Genotype x Environment Interaction and AMMI Analysis of Oil Yield Sesame (*Sesamum indicum* L.) Genotypes in Northern Ethiopia

Yirga Belay Kindeya[1, *], Firew Mekbib[2], Eyasu Abraha Alle[3]

[1]Crop Department, Humera Agricultural Research Center (HuARC), Tigray, Ethiopia

[2]College of Agriculture and Environmental Science, School of Plant Science, Department of Plant Breeding and Genetics, Haramya University, Dire Dawa, Ethiopia

[3]Crop Department, Tigray Agricultural Research Institute (TARI) General Director, Tigray, Ethiopia

Email address:
yirgabelay66@gmail.com (Y. B. Kindeya), yirgabelay@ymail.com (Y. B. Kindeya), firew.mekbib@gmail.com (F. Mekbib),
eyasuabraha@gmail.com (E. A. Alle)
*Corresponding author

Abstract: The study was conducted to evaluate the nature and magnitude of Genotype x Environment Interaction (GEI) for oil yield of sesame genotypes and to identify stable and promising genotypes for general and specific adaptations across sesame growing areas of northern Ethiopia: Humera, Dansha, Maykadra, Sheraro, Wargiba and Gendawuha. Randomized Complete Block Designs (RCBD) with three replications across all the environments used. Seventeen white seeded sesame genotypes were evaluated in all locations. The combined analysis of variance revealed that highly significance difference (p<0.001) among genotypes, environments and GEI for oil yield. The grand mean oil yield over six environments was 296.6kg/ha and the mean oil yield of genotypes across six environments ranged between 125.48kg/ha in Humera to 531.21kg/ha in Sheraro, respectively. High mean oil yield variation was detected among genotypes ranged between 193.6 kg/ha for G8 and 409.4kg/ha for G1 respectively. The oil yield of genotypes varied to different environments with rank changed, this variation among genotypes indicating that selection should be based on mean oil yield performances of the genotypes to their respective environments. According to stability models, AMMI Stability Value (ASV), Yield Stability Index (YSI) and Environmental Index (EI) land racegumero and HuRC-4 were identified as the most stable and higheroil yield were recommended for wider areas. While, HuRC-2and Acc 227880 were unstable accompanied with high oil yield performance will be recommended for specific environments.

Keywords: ASV, GEI, Oil Yield, Northern Ethiopia, White Seeded Sesame, YSI

1. Introduction

Sesame (*Sesamum indicum* L.*)* belongings to family Pedaliaceae, is an important and ancient oil-yielding crop. It has an edible seed and has high quality oil [1]. Sesame in differentcountries has different names; til (Hindi), hu ma (Chinese), sesame (French), goma (Japanese), gergelim (Portuguese) and ajonjoli (Spanish) [2]. In Ethiopia sesame known as *Selit* in Amharic and Tigrigna, *Sallet* in Affan Oromo [3, 4] Reported that cultivars grown at numerous sites

in the USA showed significant sesame GEI of oil content. A study on oil yield of sunflower for stability and adaptability at eight locations in Pakistan indicated that the GEI contributed about 85.45% of total variation, which is an indication that a stability analysis of genotypes with respect to oil yield based on location index is important [5]. Variety development and agronomic research in Ethiopia has resulted in the development of high yielding varieties out of introduced, locally collected and segregating populations using multi-location testing and verification. A considerable

variation in oil yield is observed on released varieties and elite genotypes under trial across locations [6].

The yield is low as compared to other oilseeds, due to mainly the lack of improved varieties for use by the farmers, erratic rainfalland pests [7]. Sesame genotypes showed different performance under different sesame growing environments. Failure of genotypes to respond consistently to variable environmental conditions is attributed to GEI [8]. A considerable variation on oil yield was observed on released varieties and elite genotypes under trial across locations. However, studies on the effects of GEI in sesame oil yield are quite few [6] Assessing any genotype performance without including its interaction with the environment is incomplete and limits the accuracy of measured parameter estimates. Study on the effect of GEIin globally market demanded white seeded genotypes oil yield worldwide and in Ethiopia is no or

limited. So this experiment was done (i) to evaluate the magnitude and nature of GEI oil yield of different white seeded sesame genotypes, (ii) to identify stable and oil yield performance of white seeded sesame genotypes across different sesame growing environments.

