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Graphical presentation for describing yield stability in sesame

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Abstract
The presence of genotype × environment (G × E) interaction is a main challenge to plant breeders, since large interaction could reduce earning from selection and complicate the identification of superior genotypes. This investigation aimed to identify the superior sesame genotypes with both mean performance and response to improving environment and high stability besides, to compare between the applications of graphical presentation by AMMI and GGE biplot analyses to determine high yielding and stable genotypes. Twenty sesame genotypes were grown in a randomized complete block design with three replications during four summer seasons (2014 through 2017) in three locations (Shandaweel, El-Mtaana and Al-Eweinat). Results showed significant mean squares for genotypes, environments and (G × E) interaction indicating that the tested genotypes showed different responses to the environmental conditions. Pooled analysis showed that 30.20% of the total sum of squares was attributed to environment while the genotype and GxE interaction items explained 37.36% and 11.19%, respectively. Using Additive Main Effect and Multiplicative Interaction (AMMI) method, the highest seed yield and stable genotypes were N.A.310-2 (G15), N.A.308 (G18), N.A. 167 (G8), H104 F2-7 (G3), and H102 F2 (G1). The GGE biplot suggested the existence of two mega-environments including seven and five environments with wining genotypes G13 (N.A.245-2) and G16 (N.A.497), respectively. According to mean vs. stability graph, N.A.310-2 (G15), N.A. 128 (G5), H102 F2 (G1), H106 F4 (G4) and N.A. 153 (G6) were better genotypes demonstrating higher seed yields and higher stability of performance across the tested locations. Concerning the discriminating power vs. representativeness graph, it is observed that Environment (E2) (Representative as ideal environment) is ideal for selecting superior genotypes. On the other hand, E3 could be useful in selecting unstable genotypes.

Keywords: SESAME, (*Sesamum indicum* L.), AMMI and GGE biplot analyses, AMMI stability value (ASV).

Introduction
Sesame is used by humans as a food. This important annual oilseed crop has been cultivated for centuries, particularly in the developing countries of Asia and Africa, for its high content of both excellent quality of edible oil (42– 54%) and protein, (22 to 25%) (Desphande *et al* 1996 and Anilakumar *et al* 2010) [3, 1].

Sesame seed is one of the world's most important and oldest oil seed crops known to man. The genus Sesamum is a member of the Pedaliaceae family, which contains 16 genera and 60 species (Pathak *et al* 2014) [21].

The adaptability of a genotype over diverse environments is an important target in most breeding programs. A genotype is considered to be more adaptive or stable if it has a high mean yield but low degree of fluctuation in yielding ability when grown across diverse environments. When the genotypes are consistently responding to variable environmental conditions, this is attributed to the magnitude of the genotype x environment interaction (GEI). Knowledge of GEI is advantageous to have a cultivar that gives consistently high yield in a broad range of environments and to increase efficiency of breeding program and selection of superior genotypes (Mohammed *et al* 2015) [17].

Several methods have been proposed to analyze GEI or phenotypic stability. These methods could be divided into two major groups, univariate and multivariate stability statistics. Joint-regression is the most popular among univariate methods because of its simplicity of calculation and application, whereas Additive Main Effect and Multiplicative Interaction (AMMI) is a multivariate approach, gaining popularity and is currently the main alternative to joint-regression model in many breeding programs.

It is widely used for G x E investigation of multi environment cultivar traits (Laurentin and Montilla 1999) [13].

Thus, (AMMI) (Gauch and Zobel 1996) [6] allows a more detailed evaluation of the genotypes x environment interaction. Also, it is relatively simple, making it possible to study the stability behavior of genotypes, as well as inferring the degree of divergence between cultivars and environments under evaluation.

The genotype x environment interaction is of high importance. It gives information about the impact of different environments on genotype performance and has an important role in assessing stability of breeding materials (Moldoven *et al* 2000 and Mortazavian *et al* 2014) [19].

Genotypic main effect plus genotype by environment interaction GGE-biplot display both G (Cultivars) and GE (interaction among environments and cultivars), which are the two sources of variation that are relevant to cultivar evaluation (Gauch and Zobel 1996a, [6] and Yan and Kang 2003) [28]. The analysis of GGE-biplot is used because it has the ability to graphically better explain the cultivars and cultivars by environment components of variance. It is of higher efficient tool in discriminating cultivars and environments (Yan *et al* 2007) [30].

Yan (2001) [29] reported that the GGE biplot helped to investigate: (1) ranking the cultivars based on their performance at any given environment, (2) ranking the environments based on the relative performance of any given cultivar, (3) comparing the performance of any pair of cultivars in different environments, (4) identifying the best cultivar in each environment, (5) grouping the environments based on the best cultivars, (6) evaluating the cultivars based on both average yield and stability, (7) evaluating the environments based on both discriminating ability and representativeness, and (8) visualizing all of these aspects for a subset of the data by removing some of the cultivars or environments. GGE biplot has been applied to visual analysis of genotype × environment data. Therefore, GGE biplot is widely used by plant breeders to analyze mega environment evaluation and ranking genotypes.

AMMI and GGE models help to understand complex genotype by environment (G × E) interactions, and determine which genotype has been in which environments, also help when grouping environments with the similar winners into mega environments (Pourdad and Moghaddam 2013) [23].

