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AMMI and GGE Bi-plot Analysis for Seed Yield and Oil Content of Sesame (*Sesamum indicum* L.) Genotypes in Tigray, Northern Ethiopia

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Abstract

Seventeen sesame genotypes were tested at ten environments in Tigray, Northern Ethiopia during 2014-2015 cropping seasons. Randomized Complete Block Designs (RCBD) with three replications was used in the study. According to the GGE bi-plot different sesame growing environments grouped into two mega-environments: The first mega-environment contained the favorable environments Dansha area with a vertex G4 and Sheraro area with winner G3 and the second environment included medium to low environments E2 (Humera-2), E4 (Dansha-2), E5 (Sheraro-1), E7 (Wargiba-1), E8 (Wargiba-2) and E9 (Maykadra) for seed yield. Three mega-environments identified for oil content: The 1st environment contained G12, G7 and G2 in the mega-environment group of Humera, Dansha and Gendawuha, The 2nd environment, Sheraro location contained G9 and the 3rd environment Wargiba, was containing G17. G1 (HuRC-4) identified as an "ideal" genotype and E1 (Humera-1) also identified as an ideal environment the most representative of the overall environments and the most powerful to discriminate genotypes. The multivariate approaches AMMI and GGEbi-plot were better for partitioning the GEI into the causes of variation. According to different stability models, G1, G7, and G3 were high yielder and the most stable both in terms of seed yield and oil content. Moreover, showed yield advantages over the released and local varieties. The stable genotypes recommended for wider areas while G14 and G4 were for specific favorable environments Sheraro and Dansha, respectively.

Keywords: AMMI; ASV; GGE biplot; Oil content; Seed yield; Sesame; YSI.

1. Introduction

Sesame (*Sesamum indicum* L.) is an annual, indeterminate plant with a diploid chromosome number of 2n=2x=26 and belonging to family *Pedaliacea*. It is a Sanjayrao Khairnar and Arjanbhai Monpara 2 plant breeder's dream crop because it presents a great genetic variability Janick and Whipkey [1]. The additive main effects and multiplicative interaction

(AMMI) method integrates analysis of variance and principal components analysis into a unified approach Gauch [2]. According to Zobel, *et al.* [3] it can be used to analysis METs. The AMMI method is used for three main purposes. The first is model diagnoses, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool of diagnosing other models as sub cases when these are better for particular data sets Gauch [2]. Secondly, AMMI clarifies the GEI and summarizes patterns and relationships of genotypes and environments Zobel, *et al.* [3].The third use is to improve the accuracy of yield estimates. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replicates by a factor of two to five Zobel, *et al.* [3].

AMMI stability value (ASV) was calculated in the excel spread sheet using the formula developed by Purchase [4]:

$$\mathrm{ASV} = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(\mathrm{IPCA1}_{score})\right]^2 + (\mathrm{IPCA2}_{score})^2}$$

Where, ASV= AMMI's stability value, SS=sum of squares, IPCA1=interaction of principal component analysis one, IPCA2 = interaction of principal component analysis two. Similarly Yield stability index (YSI) was also computed by summing up the ranks from ASV and mean seed yield Farshadfar, *et al.* [5]:

YSI= RASV+RGY

Where: RASV is rank of AMMI stability value and RGY is rank of mean seed yield to statistically compare the stability analysis procedures used in the study, the Spearman's coefficient of rank correlation (r_s) Steel and Torrie [6] was estimated using SPSS version 16 statistical software.

The seed yield data were subjected to AMMI analysis, which combines analysis of variance (ANOVA) with additive and multiplicative parameters in to a single model Gauch [2]. After removing the replicate effect when combining the data, the genotypes and environments observations are partitioned in to two sources: Additive main effects for genotypes and environments; and non-additive effects due to genotype by environment interaction. A bi-plot showing the genotype and environmental means against IPCA1 was also performed *via* this model using GenStat (V16). The AMMI model is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^{n} \lambda_k \alpha_{ik} \gamma_{jk} + \theta_{ij} \quad \text{Where:}$$

Y_{ij} is the observed mean yield of i^{th} genotype in the j^{th} environment; μ is the grand mean; G_i is the i^{th} genotypic effect; E_j is the j^{th} environment effect; λ_k is the eigen value of the principal component analysis (PCA) axis k; α_{ik} and γ_{jk} are the i^{th} genotype j^{th} environment PCA scores for the PCA axis k; θ_{ij} is the residual; n is the number of PCA axes retained in the model. The number n is judged on the basis of empirical consideration of F-test of significance

GGE bi-plot is a data visualization tool, which graphically displays a G x E interaction in a two way table Yan and Rajcan [7]. GGE bi-plot is an effective tool for: 1) mega-environment analysis (e.g. “which-won-where” pattern), whereby specific genotypes can be recommended to specific mega-environments Yan and Kang [8], 2) genotype evaluation (the mean performance and stability), and 3) environmental evaluation (the power to discriminate among genotypes in target environments). Sabaghnia, *et al.* [9] and Farshadfar, *et al.* [10] in wheat; Munawar, *et al.* [11] and Fiseha, *et al.* [12] in sesame are among the many authors who used GGE bi-plot to identify mega environments, to evaluate the genotypes and to test the environments.

GGE bi-plot is able to show the best genotype with the highest yield in a quadrant containing identical locations (Mega-Environments), genotype average performance and stability, ideal genotype and ideal location to increase yield and specific location. Visualization of GGE biplot is very useful to evaluate and find the most stable genotypes Farshadfar, *et al.* [10]. Genotypes laid in the concentric area are the most stable compared to the genotypes laid outside, even though the environmental effect was very strong Untung, *et al.* [13]. An ideal genotype is defined as one that is the highest yielding across test environments and absolutely stable in performance (that ranks the highest in all test environments Farshadfar, *et al.* [14]. Although such an “ideal” genotype may not exist in reality, it could be used as a reference for genotype evaluation Mitrovic, *et al.* [15]. A genotype is more desirable if it is located closer to “ideal” genotype Mitrovic, *et al.* [15] and Kaya, *et al.* [16].

