SciencePG
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Research Article

Genotype by Environment Interaction and Grain Yield Stability of Sesame (*Sesamum indicum* L.) Genotypes in Hararghe Zones, Eastern Oromia

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Abstract

Sesame 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. Multi-environment yield trials are widely used for selecting superior sesame advanced lines to be released as a new variety for target environments in Ethiopia sesame breeding programs. The study was conducted for two years at Mechara, Milkaye, Ibsa and Fadis in 2021, 2022 cropping season. Total of 18 sesame genotypes including standard checks were planted in Randomized Complete Block Design with three replications. The objective of the experiment to estimate the magnitude of GEI and to select stable and adaptable genotypes for the target environment(s). AMMI analysis of variance revealed that, there were highly significant (p< 0.001) differences among environments, genotypes and genotype by environment interaction for grain yield. Genotype G15 (972kgha^{-1}) was showed the mean yield performance across the test environment with 46.67% yield advantage over average yield, the most stable. Milkaye was identified as high yielding and best desirable testing environment for sesame production. Therefore, genotype G15 was proposed as candidate variety for verification trial and possible release and it can be used as parent material in the future breeding program.

Keywords

Sesame (*Sesamum indicum* L.), Genotype, AMMI, GGE Bi-plot, GEI, Seed Yield

1. 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. Sesame is 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 [3]. In Ethiopia, Sesame is important oil crop in terms of both area coverage and production [6] the target of sesame breeding in Ethiopia is to develop varieties that meet the demands of sesame growers, processors, and consumers.

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 and stable environments. Multi-environment yield trials are widely used for selecting superior sesame advanced

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lines to be released as a new variety for target environments in Ethiopia sesame breeding programs. Information on the adaptation and stability of the genotypes over seasons and over sites is useful for recommending the varieties that should be grown under particular production environments and predicting the yield expectations of the test genotypes. A Genotype is considered to be the most adaptive or stable one if it has a high mean yield but a low degree of fluctuation in yielding ability when grown over diverse environments [2]. A significant portion of the resources of crop breeding is devoted determining GEI through replicated multiplication trial.

Multi environment yield trial can be analyzed to extract more information on stability, adaptability and yield performance using various statistical methods and software used by different investigators [9, 17]. AMMI model and GGE bi plot analysis are shows visual examination of the relationships among the test environments, genotypes and the genotype by environment interactions [7]. Therefore; the objectives of this study was to estimate the magnitude of GEI and to select stable and adaptable sesame genotype/s for the target environment(s).

2. Materials and Methods

2.1. Study Site

The experiment was conducted at three locations; Milkaye and Mechara on station, (Daro labu district), Ibsa (Hawi Gudina district) and East Hararghe Fedis on station during 2021 and 2022 main cropping season.

2.2. Treatments and Experimental Design

Total of sixteen genotypes including two standard checks tested using Randomized Complete Block design (RCBD) with three replications. A plot size of 6 rows with row spacing of 1.8meter and row length of 2.5m was used and the four middle rows were used for data collection. For statistical analysis, yield from net plot area of $2m^2$ was harvested and converted into tonha^{-1} base at 10% grain moisture content. Seed rate of 5 kgha^{-1} was used and planted by drilling. Fertilizer was applied at 100 kg ha-1of NPS and 50 kg ha-1 urea at planting.

Table 1. List of Genotypes tested.

SN.	Genotype code	Genotype name	Source
1	G1	BKC 104-1	BARC
2	G2	BKC 138-1	BARC
3	G4	ACC-EW-023 (2)	BARC
4	G6	EW006*BG006-2-1-1	BARC
5	G7	BKC 010-2	BARC
6	G8	EW002 * Wama-10-2-1	BARC
7	G9	BKC 102-1	BARC
8	G10	MTM-12 13 23 (2)	IEB
9	G11	EW002 * Dicho -5-3	BARC
10	G12	BKC 010-2	BARC
11	G13	Dicho *EW006-9-1	BARC
12	G14	MTM-23 13 12 (3)	IEB
13	G15	BG006 * 010-1-2-2-1	BARC
14	G16	Obsa*EW023(2)-2-1-1	BARC
15	G18	BKC 112-1	BARC
16	G3	EW002 *Obsa 21-1	BARC
17	G5	Bha Zeyit	HU(Standard check)
18	G1	Bha Necho	HU(Standard check)

2.3. Data Collected

2.3.1. Phenological Parameters

Days to flowering was recorded by counting the number of days after emergence when 50% of the plants per plot had the first open flower. Days to maturity was recorded when 90% of capsule matured per plot.