The goal of this study was to identify the superior sesame genotypes with both mean performance and high stability, and to compare between the application of the AMMI and GGE biplot analyses to determine sesame high yielders and more stable.

Materials and Methods

Experimental design and plant materials

Nineteen promising genotypes of sesame and one check cultivar (Shandaweel 3) were planted in the four summer seasons of 2014, 2015, 2016 and 2017, at the agriculture research stations of Shandaweel, El-Mtaana and Al-Eweinat. The aim of the study was to identify the superior sesame genotypes regarding mean performance and high stability. Sesame genotypes were planted in a randomized complete block design (RCBD) with three replications. The details of tested genotypes are shown in Table 1. Sowing was done by hand in rows 4 m long and 50 cm apart and 20 cm between plants. The plot area was 4 x 2.5 m = 10 m^2. In all experiments, weeds were controlled by hand as needed. All other cultural practices were done as recommended.

Recorded variables

At harvest, the plants of each plot were harvested to measure seed yield in kilograms per plot. which was adjusted to calculate yield in ardab per feddan (ardab = 120 kg and one feddan = 4200m^2).

Statistical analysis

Regular analysis of variance of RCBD as outlined by Gomez and Gomez (1984) [9] was separately conducted for each environment. The homogeneity of individual variances was verified using Bartlett test (1937) [2] prior to the combined analysis. Accordingly, the combined analysis of variance across twelve environments was worked out. The detection of significant interaction between genotypes and environments (GxE) helps us to discover the stability of yield performance for the tested genotypes.

Table 1: The details of the studied sesame genotypes under study

Genotypes				Main description			
N	**Name**	**Origin**	**No. of capsules / leaf axel**	**Branching habit**	**Seed color**	**Shattering**	**Tolerant for welting disease**
1	H102F2	Egypt	Three	Non branched	Brown	Indehiscent	Tolerant
2	H102F46	Egypt	Three	Non branched	Brown	Dehiscent	Susceptible
3	H104F7-2	Egypt	Three	Non branched	Brown	Dehiscent	Susceptible
4	H106F4	Egypt	Three	Non branched	Brown	Indehiscent	Tolerant
5	Local128	AlfaYom	Single	Branched	White	Dehiscent	Tolerant
6	Local153	Al- Sharqia	Single	Branched	White	Dehiscent	Susceptible
7	Local156	Al- Sharqia	Single	Branched	Creamy	Indehiscent	Tolerant
8	Local167	Al- Sharqia	Single	branched	Brown	Indehiscent	Susceptible
9	Local219	Al- Sharqia	Single	branched	White	Dehiscent	Susceptible
10	N.A.550	FAO	Three	branched	White	Dehiscent	Tolerant
11	N.A.612	Greece	Three	branched	Brown	Indehiscent	Tolerant
12	H436	Egypt	Three	branched	Brown	Indehiscent	Tolerant
13	N.A.245	Ethiopia	Single	Non branched	Brown	Dehiscent	Tolerant
14	N.A.288	Egypt	Single	branched	White	Dehiscent	Tolerant
15	N.A.310	U.S.A	Three	Non branched	White	Indehiscent	Tolerant
16	N.A.497	INDIA	Single	branched	Brown	Indehiscent	Tolerant
17	Local127	AlfaYom	Single	Non branched	White	Dehiscent	Susceptible
18	N.A.308	U.S.A.	Single	branched	Brown	Indehiscent	Tolerant
19	N.A.355	U.S.A	Single	branched	Brown	Indehiscent	Tolerant
20	Shandaweel3	Local variety	Three	Non branched	White	Indehiscent	Tolerant

Stability analyses

Two graphical and visual analyses were applied to identify the stable genotypes to be incorporated in the sesame breeding programs. The first method was Additive Main Effects and Multiplicative Interaction (AMMI) and the second one was Genotypic Main Effect plus Genotype by Environment interaction (GGE biplot).

AMMI model can be written using the formula:

$$Y_{ij} = \mu + g_i + e_j + \Sigma \lambda_k \gamma_{ik} \delta_{jk} + \varepsilon_{ij},$$

Where Y_{ij} is the yield of i-th genotype in the j-th environment; μ is the grand mean; g_i and e_j are the deviations of genotype and environment from the grand mean, respectively. λ_k is the eigenvalue of the principal component analysis (PCA) for axis k; γ_{ik} and δ_{jk} are the genotype and environment principal components scores for axis k; N is the number of principal components in the AMMI model; ε_{ij} is the residual term. Genotype and environment PCA scores are expressed as unit vector times the square root of λ_k (genotype PCA score $=\lambda_k \delta_{ik}$, environment PCA score$=\lambda_k$,). To interpret G x E interaction, correlation analysis was conducted between genotypic and environmental scores of the first and second interaction principal component axes (IPCA1 and IPCA2) from the AMMI model, (Gauch and Zobel 1997) [8].

AMMI stability value of the i^{th} genotype (ASV_i) was calculated for each genotype and each environment according to the relative contribution of $IPCA_1$ to $IPCA_2$ to the interaction SS according to Purchase *et al* (2000) [24] as follows:

$$ASV = \{[(SSPC1/SSPC2)\ (GPCA_1\ score)]^2 + (GCPA_2\ scores)^2\}\ ½$$

Where; ASV = the distance from zero in a two dimensional scatter diagram of $IPCA_1$ against $IPCA_2$. $SSPC_1/SSPC_2$ is the weight given to the $IPCA_1$-value by dividing the $IPCA_1$ sum of squares by the $IPCA_2$ sum of squares.