AMMI method integrates analysis of variance and principal components analysis into a unified approach [9]. According to [10, 11] 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 [9]. Secondly, AMMI clarifies the GEI and summarizes patterns and relationships of genotypes and environments [10, 11].
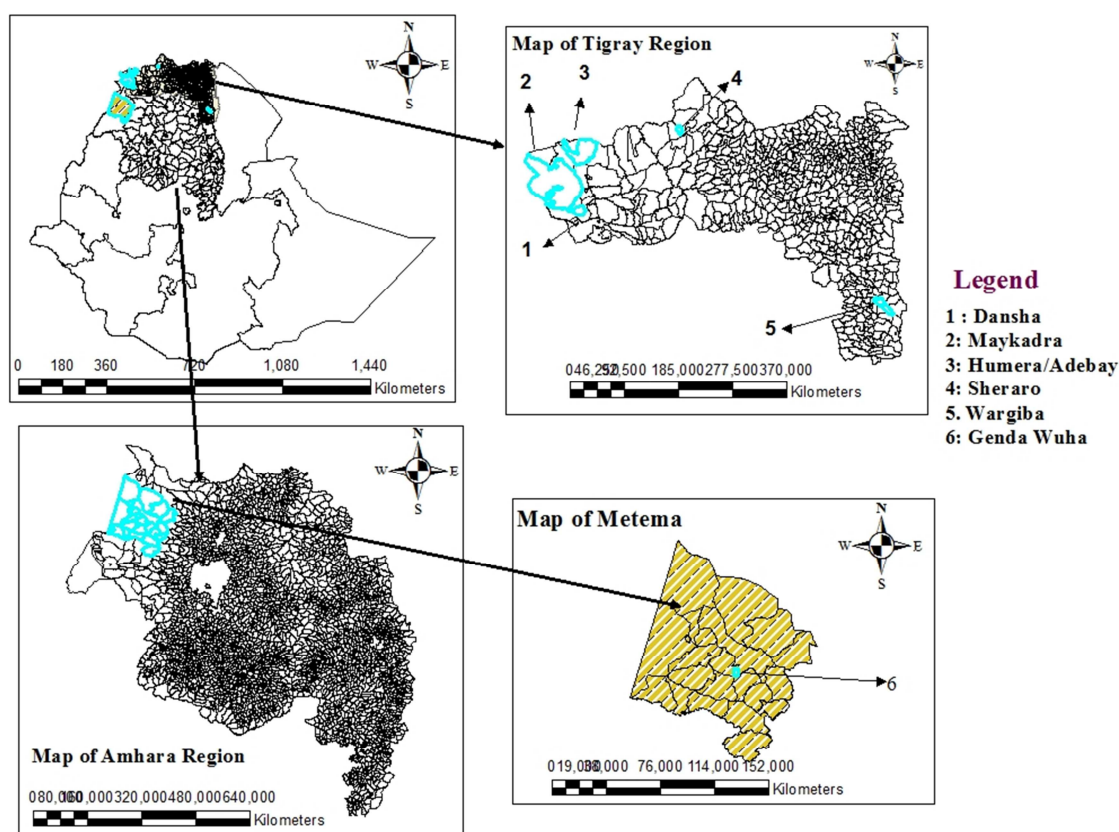
2. Materials and Methods

Figure 1. Map of test sites in Northern Ethiopia.

Table 1. Agro-climatic and soil types of experimental 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 Characteristics	Vertisol	Chromic vertisol	Chromic Vertisol	Vertisols	NA	Vertisol

Source: [12] Meteorology data for (Dansha, Humera, and Maykadra): [13] IPMS Ethiopia, (for Gendawuha). NA=Not Available.