2. Materials and Methods

The experiment was conducted in Tigray, Northern Ethiopia presented below (Table 2)

Table-1. Agro-climatic and soil types of six tested locations in Northern Ethiopia

Description	**Locations**					
	Dansha	**Maykadra**	**Humera**	**Sheraro**	**Wargiba**	**Gendawuha**
Altitude(m.a.s.l)	696	646	609	1028	1578	760
Latitude (°N)	13°36'	14°02'	14°15'	14°24'	12° 41'	12°
Longitude (°E)	36°41'	36°35'	36°37'	37°45'	39° 42'	36°
R.F. (mm)	888.4	NA	576.4	1000	750	850-1100
Temp. (°C)	28	NA	18.8-37.6	18.8-34.9	18-25	19.5-35.7
Soil type	Vertisol	Chromic vertisol	Chromic Vertisol	Vertisols	NA	Vertisol

Source: Bereket. and Yirgalem [17] Meteorology data (Dansha, Humera, and Maykadra): IPMS-ETHIOPIA [18] (for Gendawuha), NA=Not Available

Table-2. The Study locations in Northern Ethiopia in 2014-2015 cropping season

Location	**District**	**Year**	
		2014	**2015**
Humera	K/Humera	E1	E2
Dansha	Tsegede	E3	E4
Sheraro	T/Adyiabo	E5	E6
Wargiba	R/Azebo	E7	E8
Maykadra	K/Humera	-	E9
Gendawuha	Metema	-	E10

Note: K/Humera=Kafta Humera, T/Adyiabo=Tahtay Adyiabo, R/Azebo=Raya Azebo. E1=Humera, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

2.1. Experimental Genotypes

Seventeen sesame planting materials were used in the study presented (Table 3).

Table-3. Description of genotypes used in the study

Genotype (G)	Code	Status	Sources
HuRC-4	G1	Advance line	HuARC
Acc202514	G 2	Advance line	HuARC
Land race Gumero	G 3	Advance line	HuARC
Abuseffa	G 4	Advance line	HuARC
HuRC-1	G 5	Advance line	HuARC
Rawyan -2	G 6	Advance line	HuARC
HuRC-3	G 7	Advance line	HuARC
Acc 202300	G 8	Advance line	HuARC
Kefif	G 9	Advance line	HuARC
Acc111824	G 10	Advance line	HuARC
Acc 111518	G 11	Advance line	HuARC
Acc 27913	G 12	Advance line	HuARC
Gumero	G 13	Advance line	HuARC
HuRC-2	G 14	Advance line	HuARC
Acc 227880	G 15	Advance line	HuARC
Setit -1(Standard check)	G 16	Released	HuARC
Hirhir (Local check)	G 17	Local	HuARC

Source: Humera Agricultural Research Center [19] Annual report

2.2. Experimental Design and Management

The experiment was laid out in randomized complete block design (RCBD) with three replications. Each genotype was randomly assigned and sown in a plot area of 2m x 5m with 1m between plots and 1.5m between blocks keeping inter and intra row spacing of 40cm and 10 cm, respectively.

2.3. Data Analysis

Analysis of variance for each environment, combined analysis of variance over environments and AMMI analysis were computed using GenStat statistical softwre16th edition GenStat [20]. Unbalanced design was used for combined analysis of variance because of different locations and years in the study. The model employed in the analysis was;

$$Y_{ijk} = \mu + G_i + E_j + B_k + GE_{ij} + \varepsilon_{ijk} \text{ where:}$$

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 the jth environment; and εijk is the error term.

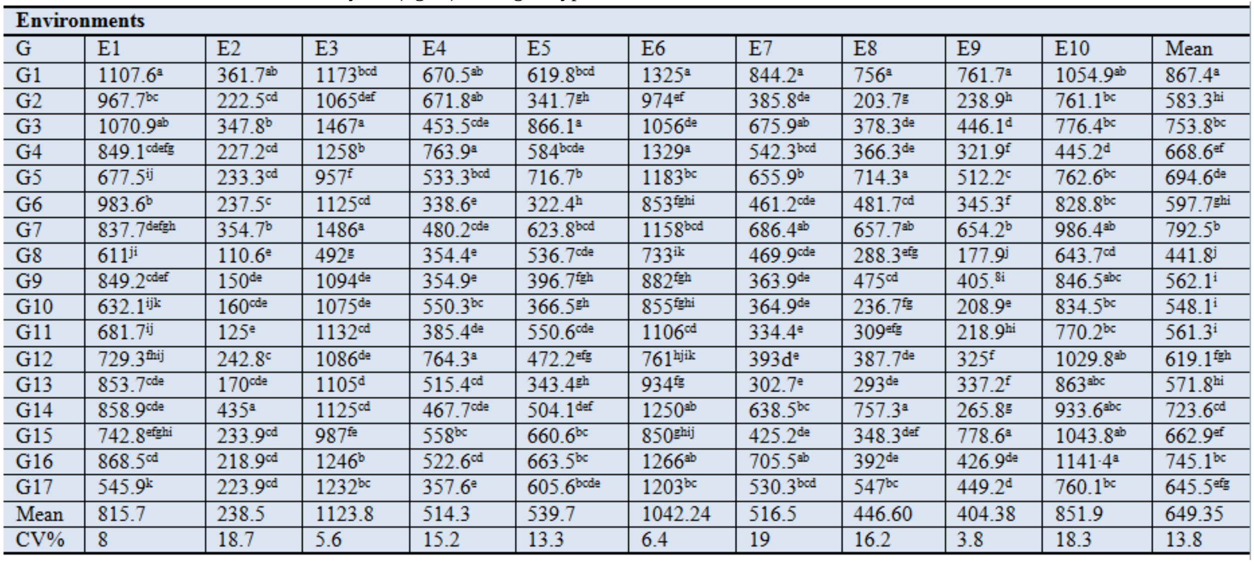
3. Result and Discussion

3.1. Mean of Genotypes for Seed Yield and Oil Content Across Ten Environments

The mean seed yield of the environments in 2014-2015 and oil content during 2015 main seasons was highly significant at ($p \leq 0.001$). Overall mean seed yield over ten environments was 649.35 kg/ha and the mean seed yield of genotypes across environments ranged between 238.5 kg/ha in E2 to 1123.8 kg/ha in E3. Among high yielded genotypes, G1, G7, and G3 showed 18.85%, 7.30% and 1.34% yield advantage over the recently released and 34.25%, 22.75% and 16.75% over the local varieties, respectively. Changing sesame yield performance with environments reported by Fiseha, *et al.* [12], Mekonnen, *et al.* [21] and Mohammed [22] in sesame.