Based on the rank of mean seed yield of genotypes (RY_i) across environments and rank of AMMI stability value ($RASV_i$) a selection index called Genotype Selection Index (GSI) was calculated for each genotype, which incorporates both mean seed yield (RYi) and stability index in a single criteria (GSIi) as (Farshadfar 2008) [4]:

$$GSIi = RYi + RASVi$$

Environmental index (Ij) was obtained by the difference between the mean of each environment and the general mean.

The GGE-biplot method as outlined by Yan *et al* 2000 [26] was used to analyze the genotype by environment interaction of yield. The biplot model can be written as follows:

$$Y_{ij} - Ý_j = \lambda 1\ \xi i1\ \eta j1 + \lambda 2\ \xi i2\ \eta j2 + \varepsilon_{ij}$$

where Y_{ij} is the average yield of a genotype (i) in an environment (j), Ýj is the average yield over all genotypes in an environment (j), $\lambda 1\ \xi i1\ \eta j1 + \lambda 2\ \xi i2\ \eta j2$ are collectively called the first principal component (PC1) and the second principal component (PC2); $\lambda 1 + \lambda 2$ are the singular values for the first and second principal components, PC1 and PC2, respectively. $\xi i1 + \xi i2$ are the PC1 and PC2 scores respectively, for genotype i; $\eta j1 + \eta j2$ are the PC1 and PC2 eigenvectors, respectively, for environment j, and ε_{ij} is the residual of the model associated with the genotype i in environment j. GGE-biplot is constructed by plotting the PC1 scores against the PC2 scores for each genotype and each environment.

Results and Discussion

Analysis of variance

As shown in Table (2) and Fig (1), the test of homogeneity using Bartlett and Levene methods, (Bartlett, 1937) [2] and (Levene, 1960) indicated no evidence for heterogeneity among error terms across environments which enable us to run combined analysis. The regular combined analysis of variance for seed yield of the 20 sesame genotypes (G) evaluated across 12 environments (E) and their (GxE) interaction is presented in Table (2). The results indicate that the main effects of genotypes, environments and their interaction (GxE) were highly significant ($P<0.01$). On the other hand, the pooled analysis showed that 30.20% of the total sum of squares was attributed to environment while the genotype and GxE interaction effects explained 37.36% and 11.19%, respectively (Table 2). The large percent of sum of squares corresponding to the environment term indicating substantial differences among tested environments. However, the ratio of the sum of squares for genotype item were nearly three times the share of interaction effect indicating wide genetic variation among the tested environments. The highly significant interaction effect gives another justification to discuss the genotype stability. However, the results showed that the value of coefficient of variation (CV% = 11.94) was located at the statistically acceptable range for seed yield (Table 2). Mohammadi *et al* (2012) [16], Pathak *et al* (2014) [21] and Yirga (2016) [31] found significant GxE interaction indicating that the sesame genotypes fluctuated in their rank performance for seed yield across the tested environments.

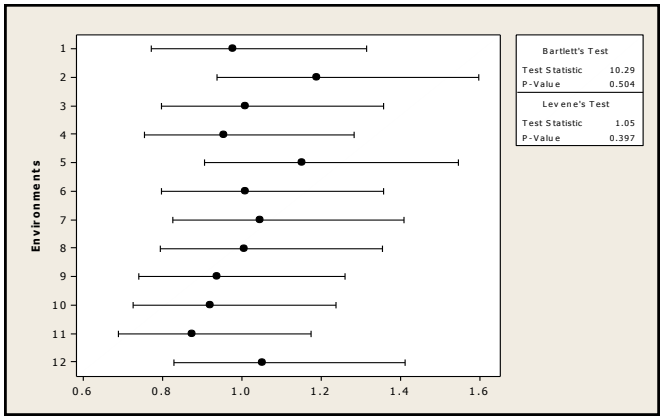

Fig 1: Test of heterogeneity among individual error terms across the tested environments using Bartlett and Levene methods.

Table 2: Regular combined analysis of variance and partitioning the proper source of variation according AMMI and Biplot models

Source of variation	DF	SS	%	MS
Environments (Env)	11	314.81	30.20	28.62**
Rep/Env	24	67.19		
Genotype (G)	19	389.35	37.36	20.49**
E X G	209	116.61	11.19	0.56**
Error	456	154.30	14.80	
Total	719	1042.26		
AMMI model				
E X G	209	116.61	100	0.56**
PC 1	29	35.4	30.36	1.22**
PC 2	27	20.2	17.32	0.75**
Residual	153	60.9	52.23	0.4 NS
Test of homogeneity				
Bartlett test	10.29 NS			
Levene test	1.05 NS			
Coefficient of variation (CV%)	11.94			

NS and **: no significant and highly significant at 0.01 probability level, respectively.