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

Location	Region	Zone	District	Year	
				2014	2015
Humera	Tigray	Western	K/Humera	E1	E2
Dansha	Tigray	Western	Tsegede	E3	E4
Sheraro	Tigray	N/western	T/Adyiabo	E5	E6
Wargiba	Tigray	Southern	R/Azebo	E7	E8
Maykadra	Tigray	Western	K/Humera	-	E9
Gendawuha	Amhara	-	Metema	-	E10

Note: K/Humera=KaftaHumera, T/Adyiabo=TahtayAdyiabo, 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.

Experimental Plant Materials Used in the Study

Table 3. Description of genotypes used in the study.

Genotype (G)	Code	Status	Sources	Seed color	Remark
HuRC-4	G1	Advance line	HuARC	White	Collection
ACC202514	G 2	Advance line	HuARC	White	Collection
Land racegumero	G 3	Advance line	HuARC	White	Collection
Abuseffa	G 4	Advance line	HuARC	White	Collection
HuRC-1	G 5	Advance line	HuARC	White	Collection
Rawyan -2	G 6	Advance line	HuARC	White	Collection
HuRC-3	G 7	Advance line	HuARC	White	Collection
Acc 202300	G 8	Advance line	HuARC	White	Collection
Kefif	G 9	Advance line	HuARC	White	Collection
Acc111824	G 10	Advance line	HuARC	White	Collection
Acc 111518	G 11	Advance line	HuARC	White	Collection
Acc 27913	G 12	Advance line	HuARC	White	Collection
Gumero	G 13	Advance line	HuARC	White	Collection
HuRC-2	G 14	Advance line	HuARC	White	Collection
Acc 227880	G 15	Advance line	HuARC	White	Collection
Setit -1 (Standard check)	G 16	Released	HuARC	White	Collection
Hirhir (Local check)	G 17	Local	HuARC	White	Collection

Source: Humera Agricultural Research Center (HuARC) (2014) [14].

2.1. Experimental Design and Management

The experiment was laid out in randomized complete block design (RCBD) with three replications in all testing sites. 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 10cm, respectively. Each plot had a total area of $10m^2$ and total of five rows and $6m^2$ net plot area with three harvestable rows. Each experimental plot received the same rate of DAP (100 kg/ha) and Urea (50 kg/ha) fertilizer and all managements were done equally and properly as per the recommendations for the study areas.

2.2. Data Collection

From the harvestable three rows ten plants were selected randomly and tagged to collect data of plant height, length of capsule bearing zone, number of branches, number of capsules and seeds per capsule. The three experimental rows were harvested, tied in sheaves and were made to stand separately until the capsules opened. After the sheaves have dried out fully and all of the capsules opened, seeds were tipped out onto sturdy cloths or canvases and threshing was accomplished by knocking the sheaves. Oil yield was calculated by multiplying seed yield (kg/ha) and oil content

(%) from each plot.

2.3. AMMI Analysis

AMMI analysis, which combines analysis of variance (ANOVA) with additive and multiplicative parameters in to a single model [10]. Principal component analysis (PCA) is analyzes a data table in which observations are described by several inter-correlated quantitative dependent variables [15]. The variance explained by each principal component is expressed in terms of its eigenvalue. For this reason, principal components are usually arranged in order of decreasing eigenvalues or declining information content. From this point of view the most informative principal component is the first and the least informative is the last and each principal component are uncorrelated. Principal component analysis combined with cluster analysis was effective in forming sub groups among populations and explaining the associations of the traits and the PCs [16]. The number of components extracted is equal to the total amount of variance in PCA which are also equal to the number of observed variables being analyzed. However, to select maximum number of PCs for better interpretation different rules set by different scholars are: (1) Eigenvalue-one criterion or Kaiser criterion[17] (If the eigenvalue is greater than 1, then each principal component explains at least as

much variance as 1 observed variable); (2) the Scree test[18] (looking for a break between consecutive PCs); (3) Proportion of variance for each component (5-10%) and cumulative proportion of variance explained (70-80%).