The grand mean oil content of the genotypes over six environments were 49.9% and the mean oil content ranged between 49% in G5 to 51.9% in G12 across the tested locations this result in line with the major requirements for sesame export are pearly white seed color and 40-50% oil content. The oil content percentage was varied among genotypes and is consistent with the previous findings: Zenebe and Hussien [23] 45.9-52-5% 24-58%, Alege and Musapha [24] 38-57% Yahaya, *et al.* [25], 45.2-52.7% Mohammed [22] and 46.4%-53.4% Mekonnen, *et al.* [21]. Gendawuha (52.5%) gave the highest mean oil content followed by Sheraro (50.99% and Dansha (50.6%) which received optimum rainfall in the 2015 main cropping season resulted in high oil content while Humera (48.2%), Wargiba (48.5%) and Maykadra (48.61%).Oil content greatly across seasons and environments among genotypes. This result is in agreement with Zenebe and Hussien [23] and Mekonnen, *et al.* [21]. To improve the oil content of sesame genotypes, selection should be based on high seed yield with relatively high oil content or cross-breeding of high seed yielded with high oil content genotypes.

Table-4. Mean yield (kg/ha) of 17 genotypes across 10 environments in 2014-2015 main season



Environments										
G	E1	E2	E3	E4	E5	E6	E7	E8	E9	E10	Mean
G1	1107.6^{a}	361.7^{ab}	1173^{bcd}	670.5^{ab}	619.8^{bcd}	1325^{a}	844.2^{a}	756^{a}	761.7^{a}	1054.9^{ab}	867.4^{a}
G2	967.7^{bc}	222.5^{cd}	1065^{def}	671.8^{ab}	341.7^{gh}	974^{ef}	385.8^{de}	203.7^{g}	238.9^{h}	761.1^{bc}	583.3^{hi}
G3	1070.9^{ab}	347.8^{b}	1467^{a}	453.5^{cde}	866.1^{a}	1056^{de}	675.9^{ab}	378.3^{de}	446.1^{d}	776.4^{bc}	753.8^{bc}
G4	849.1^{cdefg}	227.2^{cd}	1258^{b}	763.9^{a}	584^{bcde}	1329^{a}	542.3^{bcd}	366.3^{de}	321.9^{f}	445.2^{d}	668.6^{ef}
G5	677.5^{ij}	233.3^{cd}	957^{f}	533.3^{bcd}	716.7^{b}	1183^{bc}	655.9^{b}	714.3^{a}	512.2^{c}	762.6^{bc}	694.6^{de}
G6	983.6^{b}	237.5^{c}	1125^{cd}	338.6^{e}	322.4^{h}	853^{fghi}	461.2^{cde}	481.7^{cd}	345.3^{f}	828.8^{bc}	597.7^{ghi}
G7	837.7^{defgh}	354.7^{b}	1486^{a}	480.2^{cde}	623.8^{bcd}	1158^{bcd}	686.4^{ab}	657.7^{ab}	654.2^{b}	986.4^{ab}	792.5^{b}
G8	611^{ji}	110.6^{e}	492^{g}	354.4^{e}	536.7^{cde}	733^{ik}	469.9^{cde}	288.3^{efg}	177.9^{j}	643.7^{cd}	441.8^{j}
G9	849.2^{cdef}	150^{de}	1094^{de}	354.9^{e}	396.7^{fgh}	882^{fgh}	363.9^{de}	475^{cd}	$405.^{8i}$	846.5^{abc}	562.1^{i}
G10	632.1^{ijk}	160^{cde}	1075^{de}	550.3^{bc}	366.5^{gh}	855^{fghi}	364.9^{de}	236.7^{fg}	208.9^{e}	834.5^{bc}	548.1^{i}
G11	681.7^{ij}	125^{e}	1132^{cd}	385.4^{de}	550.6^{cde}	1106^{cd}	334.4^{e}	309^{efg}	218.9^{hi}	770.2^{bc}	561.3^{i}
G12	729.3^{fhij}	242.8^{c}	1086^{de}	764.3^{a}	472.2^{efg}	761^{hjik}	$393d^{e}$	387.7^{de}	325^{f}	1029.8^{ab}	619.1^{fgh}
G13	853.7^{cde}	170^{cde}	1105^{d}	515.4^{cd}	343.4^{gh}	934^{fg}	302.7^{e}	293^{de}	337.2^{f}	863^{abc}	571.8^{hi}
G14	858.9^{cde}	435^{a}	1125^{cd}	467.7^{cde}	504.1^{def}	1250^{ab}	638.5^{bc}	757.3^{a}	265.8^{g}	933.6^{abc}	723.6^{cd}
G15	742.8^{efghi}	233.9^{cd}	987^{fe}	558^{bc}	660.6^{bc}	850^{ghij}	425.2^{de}	348.3^{def}	778.6^{a}	1043.8^{ab}	662.9^{ef}
G16	868.5^{cd}	218.9^{cd}	1246^{b}	522.6^{cd}	663.5^{bc}	1266^{ab}	705.5^{ab}	392^{de}	426.9^{de}	$1141·4^{a}$	745.1^{bc}
G17	545.9^{k}	223.9^{cd}	1232^{bc}	357.6^{e}	605.6^{bcde}	1203^{bc}	530.3^{bcd}	547^{bc}	449.2^{d}	760.1^{bc}	645.5^{efg}
Mean	815.7	238.5	1123.8	514.3	539.7	1042.24	516.5	446.60	404.38	851.9	649.35
CV%	8	18.7	5.6	15.2	13.3	6.4	19	16.2	3.8	18.3	13.8