Mean performance

Mean performance of genotypes across the tested environments are presented in Table (3). The average environmental seed yield across genotypes ranged from the lowest value of (3.66 ardab/fed.) in Alewinat 2016 to the highest value of (5.90 ardab/fed.) in Shandaweel 2017. Generally, the highest seed yield were recorded by El-Mtaana (5.25 ardab/fed.) followed by Shandaweel (5.22 ardab/fed.) and Alewinat (4.14 ardab/fed.). The mean seed yield of sesame genotypes across environments varied from 3.72 ardab/fed for genotype G11 to (6.06 ardab/fed.) for G16, with an overall mean of 4.87 ardab/fed. The results in Table (3), revealed differential performance of genotypes across the tested environments, indicating the existence of genotype environment interaction. Further stability analysis has to be carried out to identify a genotype which is stable and had high mean yield across environments.

Table 3: Mean values of seed yield (ardab/fed) of twenty sesame genotypes evaluated across three locations during the four summer seasons of 2014–2017 (representing 12 environments).

Genotype		Environment												Mean
		Shandaweel				EL Mataana				East El Ewienat				
		2014 E1	2015 E2	2016 E3	2017 E4	2014 E5	2015 E6	2016 E7	2017 E8	2014 E9	2015 E10	2016 E11	2017 E12	
H102 F2	G1	4.60	5.50	5.97	6.47	6.03	4.73	5.93	6.43	5.30	4.60	4.23	5.97	5.48
H102 F46	G2	5.13	5.07	4.67	6.00	4.27	4.53	4.00	5.63	5.13	3.20	3.67	4.50	4.65
H104 F2-7	G3	4.03	4.03	3.97	4.93	4.47	4.17	4.40	4.70	3.53	2.70	2.47	4.17	3.96
H106 F4	G4	5.10	5.53	5.67	6.27	5.13	4.97	6.27	6.23	4.10	4.60	3.97	5.67	5.29
N.A. 128	G5	5.33	6.07	6.03	6.33	6.27	5.47	6.03	6.30	4.67	3.83	4.03	5.47	5.49
N.A. 153	G6	5.60	6.13	5.80	6.00	6.07	6.00	6.07	6.20	4.57	4.00	3.93	4.47	5.40
N.A. 156	G7	5.10	4.70	4.23	5.40	4.83	5.10	4.87	5.13	4.60	3.43	2.77	4.43	4.55
N.A. 167	G8	4.73	4.67	4.60	5.87	5.10	4.17	5.00	6.33	4.10	3.80	3.73	4.17	4.69
N.A.219	G9	4.23	4.37	6.23	6.00	5.63	5.53	5.47	5.93	4.37	3.80	3.80	4.07	4.95
N.A.550	G10	4.93	4.53	4.10	5.33	4.40	4.63	4.80	5.13	3.93	2.53	3.10	5.13	4.38
N.A.612	G11	4.44	3.59	4.75	4.92	3.06	3.02	3.82	4.92	3.11	2.80	2.93	3.24	3.72
H36 F1	G12	3.49	4.36	3.99	5.36	4.47	3.67	3.78	5.63	3.85	2.73	2.73	2.79	3.91
N.A.245-2	G13	5.07	6.46	6.81	7.19	7.14	5.78	6.59	6.87	5.07	4.75	4.75	5.29	5.98
N.A.288-1	G14	5.80	4.47	4.47	6.50	5.60	5.60	5.97	6.13	6.13	4.17	4.17	5.50	5.38
N.A.310-2	G15	6.17	6.27	6.30	6.97	6.20	5.77	6.17	6.77	5.30	5.10	5.10	5.30	5.95
N.A.497	G16	6.40	6.47	6.13	6.73	5.97	6.10	6.20	6.83	5.90	5.00	5.13	5.83	6.06
N.A.127	G17	5.63	5.53	5.03	6.17	5.33	5.43	5.13	6.27	4.63	4.03	3.53	5.17	5.16
N.A.308	G18	4.25	3.29	4.84	4.91	3.89	4.62	4.03	4.91	3.81	2.90	2.64	4.14	4.02
N.A.355	G19	3.23	3.07	4.44	5.12	4.24	3.83	4.48	4.68	2.98	2.66	3.11	3.83	3.80
Shandaweel 3	G20	4.08	5.04	4.88	5.60	4.56	4.36	4.40	5.80	5.08	3.48	3.40	4.36	4.59
Mean		4.87	4.96	5.14	5.90	5.13	4.87	5.17	5.84	4.51	3.71	3.66	4.67	4.87
Location means		5.22				5.25				4.14				

MMI stability value (ASV)

AMMI Stability Value (ASV) and its respective rank for the twenty tested genotypes are presented in Table 4. Based on ASV parameter, a genotype with the least ASV is the most stable (Purchase *et al.*, 2000) [24]. Accordingly, the genotypes were found to be widely adapted and ranked (first to fifth) being, N.A.310-2 (G15), N.A.308 (G18), N.A. 167 (G8), H104 F2-7 (G3), and H102 F2 (G1), respectively.