A bi-plot showing the genotype and environmental means against IPCA1 was also performed *via* this model using [19]. The AMMI model is:

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

Where: Y_{ij} is the observed mean yield of ith genotype in the jth environment; μ is the grand mean; G_i is the ith genotypic effect; E_j is the jth environment effect; λ_k is the eigen value of the principal component analysis (PCA) axis k; α_{ik} and γ_{jk} are the ith 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.

2.4. AMMI Model

AMMI analysis were shown in common graph called biplot as described by [20] which provides a clear insight into specific GEI combination and the general pattern of adaptation of genotypes. The AMMI biplot was done by placing the genotype and environment means on the abscissa (X- axis) and the respective PCA score, Eigen vector on the Y- axis.

AMMI Stability Value (ASV)

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}}(IPCA1_{score})\right]^2 + (IPCA2_{score})^2}$$

Where, ASV=AMMI stability value, SS=sum of squares, IPCA1=interaction of principal component analysis one,

IPCA2=interaction of principal component analysis two.

2.5. Yield Stability Index (YSI)

Yield Stability Index (YSI) was also computed by summing up the ranks from ASV and mean seed yield [21] YSI=RASV+RGY, Where: RASV is rank of AMMI stability value and RSY is rank of mean seed yield to statistically compare the stability analysis procedures used in the study, the Spearman's coefficient of rank correlation [22] (r_s) was estimated using SPSS version 16 statistical software.

3. Results and Discussion

AMMI Analysis

The mean seed yield of white seeded sesame genotypes were evaluated during 2014 at four locations and in 2015 at six locations (Totally ten environments). But oil content and oil yield were evaluated during 2015 cropping season for only one year during 2015 cropping season. Mean squares of genotypes, environments and GEI were highly significant (P < 0.001), indicating the existence of differential responses of genotypes to different environments and suggests the need for the extension of G x E analysis (Table 4). This significance variation gives a chance for selecting better performing genotypes for oil yield production in sesame production areas. The AMMI model extracted four significant IPCAs leading to a cumulative of 96.42% of variation and the rest 3.68% was contributed due to noise. From the total variation environments (71.02%) followed by GEI (13.12%) and genotypes (8.81%) explained, respectively. This large percent variation showed that environment had considerable influence on oil yield variation in sesame genotypesacross locations. This result is in line with [6, 23, 7] in sesame.

Table 4. Combined AMMI analysis of variance for oil yield of 17 sesame genotypes.

Source of variation	df.	SS.	MS.	Sum of squares Explained (%)		
				Total V. E.	GEI E.	GEI cum.
Genotypes	16	813296	50831**	8.81		
Environments	5	6555320	1311064**	71.02		
Block	12	279524	23294**	3.03		
Interactions	80	1210817	15135**	13.12		
IPCA 1	20	506356	25318**		41.82	41.82
IPCA 2	18	333190	18511**		27.52	69.34
IPCA 3	16	193234	12077**		15.96	85.30
IPCA 4	14	134673	9619**		11.12	96.42
Residuals	12	43365	3614			
Error	192	370789	1931			
Total	305	9229747	30261			

Block=replication within environments. Total V. E. =Total variation explained, GEIE. =GEI explained and GEI coum. =GEI cumulative, SS=Sums of squares and MS=Means of squares.

Genotypic Adaptability and Stability Analysis

The mean seed yield of white seeded sesame genotypes were evaluated during 2014 at four locations and in 2015 at six locations (Totally ten environments). But oil content and oil yield were evaluated for only one year during 2015 cropping season. The average mean oil yield of sesame

genotypes over six environments was 296.6kg/ha and the mean oil yield of genotypes ranged between 125.48kg/ha in Humera to 531.21kg/ha in Sheraro respectively. High oil yield variation was detected among genotypes ranged between 193.6 kg/ha for G8 to 409.4kg/ha for G1 (Table 5). This variation among genotypes indicating that selection

should be based on mean oil yield performances. High yielder genotypes gave highest oil yield and low yielding genotypes gave low oil yield. Hence, the breeding strategy should be based on wider adaptive and high yielder genotypes. This result is in line with [24, 7, 8] in sesame.