G=Genotypes; G1= HuARC-4(Setit-3)(Setit-3)(Setit-3), G2= Acc202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuARC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=, Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7= Wargiba-1, E8= Wargiba-2, E9=Maykadra and E10= Gendawuha

Table-5. Mean oil content (%) of 17 genotypes across six locations during 2015 main season

	Environments						
G	**E2**	**E4**	**E6**	**E8**	**E9**	**E10**	**Mean**
G1	47.18^{d}	50.91^{bcd}	50.49^{ab}	48.2	47.7^{efg}	51.83^{bcde}	50^{fgh}
G2	48.52^{abcd}	50.27^{cdef}	50.77^{ab}	48.37	49.54^{bc}	53.74^{ab}	50.2^{abcdef}
G3	48.87^{ab}	52.03^{ab}	49.18^{b}	48.08	49.78^{b}	52.64^{abcd}	50.10^{bcdef}
G4	48.5^{abcd}	51.36^{abc}	50.51^{ab}	48.74	50.27^{ab}	52.16^{bcde}	50.26^{abcde}
G5	47.34^{d}	49.58^{ef}	50.31^{ab}	47.92	47.63^{efg}	51.37^{de}	49.03^{h}
G6	47.19^{d}	49.82^{def}	52.09^{ab}	48.67	46.9^{fg}	50.49^{e}	49.18^{gh}
G7	47.67^{bcd}	51.21^{bc}	51.81^{ab}	49.59	49.5^{bc}	52.33^{abcde}	50.35^{abcd}
G8	48.8^{abc}	49.34^{f}	51.26^{ab}	48.63	47.54^{efg}	51.42^{cde}	49.54^{defgh}
G9	49.33^{a}	49.28^{f}	52.62^{a}	48.13	46.79^{g}	51.87^{bcde}	49.67^{cdefgh}
G10	49^{ab}	50.7_{cde}	49.91^{ab}	48	47.63^{efg}	52.17^{bcde}	49.57^{defgh}
G11	48.13^{abcd}	49.47^{ef}	50.2^{ab}	48.59	47.82^{def}	52.58^{abcde}	49.46^{efgh}
G12	48.93^{ab}	52.52^{a}	51.7^{ab}	47.68	50.79^{a}	54.24^{a}	51^{a}
G13	47.32^{d}	50.46^{cdef}	51.78^{ab}	48.43	47.53^{efg}	52.3^{abcde}	49.67^{cdefgh}
G14	48.32^{abcd}	51.33^{abc}	52.03^{ab}	48.29	49.79^{b}	53.68^{ab}	50.6^{ab}
G15	48.4^{abcd}	51.29^{abc}	50.11^{ab}	49.1	50.11^{ab}	53.39^{abc}	50.4^{abc}
G16	48.56^{abcd}	50.92^{bcd}	51.43^{ab}	48.47	48.26^{de}	54.17^{a}	50.3^{abcd}
G17	47.42^{cd}	50.2^{cdef}	50.7^{ab}	49.87	48.73^{cd}	52.77^{abcd}	49.95^{bcdefg}
Mean	48.20	50.6	50.99	48.5	48.61	52.5	49.9
CV%	1.5	1.3	3.1	2.8	1.1	1.9	1.95

Values connected with the same letters in a column were not significantly different; G=Genotype, CV%= Coefficient of variability, E2= (Humera-2), E4= (Dansha-2), E6 = (Sheraro-2), E8= (Wargiba-2), E9= (Maykadra), E10= (Gendawuha)

3.2. Overall Ranking of Genotypes Using Various Stability Models

G1, G7 and G3 including the released variety (G16) and local (G17) were found the most stable and ranked 1st, 2nd, 3rd, 4thand 9th. While, G4, G8 and G15 were unstable and7th, 17th and 8thfor seed yield, respectively (Table 6). According to those models, the oil content was also varied from one environment to another. G2, G15 and G16 were the most stable and ranked 6th, 3rd and 4th. On contrary, G6, G10 and G9 were the most unstable and ranked16th, 14th and 13thformean oil content across the tested locations, respectively (Table 6).

.**Table-6.** Ranking of seed yield of sesame genotypes based on the various stability parameters

Stability analysis result															
G	**SY**	**R**	**YSI**	**R**	**ASV**	**R**	**Wi**	**R**	**Pi**	**R**	**bi**	**R**	**S^2di**	**R**	**OR.**
G1	867.4	1	6	2	5.8	5	110047	5	9036	1	0.76	6	14783.5	10	1
G2	583.3	12	23	8	11.7	11	163463	10	80169	13	1.24	16	5354.35	4	15
G3	753.8	3	13	3	10	10	233791	14	29813	4	0.89	5	20758.7	14	5
G4	668.6	7	24	9	17.1	17	341095	17	58946	9	1.11	12	4391.77	2	16
G5	694.6	6	21	6	14.8	15	188863	12	42711	6	1.09	11	10382.5	7	13
G6	597.7	11	15	4	4.9	4	123724	8	69822	11	1.13	13	37759.3	17	10
G7	792.5	2	5	1	3.8	3	115774	7	16102	2	1.08	9	4500.33	3	3
G8	441.8	17	30	10	13	13	269022	15	146926	17	0.97	3	5791.59	5	17
G9	562.1	14	16	5	2.9	2	67623	2	80574	15	1.2	15	1419.28	1	11
G10	548.1	16	23	8	7.5	7	73381	4	86227	16	0.93	4	10043.9	6	9
G11	561.3	15	21	6	6.2	6	67254	1	80386	14	1.13	13	24115.9	16	12
G12	619.1	10	24	9	14	14	202390	13	68775	10	0.57	17	12680.7	9	8
G13	571.8	13	22	7	8.9	9	70485	3	77593	12	1.05	8	16486.7	12	7
G14	723.6	5	13	3	8.3	8	169296	11	38301	5	1.09	10	16406.8	11	6
G15	662.9	8	24	9	16.4	16	270511	16	54425	8	1.02	1	12142.4	8	14
G16	745.1	4	5	1	0.8	1	114803	6	27076	3	0.99	2	17843.7	13	2
G17	645.5	9	21	6	12	12	160177	9	53505	7	0.75	7	24593.3	15	4

Note: ASV=AMMI stability value, YSI=yield stability index, bi = Eberhart and Russell [26] regression coefficient, R= Rank,OR. = Overall rank, Pi = Lin and Binns [27] cultivar performance measure, S^2di = Eberhart and Russell [26] deviation from Regression, SY= Seed yield (kg/ ha) and Wi = Wricke [28] Ecovalenc.