The least values of Genotype Selection Index (GSI) are considered as the most stable with high seed yields (Farshadfar, 2008) [4]. Based on the GSI, results in Table (4) showed that the best genotypes for both stability and high seed yield were N.A.310-2 (G15), N.A.497 (G16), H102F2 (G1), N.A. 167 (G8), and H106 F4 (G4), respectively. It is noticed that GSI is nearly similar to AMMI stability value (ASV) in identifying stable genotypes. Thus, each one of the

two stability parameters ASV and GSI is considered as substitute for each other. Consequently, it is enough to use only one of them as stability parameter. For fast and easy visualization of high yielding and stable genotypes, the authors supposed to plot the mean seed yield on the horizontal axis (abscissa) against the ASV values on the vertical axis (ordinate) in one graph (Fig. 2).

The area under graph is divided into four classes representing the interrelationship between seed yield and stability parameter of (ASV). The upper left class contains the genotypes characterized by high yielding ability (more than the mean seed yield) and stability (low ASV values). Seven out of the twenty genotypes were located in this class namely: G15 (N.A.310-2), G16 (N.A.497), G1 (H102F2), and G4 (H106 F4), G6 (N.A. 153), G5 (N.A. 128) and G17 (N.A.127). In the upper right class, three genotypes being G13 (N.A.245-2), G14 (N.A.288-1) and G9 (N.A.219) were found to be unstable (high ASV value) but they had high seed yield (more than the mean seed yield). Also, in the opposite side at the bottom, four genotypes (G7 (N.A. 156), G2 (H102 F46), G12 (H36 F1), and G10 (N.A.550) occupied the lower right class having high ASV values (unstable) and poor seed yield. Six genotypes fall in the lower left class, G8 (N.A. 167), G20 (Shandaweel3), G18 (N.A.308), G3 (H104 F2-7), G11 (N.A.612) and G19 (N.A.355). They have low ASV value and lowest seed yield. According to the stability measures ASV and GSI, G15 (N.A.310-2), G1 (H102F2) and G8 (N.A. 167) were selected as high seed yielding and most stable genotypes.

The merits of the supposed graph over each of ASV and GSI were:

1- The graph shows the high yielding ability and proper stability in the same time.
2- It is a fast, easy and effective tool to facilitate the decision making about the high yielder and stable genotypes.

There are some disadvantages of GSI as a stability parameter. One of them is the non-parametric concept of GSI parameter. Also, the complementary relationship between the two components of GSI (rank of mean seed yield and the rank of ASV) may be considered the other one. For example, although genotype G8 had a seed yield lowers than the grand mean; it was stable considering GSI statistic due to their stability proper. So, the stability parameter of GSI may be less effective compared to the supposed graph. Piepho (1996) [22] reported that the non-parametric models of stability would be used when the necessary assumptions for the parametric stability models are violated. These findings are in harmony with the result of Zeleke and Sentayehu (2017) [32], Hagos and Fetien (2011) [10], Zenebe and Hussien (2010) [33] and Fiseha *et al* (2015) [5] Mekonnen *et al* (2015) [15] in sesame.

GGE Bi-plot in sesame yield Data

Yan (2001) [29] reported that the GGE biplot is a data visualization tool, which graphically displays a GxE interaction in a two way table. Also, it is an effective tool for describing three different types of graphs as follows:

1) Mega-environment analysis (e.g. "which-won-where" pattern), shows specific adaptability of genotypes that can be recommended to specific mega-environments (Yan and kang 2003) [28] and (Yan *et al* 2007) [30].

2) Genotype evaluation (the mean performance vs. stability), which ranked the genotypes for general stability.

3) Environmental evaluation (the power to discriminate among genotypes in target environments). Several researchers automated the three aforementioned graphs in their investigations on sesame crop, among them, Munawar *et al* (2013) [20], Fiseha *et al* (2015) [5], Kang *et al* (2015) [11], Mekonnen *et al* (2015) [15], and Walter *et al* (2016).

Table 4: AMMI stability value (ASV) and its corresponding rank for the twenty tested genotypes.

Genotype		Mean	RY_i	IPCA [1]	IPCA [2]	ASV_i	$RASV_i$	GSI
H102 F2	G1	5.48	5.00	0.263	0.043	0.463	5	10.00
H102 F46	G2	4.65	12.00	-0.629	-0.598	1.254	18	30.00
H104 F2-7	G3	3.96	17.00	-0.115	0.382	0.432	4	21.00
H106 F4	G4	5.29	8.00	0.232	0.323	0.520	7	15.00
N.A. 128	G5	5.49	4.00	0.309	0.330	0.634	12	16.00
N.A. 153	G6	5.40	6.00	0.292	0.247	0.569	10	16.00
N.A. 156	G7	4.55	14.00	-0.482	0.321	0.904	15	29.00
N.A. 167	G8	4.69	11.00	0.101	-0.343	0.386	3	14.00
N.A.219	G9	4.95	10.00	0.677	0.095	1.190	17	27.00
N.A.550	G10	4.38	15.00	-0.514	0.506	1.033	16	31.00
N.A.612	G11	3.72	20.00	-0.012	-0.575	0.575	11	31.00
H36 F1	G12	3.91	18.00	0.202	-0.708	0.792	14	32.00
N.A.245-2	G13	5.98	2.00	0.838	0.038	1.469	20	22.00
N.A.288-1	G14	5.38	7.00	-0.799	0.269	1.426	19	26.00
N.A.310-2	G15	5.95	3.00	0.131	-0.225	0.322	1	4.00
N.A.497	G16	6.06	1.00	-0.266	-0.120	0.481	6	7.00
N.A.127	G17	5.16	9.00	-0.294	0.079	0.522	8	17.00
N.A.308	G18	4.02	16.00	-0.187	0.187	0.378	2	18.00
N.A.355	G19	3.80	19.00	0.388	0.255	0.726	13	32.00
Shandaweel3	G20	4.59	13.00	-0.136	-0.506	0.559	9	22.00

RY_i =rank in yield, IPCA1, 2= interaction principal component 1 and 2, ASV_i= AMMI stability value, $RASV_i$= rank of AMMI stability value, GSI= genotype selection index.