Table 5. *Means and PCA1 scores of genotypes and environments for oil yield.*

				Locations				
G	Humera	Dansha	Sheraro	Wargiba	Maykadra	Gendawuha	Mean	IPCA1
1	187.2	341.4	669.3	365	363.4	546.9	409.4	1.38011
2	119.4	337.4	494.9	98.5	118.4	407.7	260.8	-1.7776
3	182	236.4	518.5	181.9	222.4	407.6	289.5	0.14587
4	118.8	392.3	670.1	178.6	161.8	231.1	290.7	9.27948
5	119.9	264.3	595.4	342.3	244	392.1	324.8	5.1854
6	119.9	168.6	445.1	234.3	162.1	418.4	256.8	-0.3384
7	186	245.9	600.2	326.1	323.8	516.4	363.6	0.75946
8	56.9	175.3	375.9	140.2	84.6	331.7	193.6	-0.8731
9	77.8	174.9	463.9	227.6	97.7	438.4	246.1	0.29706
10	83.4	279	426.7	113.5	193.3	435.4	254.4	-4.9805
11	65.7	191	556	150.2	104.7	403.4	244.3	2.74381
12	131.7	401.3	393.7	185.1	165.2	557.2	303.5	-9.1107
13	89	261	482.5	141.9	160.3	450.8	262.8	-2.5181
14	233.6	240.1	651.6	365	132.3	500.9	350	6.09432
15	124.9	286.1	425.9	171	390.2	557.5	324	-10.054
16	118.7	266.1	650.8	187.7	206	617.8	339.1	-1.5954
17	118.2	179.5	610.1	273.3	218.9	401.8	298.3	5.36258

G14, G17, G5, G7, G1, G16, G12 and G15 had above mean oil yield in the favorable environments, while, G4, G11, G8, G10, G3, G10, G13, G2, G9 G6 were below the average mean oil yield in the unfavorable environments. G1, G7, G16, G3, G9, G6, G8 and G2 were nearly closed to the origin and the most stable with little responsive to the GEI. While, G15, G12, G4, G14 and G10 far from the origin are sensitive to environmental changes and the most unstable.

Hence, high yielder and wider stability performance genotypes are the most desirable for wider area recommendation. Environments suitability are also classified according their position found in the quadrant. Sheraro and Gendawuha on 1st and 2nd quadrant were favorable environments. Whereas, Wargiba, Humera, Dansha and Maykadra on 3rd and 4th quadrant graph were considered as unfavorable environments for oil yield production.
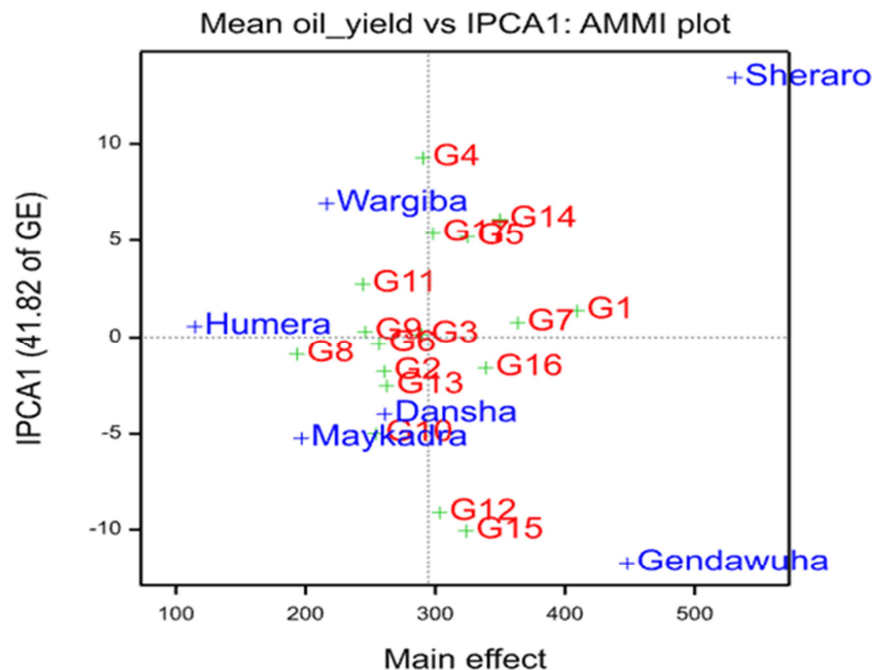
Figure 2. *AMMI biplot of IPCA1 vs. Main effects using oil yield. G1=HuRC-4, G2=ACC202514, G3=Land race Gumero, G4=Abuseffa, G5=HuRC-1, G6=Rawyan -2, G7=HuRC-3, G8=Acc 202300, G9=Kefif, G10=Acc111824, G11=Acc 111518, G12=Acc 27913, G13=Gumero, G14=HuARC-2, G15=Acc 227880, G16=Setit -1, G17=Hirhir.*