AMMI analysis of variance of ten environments for seed yield and six locations were presented in (7). Showed highly significance variation at ($P \leq 0.001$) among genotypes, environments and GEI for seed yield and oil content. From the total variation, 69.73%, 14.68%, 9.58% were explained by environments, GEI and genotypes for seed yield and 61.6%, 13.64%) and 6.55%) for oil content, respectively. The result is agreed with the previous findings Mohammed, *et al.* [29] and Mekonnen, *et al.* [21] in sesame. This showed that the significances influence of environments on yield and oil content performance of sesame genotypes in different locations of northern Ethiopia indicating the need to test sesame genotypes under various environments. The four IPCAs were highly significant leading to a cumulative 99.8% variation and the rest 2.62% was contributed due to noise for seed yield and three IPCs significance leading to a cumulative contribution of 83.7% variation and the rest due to noise for oil content. AMMI with only the two interaction principal component axes was the best predicative model for both seed yield and oil content. This is in harmony with Zobel, *et al.* [3].

Table-7. AMMI's ANOVA for seed yield (kg/ha) of 17 genotypes during 2014-2015

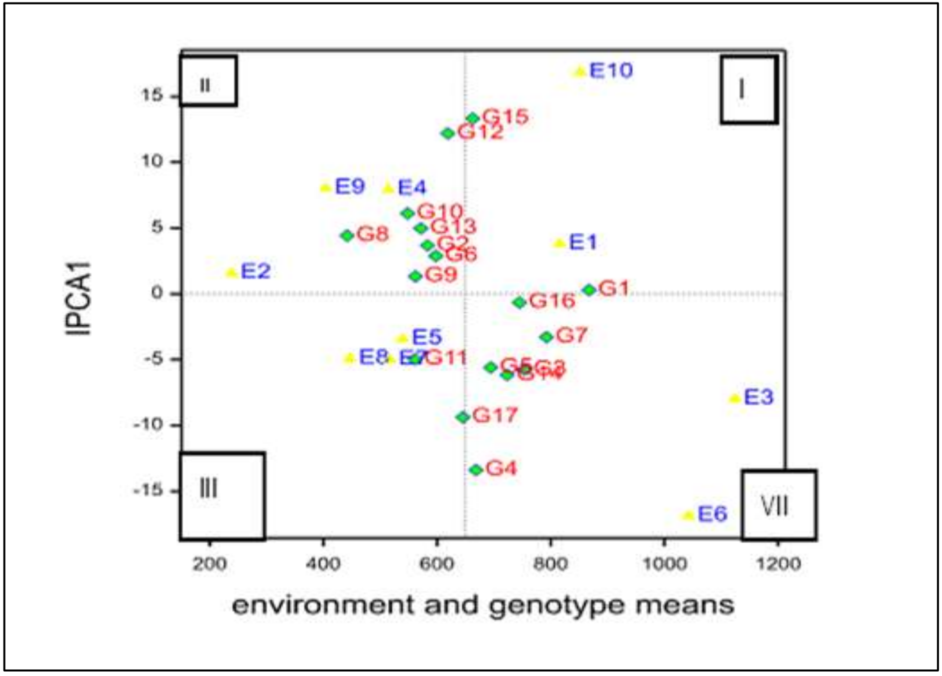
Source of variation	**df.**	**SS.**	**MS.**	**Sum of squares % explained**		
				Total V.E	**GEIE**	**GEI Cmu.**
Genotypes	16	5367408	335463**	9.58		
Environments	9	39066091	4340677**	69.73		
Block within Envir.	20	1306032	65302**	2.33		
Interactions	144	8225103	57119**	14.68		
IPCA 1	24	4234567	87589**		51.56	51.48
IPCA 2	22	1849997	84091**		22.49	73.97
IPCA 3	20	1250159	62508**		15.2	89.17
IPCA 4	18	1121227	62290**		10.63	99.8
Residuals	8	78316	4789^{ns}			
Total	281	62498900	5099828			

** Significance at ($p \leq 0.001$) respectively. Block =replication within environments. Total V.E. =Total variation explained, GEIE. =GEI explained and GEI cum. = GEI cumulative, SS= Sums of squares and MS=Means of squares

G15, G1, G16, G3, G4, G5, G14, G17 and G7 recorded seed yield above grand mean in the favorable environments, while eight genotypes G12, G8, G10, G2, G13, G6, G9 and G11 were below the grand mean and low yield in the unfavorable environments (Figure 1). Stable genotypes were adaptive to wider areas and give consistency mean yield across the test locations. G1, G7, G2, G3, G6, G9 and G16 were found nearly closer to the origin and the most stable with little responsive to the GEI. Genotypes far from the origin are sensitive to environmental changes. Hence, G4, G10, G8, G11, G12, G13, G17, G15 and G14 were the unstable. In contrast, G1, G7, G 16 and G3 were the most stable in the favorable environments. G8 and G11 were unstable with low yield in the unfavorable environments. Therefore, genotypes with high yield and wider stability performance are the most desirable for wider area.

Environments suitable to sesame production are classified according their position found in the quadrant (Figure 1). Environments on 1st and 2nd quadrant, E1, E3, E6, and E10 were favorable. Whereas, E9, E4, E2, E5, E8 and E7 in 3rd and 4th quadrant of the graph were considered as unfavorable environments.