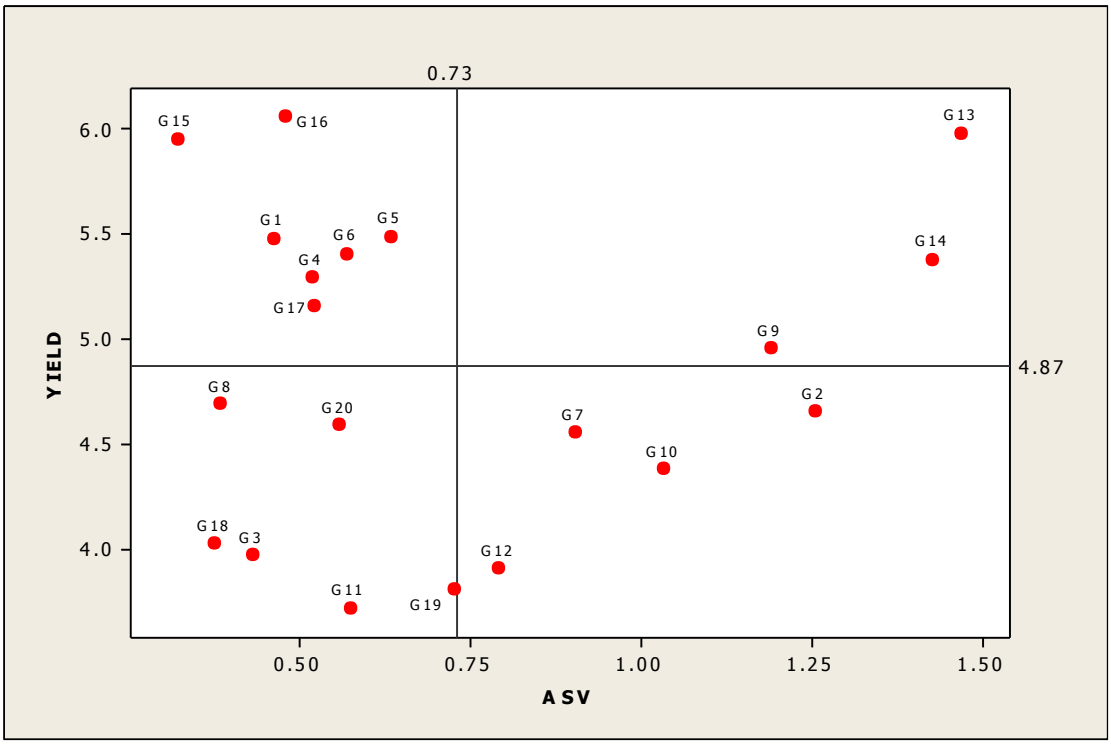

Fig 2: AMMI stability value (ASV) for the twenty sesame tested genotypes.

"Which-won-where" pattern of GE interaction in sesame yield data

GGE biplot analysis displays the main effect of genotypes (G) and genotype by environment interactions (GE) which are the most important sources of variation for genotypes evaluation in multi environment trials of the twenty tested sesame genotypes. Analysis of GGE biplot produces best polygons to view the GE interaction pattern (Yan and Kang 2003) [28]. Visualization of the pattern in the polygon view is helpful to estimate possible existence of different mega-environments in the target environment (Yan *et al* 2000 and Yan and Tinker 2006) [26, 27]. The "which-won-where" view of the GGE biplot (Yan *et al* 2000) [26] is an effective visual tool in mega-environment analysis.

Yan *et al* 2007 [30] reported that an irregular polygon and a set of lines drawn from the biplot origin and intersecting each of the sides at right angles. The vertices of the polygon are the genotype markers located farthest away from the biplot origin in various directions, such that all genotype markers are contained within the resulting polygon. A line that starts from the biplot origin and perpendicularly intersects a polygon side represents the set of hypothetical environments in which the two cultivars defining that side perform equally; the relative ranking of the two cultivars would be reversed in environments on opposite sides of the line. Therefore, perpendicular lines to the polygon sides divide the biplot into sectors, each having its own winning cultivar. The winning cultivar for a sector is the vertex cultivar at the intersection of the two polygon sides whose perpendicular lines form the border of that sector; it is positioned usually.

The results of a pattern of "which-won-where" of a biplot (Fig. 3) provides a good visual assessment of GGE with PCA1of 78.09% and PCA2 of 6.78% explaining 84.78% of the total GE sum of squares indicating goodness of fit of the graph.

Connecting the genotypes on a GGE biplot forms an irregular polygon and the perpendicular exactly upright lines to the sides of the polygon divide it in seven sectors of the 20 tested genotypes and 12 studied environments.

