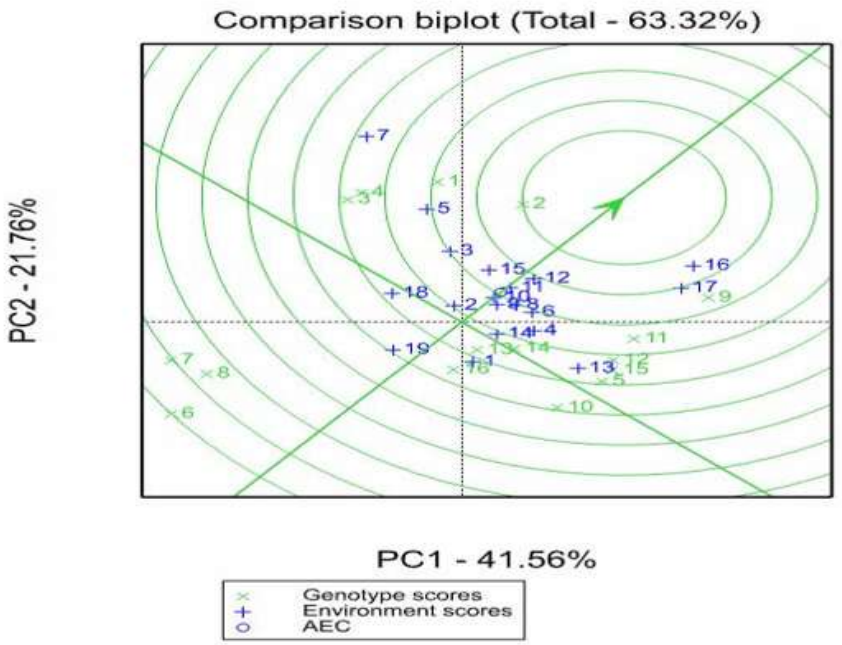

Figure 4. GGE-biplot showing the "ideal" genotype

Evaluation of Environments based on the Ideal Environment

Environment E16 and E17 were close to the ideal environment (Figure 5), therefore, it should be regarded as the most suitable to select widely adapted genotypes. E19, E18, and E7 were far from the ideal environment and considered as undesirable.

The ideal environment is representative and has the highest discriminating power (Yan and Tinker, 2006). Similar to the ideal genotype, the ideal environment is located in the first or near to the first concentric circle in the environment-focused biplot, and desirable environments are close to the ideal environment.

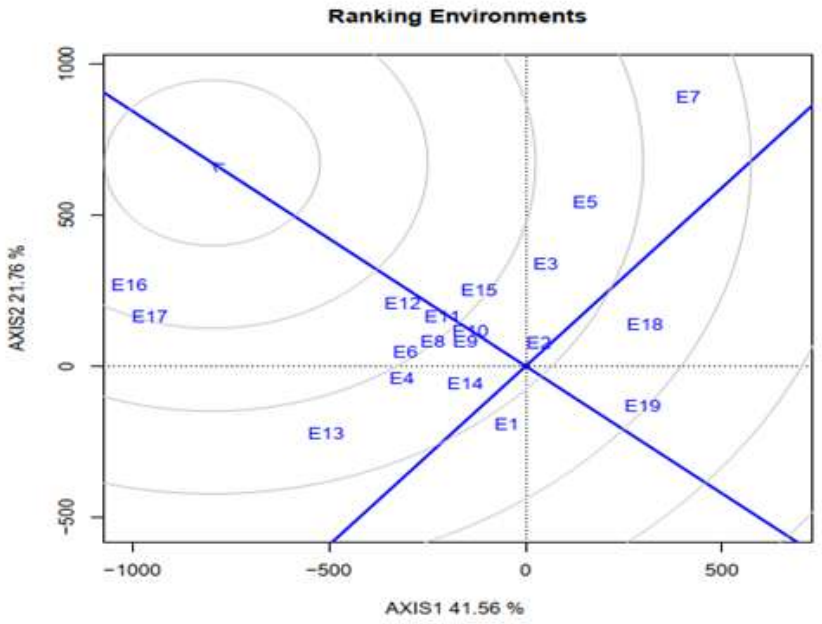

Figure 5. GGE-biplot showing the "ideal" environment

Conclusion and Recommendations

The present experiment showed the performance of sesame varieties was different in different environments due to the existence of large VEI. The existence of different winner genotypes in different environments complicates the selection process and national varieties recommendation in the breeding programs. The VEI analysis results suggested sesame producing environment in Ethiopia is classified into six mega-environments and that different genotypes should be selected and deployed for each. Overall Obsa had the highest mean yield, followed by Setit-1, on the other hand, Setit-1, MECHAL, BENSHANGUL-1, BAHA ZEYT were highly stable genotypes. Setit-1 was the "ideal" genotype in terms of yields and stability across variable environments. Hence, it is the most desirable genotype reliably recommended for farmers' for ultimate use. It can also be utilized as source material for future sesame breeding that targets high-yielding and stable genotypes. Based on the test environment, consistently Environment E16 (Tach Armacho 2017/18) and E17 (Tach Armacho 2018/19) were close to the ideal environment, therefore, it could be regarded as the most suitable to select widely adapted genotypes. The findings of this study provide useful information for sesame breeding and commercialization in Ethiopia.

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