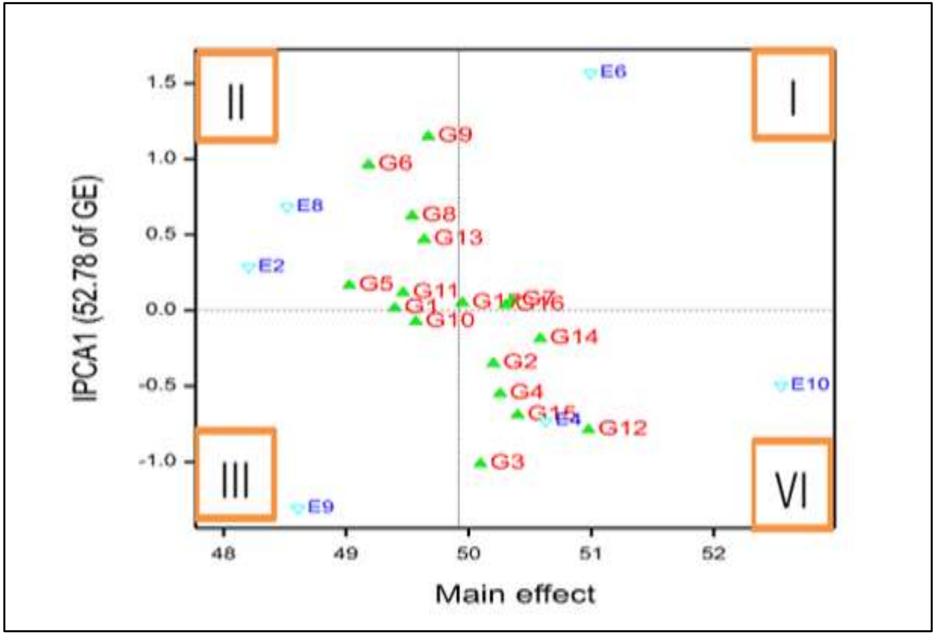
Figure-1. AMMI1bi-plot showing Genotype and Environment means seed yield against IPCA1



G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. Environments: E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2,E7=Wargiba-1,E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

E10, E4 and E6 were favorable environments, while E2, E9 and E8 were unfavorable environments for mean oil content. Due to environmental factors the oil content varied among genotypes. Hence, G1, G5, G6, G8, G9, G10, G11 and G3 had low mean oil content in the unfavorable environments and G1, G5, G10 and G11 were the most stable found close to the origin. Whereas, G2, G4, G7, G12, G13, G14, G15, G16 and G17 were in the favorable environments and G17, G16, G7 and G14 were the most stable. Hence, improving the oil content selection should be based on high seed yield with relatively high oil content genotypes or cross breeding of high seed yielder with high oil content genotype. This is in harmony with the result of Mekonnen, *et al.* [21] in sesame.

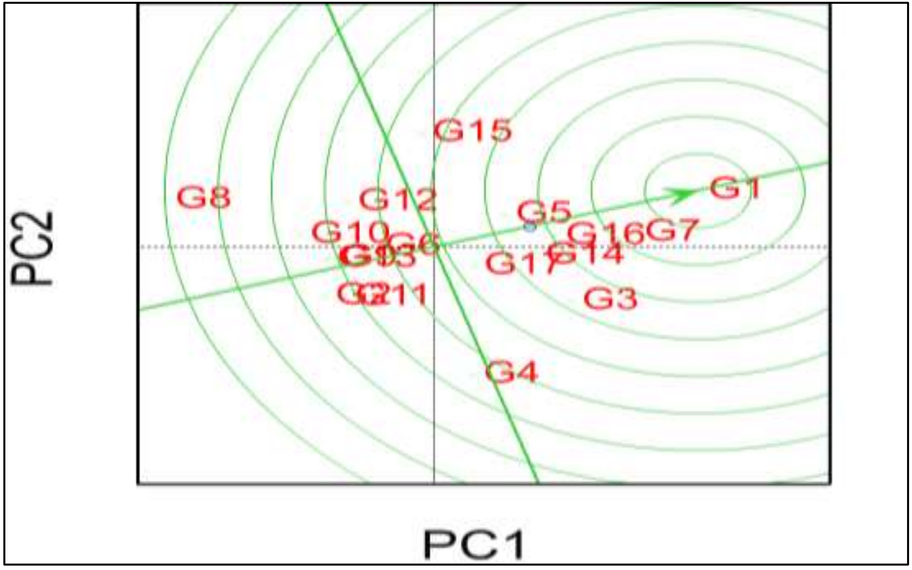
Figure-2. AMMI1 showing Genotype and Environment means for oil content (%) in 2015



G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. E2=humera-2, E4=Dansha-2, E6=Sheraro-2, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