Environments that fall in different sectors have different best genotypes (Gauch and Zobel 1996b [7] and Kaya *et al* 2002 [12] and Yan *et al* 2007 [30]).

Based on the data obtained the twelve environments (three locations and four seasons) used in this study, two mega-environments were determined as all environments were located in two sectors. Two mega environments with different winning cultivars produced in Fig. 3. The first mega environment includes environments E3, E5, E7, E10, E11, E4 and E8 while the second mega environment includes E2, E6, E12, E9 and E1.

Genotypes located near the biplot origin are less responsive to the change of environments i.e., they showed small interaction.

G13 (N.A.245-2) the vertex genotype in this investigation winner was the highest yielding at E3, E5, E7, and E8. G16 (N.A.497) was the highest yielding genotype winner in the other environments (E6, E12, E9, and E1, E2).In this regard, the best genotypes were G9 (N.A.219), G13 (N.A.245-2), G15 (N.A.310-2), G4 (H106 F4), G5 (N.A. 128), G6 (N.A. 153) and G16 (N.A.497) where they are on the right side of the polygon in some environments by contrast, the poorest genotypes were G19 (N.A.355), G11 (N.A.612) and G10 (N.A.550) in all environments since they had the greatest distance away from the origin of the biplot as reported by Yan and Kang (2003) [28]. These results are similar to those are Mekonnen *et al* (2015) [15], Walter *et al* (2016) [25] and Yirga (2016) [31].

Ranking of sesame genotypes based on yield and stability performance

The view (mean *vs.* stability) is a powerful tool for visual evaluation of genotypes based on their mean performance and stability across environments at the same time.

The straight line with a single arrow (abscissa) passes through the biplot origin refers to average environment

coordinate (AEC), (Fig. 4). The arrow direction points to higher mean performance for genotypes. The small circle that spotted on this line represents the average of environment PC1 and PC2 scores. It is defined by the average coordinates of all test environments in the biplot. However, the other line (ordinate) passes through the biplot origin and is perpendicular to the AEC line indicates that the stability is proper. Thus, a genotype located closer to AEC line in the two directions had more stable yield and vice versa.

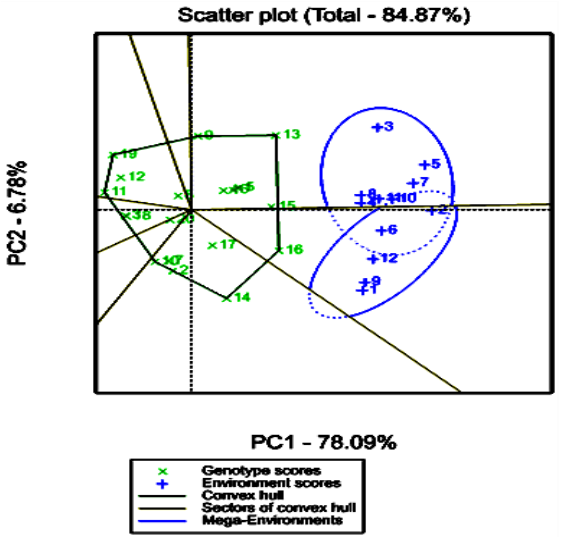

Fig 3: GGE biplot identification of winners from twenty sesame genotypes and their related mega-environments.

Ten out of the twenty genotypes located in the right side of the origin point indicating that their seed yields surpass the above-average mean. These genotypes in a descending order, were ranked as follows: N.A.497 (G16) > N.A.245-2 (G13) > N.A.310-2 (G15) > N.A. 128 (G5) > H102 F2 (G1) > N.A. 153 (G6) > N.A.288-1 (G14) > H106 F4 (G4) > N.A.127 G17 > N.A.219 (G9), whereas the remaining genotypes had below-average mean yield and located in the left side of origin point, (Fig.3).

Concerning the stable genotype regardless the yield, ten genotypes located very close to AEC line being N.A.310-2 (G15), N.A. 128 (G5), H102 F2 (G1), H106 F4 (G4), N.A. 153 (G6), N.A. 167 (G8), Shandaweel3 (G20), H104 F2-7 (G3), N.A.308 (G18) and N.A.612 (G11) reflecting their above average stability while the other genotypes exhibited average stability because they were placed away from AEC abscissa. It is observed that each of N.A.497 (G16) and N.A.245-2 (G13) were the highest yielding genotypes but they were less stable while N.A.612 (G11) was not stable and it was extremely poorly yielded (the last yielding genotype).

It could be concluded that N.A.310-2 (G15), N.A. 128 (G5), H102 F2 (G1), H106 F4 (G4) and N.A. 153 (G6) were characterized by high-yielding performance and were among the most stable genotypes. The current results are in a parallel line with those obtained by Yirga (2016) [31], Munawar *et al* (2013) [20], Fiseha *et al* (2015) [5], Kang *et al* (2015) [11], Mekonnen *et al* (2015) [15], and Walter *et al* (2016) [25].

Often, GGE biplot graph is clear and understandable when few genotypes and environments are used. When many genotypes and environments are used, this graph become so crowded that can be difficult to visualize and interpret.