AMMI Stability Value (ASV)

AMMI stability value (ASV) was developed by Purchase to quantify and rank the genotypes on the basis of their yield stability. Genotypes with least ASV scores are the most

stable, on the other hand, genotypes with high ASV score are unstable once[25]. According to this model, G3, G8, G16, G1 and G9 were the most stable. G4 were the most unstable followed by G10. G14, G12 and G15 (Table 5). Similar results were reported [16] in maize, [24, 7] in sesame. Stable genotypes will be recommended for seed yield, oil content and oil yield in different sesame growing environments of northern Ethiopia. The favorable environments also suitable for seed yield, oil content and oil yield production. Investors,

farmers, researchers will benefit from this result.

Yield Stability Index (YSI)

Genotypes with lowest estimated value are desirable and considered as the most stable. Based on YSI, G1, G3, G7, G14 and G16 were stable and ranked 1st, 3rd, 3rd, 5th, and 2nd. Conversely, G4, G10 and G11 were unstable ranked 10th, 11th and 9th, respectively (Table 6). Similar results were reported [23, 24] in sesame.

Table 6. Oil yield, AMMI Stability Value (ASV), Ranks, IPCA1 and IPCA2 scores.

G.	OY	R	IPCA1	IPCA2	IPCA1SS	IPCA2SS	ASV	R	YSI	R
G1	409.4	1	1.38011	2.54712	506356	333190	3.3	4	5	1
G2	260.8	12	-1.77762	-7.43663	506356	333190	7.91	10	22	8
G3	289.5	10	0.14587	-0.46914	506356	333190	0.52	1	11	3
G4	290.7	9	9.27948	-11.8884	506356	333190	18.4	17	26	10
G5	324.8	5	5.1854	1.87995	506356	333190	8.1	11	16	4
G6	256.8	13	-0.33844	4.02139	506356	333190	4.05	6	19	6
G7	363.6	2	0.75946	5.19844	506356	333190	5.33	9	11	3
G8	193.6	17	-0.87309	-0.36236	506356	333190	1.38	2	19	6
G9	246.1	15	0.29706	3.49653	506356	333190	3.53	5	20	7
G10	254.4	14	-4.98051	-2.91633	506356	333190	8.11	13	27	11
G11	244.3	16	2.74381	-0.08792	506356	333190	4.17	7	23	9
G12	303.5	7	-9.11068	-4.38595	506356	333190	14.5	15	22	8
G13	262.8	11	-2.51813	-1.67903	506356	333190	4.18	8	19	6
G14	350	3	6.09432	4.09282	506356	333190	10.1	14	17	5
G15	324	6	-10.0542	2.09433	506356	333190	15.4	16	22	8
G16	339.1	4	-1.59542	2.01329	506356	333190	3.15	3	7	2
G17	298.3	8	5.36258	3.88195	506356	333190	9.03	12	20	7

OY=oil yield, R=rank, ASV=AMMI stability value, IPCA1=, interaction principal component analysis one, IPCA2=, interaction principal component analysis two, IPCASS1=interaction principal component analysis sum square one, IPCASS2=interaction principal component analysis sum square two.