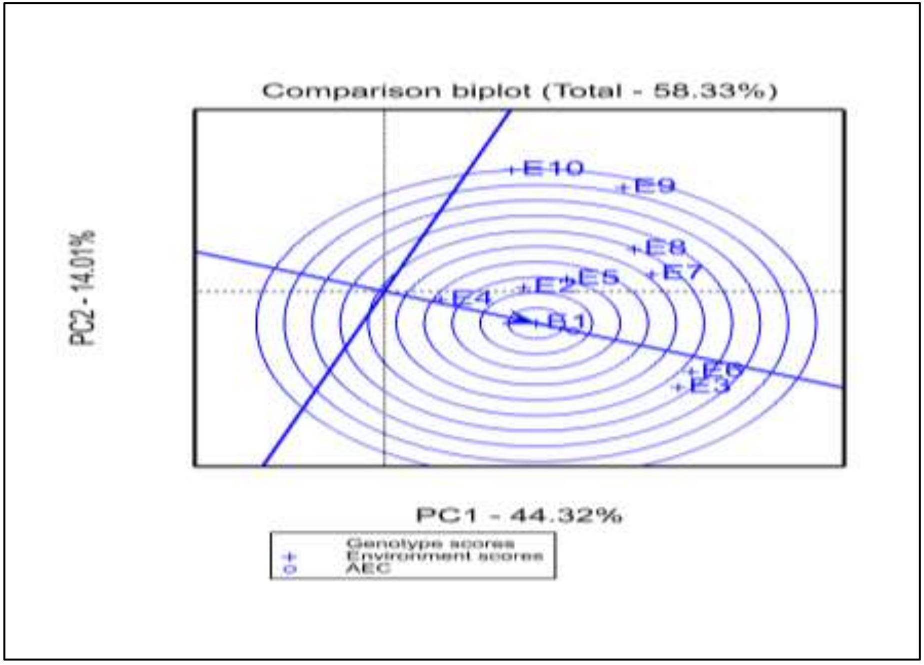
GGE bi-plot was determined using GenStat software version 16 for both seed yield and oil content. From this study G1 (HuRc-4) was the "ideal" genotype, the highest mean seed yield and the most stable across variable environments. Genotypes closer to the ideal genotype were the stable ones, while genotypes far from the ideal genotypes were unstable. A genotype is more desirable if it is located closer to the ideal genotype. A similar result was reported by Kaya, *et al.* [16]; Mitrovic, *et al.* [15]; Farshadfar, *et al.* [14]. G7, G3, G5, G16, G17 and G14 were plotted to the ideal genotype considered as desirable genotypes, while G15 and G4 were high yielding genotypes associated with genotypic instability (Figure 3). E1(Humera -1) had the longest vector with small IPCA, which fell into the center of concentric circles was considered as an ideal environment in terms of being the most representative of the overall environments and the most powerful to discriminate genotypes. The concentric circles on the bi-plot help to visualize the length of the environment vectors, which are proportional to the standard deviation within the respective environments and is a measure of the discriminating ability of the environments Asnake, *et al.* [30]. An environment is more desirable and discriminating when located closer to the center circle or to an ideal environment Naroui, *et al.* [31]. E2, E4, E5, E7 and E8 were closer to the ideal environment. E3, E10, E6, E4 and E9 were far from the ideal environment and considered as unstable (Figure 4). This result was in line with Yan, *et al.* [32] and Fiseha, *et al.* [12] presented in (Figure 3).

Figure-3. (GGE-bi-plot showing the "ideal" genotype



G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir

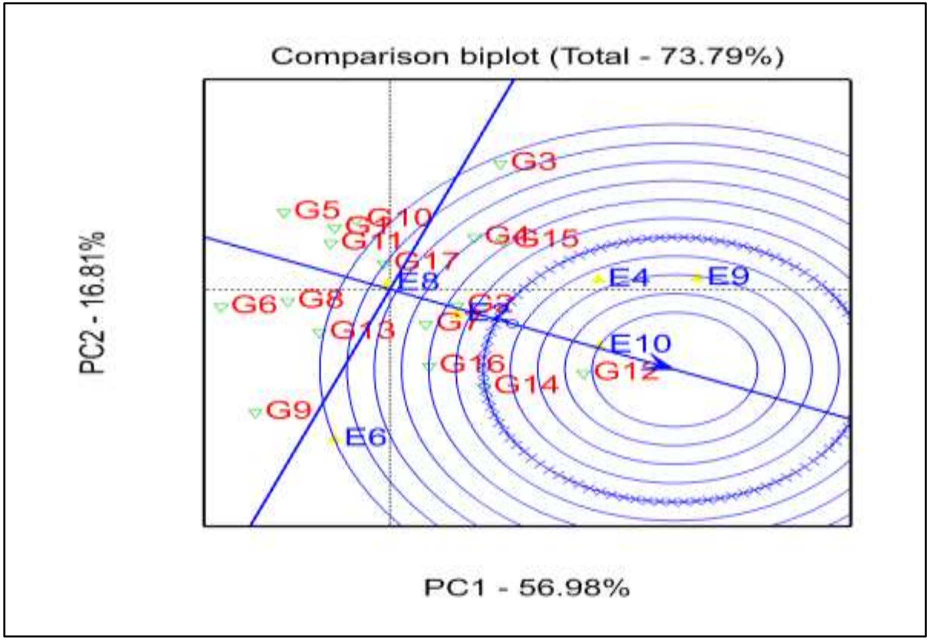
Figure-4. GGE-bi-plot based on the ranking of environments relative to an ideal environment



E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

The mean oil content of genotypes were inconsistent across locations due to environmental factors. G12 was ideal genotype for oil content and G14, G16, G7, G2 and G5 were stable, while G3 had high oil content and unstable. E10 was the ideal environment followed by E4 and E9 and the most stable for oil content. On the other hand, E2, E6 and E8 were plotted far from the ideal environment considered as unstable and unfavorable environments (Figure 5).

Figure-5. GGE-biplot based on the ranking of environments and genotypes for oil content relative to an ideal environment and ideal genotype.

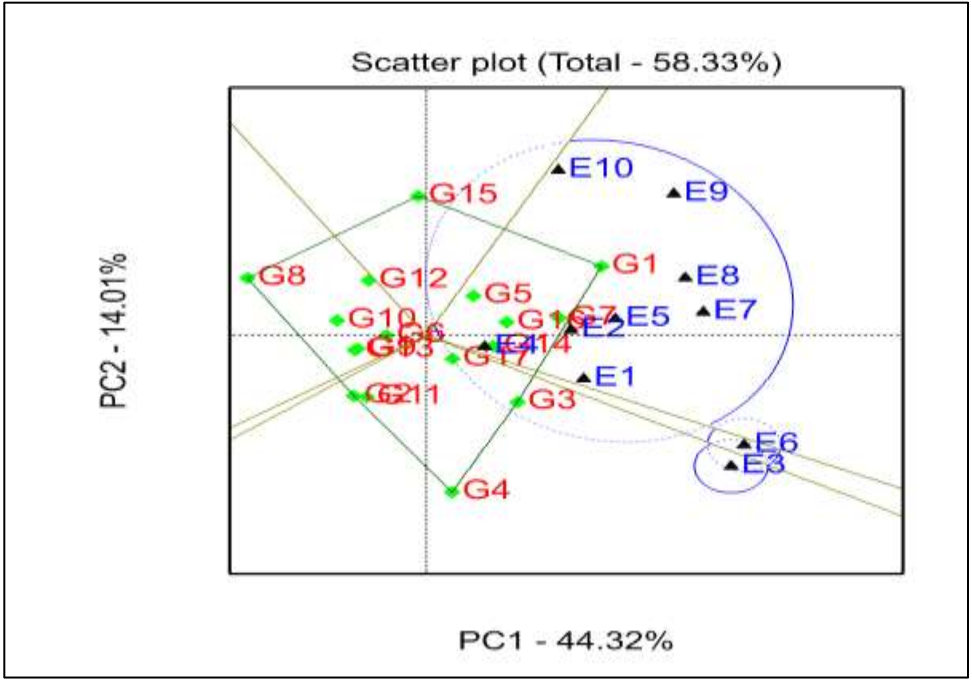


E2=humera-2, E4=Dansha-2, E6=Sheraro-2, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha. G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. Environments: E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