Test of environments (discriminating power vs. representativeness)

The objective of test-environment evaluation is to identify test environments that effectively discriminated the excellent genotypes for a mega-environment. An "ideal" test environment should be selected for discriminating of the genotypes and representative of the mega-environment. This graph (discriminating power vs. representativeness) is based on environment-focused scaling. This type of average environment coordination (AEC) could be referred to as the "Discriminating power vs. Representativeness" view of the GGE biplot. Test environments could be used to explain the following:

Test environments may be classified into some kinds or types, type (1) useless environment that has short vectors and provides little or no information about the genotypes and, therefore, should not be used as test environments; representative environments have long vectors and small angles with the AEC abscissa and are ideal for selecting superior genotypes. If budgetary constraints allow only a few test environments, representative environments are the first choice. Not representative environments (type 3) have long vectors and large angles

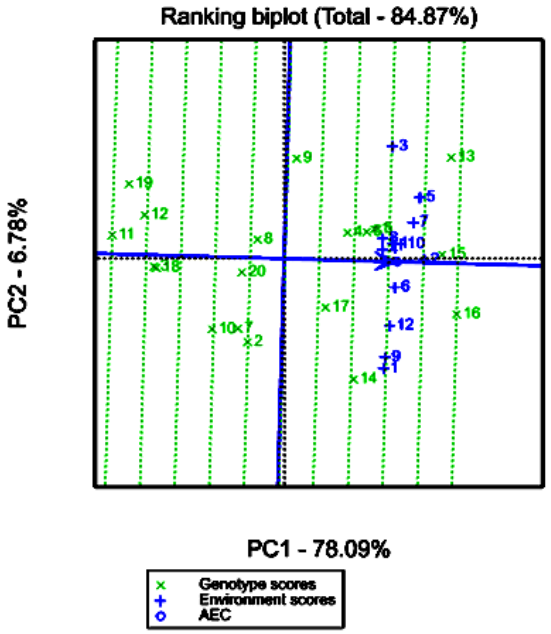

Fig 4: GGE biplot ranking genotypes (mean vs. stability) from twenty sesame genotypes.

Note that, AEC abscissa they cannot be used in selecting superior genotypes, but are useful in selecting unstable genotypes.

2- Useful test environments should be further examined for their uniqueness. Some environments may never provide unique information, as they are always similar to some other environment(s) in separating and ranking the genotypes. Some (not all) of these environments can be dropped without losing much information about the genotypes**.**

3- Testing cost could be reduced and efficiency improved by using a minimum set of test environments.

4-Test environments could be visually ranked for their usefulness in identifying superior genotypes based on the distances on the GGE biplot between their markers and the marker of the ideal test environment.

This follows from the fact that when SVP = 2, the cosine of the angle between any environment vector and the "average environment axis" approximates the correlation coefficient between the genotype values in that environment and the genotype means across the environments (Yan *et al.*, 2007) [30].

Fig. 5 showed that the test environment is classified into three types. Six environments (E8, E4, E6, E12, E9 and E1) have short vectors and were highly correlated in their ranking of the genotypes, indicating that these environments produced similar information about the genotypes; therefore, it should not be used as test environments. These environments were below type 1 (Useless environments).

Yan (2001) [29] defined an "ideal" test environment, which is a virtual environment that has the longest vector of all test environments (most discriminating) and is located on the AEC abscissa (most representative) (e.g., E2) in our study. Accordingly, in Fig. 5, E2, E5 and E7 have long vectors and small angles with the AEC abscissa and they are ideal for selecting superior genotypes, they were representative environments.

Environment 3 has long vector and large angle with the AEC abscissa and it cannot be used in selecting superior genotypes, but it is useful in selecting unstable genotypes. In addition, graph 3 visually ranked usefulness environments, for example E2 may be observed as an ideal test environment (Representative). On the other hand, E3 may be regarded as un-useful environment (Useless). These findings are similar to those of (Yan *et al* 2007) [11], Kang *et al.* (2015) [11] and Walter *et al* (2016) [25].

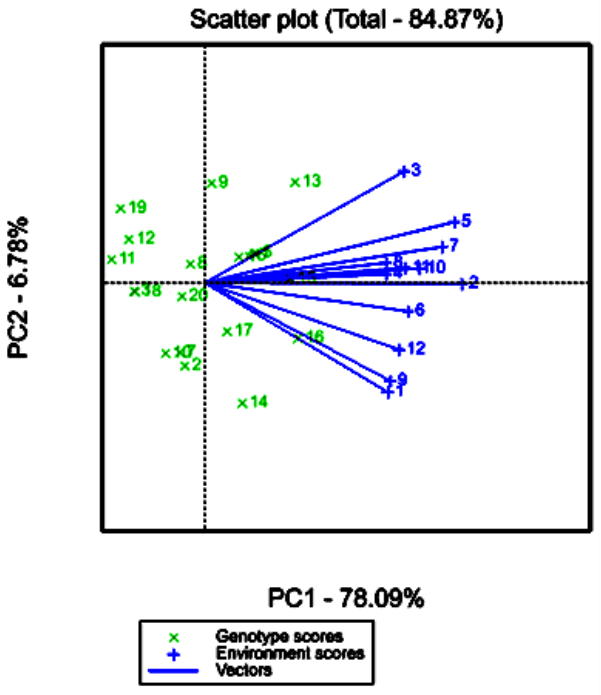

Fig 5: Test environments, the "discriminating power *vs.* representativeness"

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