Ranking of seed yield, oil content, oil yield and ASV

The ranking order of the seventeenwhite seededgenotypesfor oil yield, based on the different stability parameters is indicatedin Table 7. The mean oil yield (kg/ha) together with the mean oil content (%) and mean seed yield (kg/ha) were used for ranking of genotypes. Based on the ranking procedure, a variety that had high mean oil yield (greater than the grand mean) with least overall ranking (OR) was considered as the most stable genotype for oil yield across all environments. Whereas, genotypes had high mean

oil yield with large overall ranking value was considered to have specific adaptation in favorable environments for oil yield. As a result, genotypes G1, G16, G7 and G3were showed highest mean oil yield with lowest overall rank and the most stable genotypes for oil yield across environments. Whereas, G6, G8, G9 and G10 had high overall rank and below average mean oil yield. Genotypes below average mean oil yield and high overall rank can be considered as poorly responsive and unstable genotypes in table 7.

Table 7. Overall ranking ofSY (kg/ha), oil content (%), oilYield (kg/ha), ASV and YSI ranks.

G	SY	R	OC	R	OY	R	ASV	R	SYI	R	OR
1	867.4	1	50.17	12	409.4	1	3.3	4	5	1	2
2	583.3	12	51.07	6	260.8	12	7.91	10	22	8	10
3	753.8	3	50.73	9	289.5	10	0.52	1	11	3	4
4	668.6	7	50.86	7	290.7	9	18.4	17	26	10	11
5	694.6	6	49.7	17	324.8	5	8.1	11	16	4	8
6	597.7	11	49.73	16	256.8	13	4.05	6	19	6	12
7	792.5	2	51.13	5	363.6	2	5.33	9	11	3	3
8	441.8	17	49.98	15	193.6	17	1.38	2	19	6	14
9	562.1	14	50.09	14	246.1	15	3.53	5	20	7	13
10	548.1	16	50.1	13	254.4	14	8.11	13	27	11	16
11	561.3	15	50.21	11	244.3	16	4.17	7	23	9	15
12	619.1	10	51.86	1	303.5	7	14.5	15	22	8	6
13	571.8	13	50.47	10	262.8	11	4.18	8	19	6	10
14	723.6	5	51.48	2	350	3	10.1	14	17	5	5
15	662.9	8	51.23	4	324	6	15.4	16	22	8	7
16	745.1	4	51.24	3	339.1	4	3.15	3	7	2	1
17	645.5	9	50.84	8	298.3	8	9.03	12	20	7	9

G=genotype, SY=seed yield, R=rank, OC=oil content, OY=oil yield, ASV, AMMI Stability Value, SYI –stability yield index, OR=overallrank.

4. Conclusion

Environmentshad above average meanoil yield wereconsidered as favorable. while, below the average mean oil yield were unfavorable environments. Stable genotypes were adaptive to wider areas and gave consistency mean oil yield across the tested locations. Therefore, G1, G7, G16, G3, G9, G6, G8 and G2 were found nearly closerto the origin and the most stable with little responsive to the GEI. While, Genotypes far from the origin were sensitive to environmental changes and unstable and suitable to specific areas. According to the stability models, AMMI, ASV, YSI, G7 (land race gumero) andG1 (HuRC-4) was identified as the most stable with high oil yield will berecommended for wider sesame growing environments where as G14 (HuRC-2) and G15 (Acc 227880) will be for favorable environments.

Abbreviations

ASV=AMM Stability Value, GEI=Genotype x Environment interaction, METs=Multi Trial Environments, YSI=Yield Stability Index

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