3.3. 'Which-Won-Where' Pattern and Mega-environment Identification

The ten environments fell into six sectors with different winner genotypes and the bi-plot showed that four vertex genotypes, G4, G15, G1 and G8. From winner genotypes except G8 were high yielding in favorable environments. The GGE biplot identified two different sesame growing mega-environments. The first mega-environment containing overlapping environments with highest yielding environment (E3) in Dansha area with a vertex genotype G4 and the higher yielding environment (E6) in Sheraro area with winner genotype G3; and second environment includes medium E1 and E10 to low yielding E2, E4, E5, E7, E8 and E9 environments, respectively with the winner genotype G1 (Figure 5).

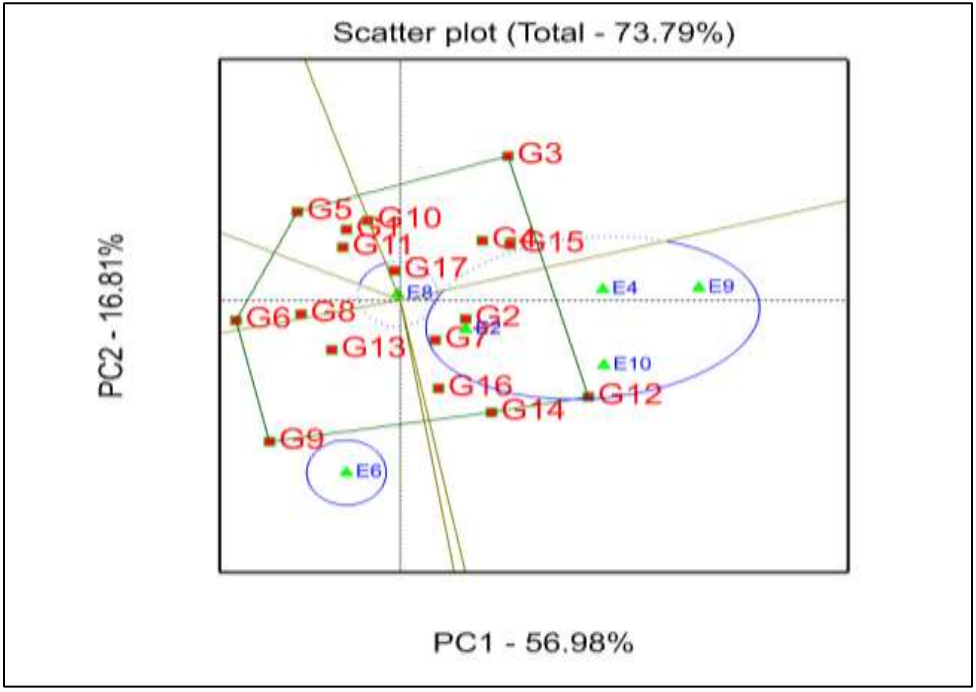
Figure-6. Which-Won-Where View of GGE bi-plot genotypes and environments of yield



G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuRC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir. E1=Humera-1, E2=Humera-2, E3=Dansha-1, E4=Dansha-2, E5=Sheraro-1, E6=Sheraro-2, E7=Wargiba-1, E8=Wargiba-2, E9=Maykadra, E10=Gendawuha

According the GGE bi-plot six sections with five vertex genotypes G3, G5, G6, G12 and G9 and identified three different sesame growing mega-environments for oil content: The first environment containing G12, G7 and G2 in the mega-environment group of E2 (Humera-2), E4 (Dansha) and E10 (Gendawuha). The second environment E6 (Sheraro-2) containing G9 and third environment E8 (Wargiba), containing G17 presented in (Figure 7).

Figure-7. The environment-vector view of the GGE bi-plot to show similarities of oil content



E2 =Humera-2, E4=Dansha-2, E6=Sheraro-2, E8=Wargiba-2, E9 =Maykadra, E10 =Gendawuha. G1= HuRC-4, G2= ACC202514, G3= Land race Gumero, G4= Abuseffa, G5= HuRC-1, G6= Rawyan -2, G7= HuRC-3, G8= Acc 202300, G9= Kefif, G10= Acc111824, G11= Acc 111518, G12= Acc 27913, G13= Gumero, G14= HuARC-2, G15= Acc 227880, G16= Setit -1, G17= Hirhir

4. Summaryand Conclusion

According to the GGE bi-plot different sesame growing environments grouped into two for yield production: The first environment containing the favorable environment Dansha area with a vertex G4 and Sheraro area with winner G3; and second environment includes medium to low environments E2 (Humera-2), E4 (Dansha-2), E5 (Sheraro-1), E7 (Wargiba-1), E8 (Wargiba-2) and E9 (Maykadra). GGE bi-plot classified three different sesame growing mega-environments for oil content production: The 1st environment containing G12, G7 and G2 in the mega-environment group of Humera, Dansha and Gendawuha. The 2nd environment, Sheraro containing G9 and the 3rd environment Wargiba contained G17. AMMI model and GGE bi-plot were better for partitioning the GEI into the causes of variation. G1, G7, and G3 were high yielder and the most stable both in terms of seed yield and oil content. Moreover, showed yield advantage over the standard and local check. Hence, G1, G7 and G3 were recommended for wider environments and G14 and G4 for favorable environments Sheraro and Dansha, respectively.

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