2.3.2. Grain Yield and Yield Components

Four central rows were harvested for determination of grain yield. Grain yield was adjusted to 8% moisture content. Five plants were randomly selected from the four central rows to determine yield and yield components, which consisted of number of capsule per plant and number of branch plant. Capsules number per plant was determined by counting capsules of the five randomly selected plants. While number of primary branch was recorded by counting the total of number of branch per plant from five randomly selected plants.

2.4. Data Analysis

Different statistical software packages were used to analyses the data. [12] Was used for analysis of variance of the individual environments and the combined data over locations. Gen Stat 18th edition AMMI and GGE bi-plot analysis.

AMMI Stability Value (ASV) was calculated for each genotype according to the relative contribution of the principal component axis score (IPCA 1 and IPCA 2) to the interaction sum of squares [11].

Genotype Selection Index (GSI) was calculated based on the rank of mean grain yield of genotypes (rYLD) across environments and the rank of AMMI stability value (rASV) a selection index (GSI) was calculated for each genotype in which it incorporates both mean grain yield and stability index in a single criterion (as GSI= rASV + rYLD).

The combined analysis of variance across environments was done in order to determine differences between sesame genotypes data of each trait was subjected to combined analysis of variance to estimate the effect of environmental, genotype and genotype x environment interaction by using the following statistical model:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{k(j)} + e_{ijk}$$

Where Yijk = observed value of genotype i in block k of environment (location) j, μ = grand mean, G_i = i[th] genotype effect, E_j= j[th] environment or location effect, GE_{ij} = the interaction effect between i[th] genotype and j[th] environment, $B_{k(j)}$= the effect of block k in location (environment) j, e_{ijk} = error (residual) effect of genotype i in block k of environment j.

3. Result and Discussion

The combined analysis of variance revealed that high significant (P<0.001) variation among genotypes, locations and GE interaction for mean grain yield of sesame genotypes (Table 2). The significance of GEI for grain yield indicates that genotypes responded differently to the tested environments. Furthermore, they have explained that the significances variation among the environments indicate that these locations can be used as testing stations for different environments while significant differences among genotypes reveals the differential response of genotypes to different environments.

Table 2. The combined ANOVA for grain yield of sesame genotypes over locations and years.

Source of variation	DF	SS	MS	F. Value	Pr (>F)
Replication	1	65409	65409	1.455	0.23001 ns
Location	6	11695900	1949317	43.357	0.0001***
Genotype	17	2453684	144334	3.21	0.0001***
Replication (with in Location)	6	8558774	142646	3.173	0.00622 **
Location* Genotype(Interaction)	102	7387124	72423	1.611	0.00552 **
Residuals	126	5664890	44959		

Key: ** = highly significant and ns= non-significant, DF.=degree freedom, SS= Sum of square, MSS= Mean Sum of square

3.1. Yield Performance Across Environments

The performance of the tested sesame genotypes for grain yield across location and year presented in (Table 3). The average grain yield ranged from the lowest 240kgha-1 at McARC on station in year-2 to the highest 1152.7kgha[-1] Milkaye site in year-1, with grand mean of 722.36kgha-1. The grain yield across environments ranged from the lowest

of 589.35 kgha-1for G4 to the highest of 971.83 kgha^{-1} for genotype G15. This wide variation might be due to their genetic potential of the genotypes. Genotype G15 was the top ranking genotype in all environments across the years (Table

3), The difference in yield rank of genotypes across the environments exhibited the high crossover type of genotypes x environmental interaction [4, 15].

***Table 3.** Combined mean yield of sesame genotypes across four locations over two years (2021 -2022).*

Genotype	McARC year 1	McARC year 2	Milkaye year1	Milkaye year 2	Ibsa year 1	FARC year 1	FARC year 2	Over all Mean	Yield Ava.%
ACC-EW-023 (2)	538.19	402	756.94	548	723.95	777.76	396.7	589.35	0
BG006 * 010-1-2-2-1	611.11	635	815.97	744	765.62	822.22	766.7	734.72	8
Bha Necho	434.02	485	736.11	738	683.33	764.81	912.5	675.37	0
Bha Zeyit	395.83	610	652.77	915	578.12	942.59	575	662.573	0
BKC 010-2	625.00	619	847.22	475	781.25	900.00	488.3	672.42	0
BKC 102-1	604.16	479	809.02	810	765.62	752.78	487.5	668.29	0
BKC 104-1	847.22	615	1104.16	715	923.95	834.72	554.2	794.23	17
BKC 112-1	722.22	638	947.91	765	890.62	796.29	745.8	781.05	15
BKC 138-1	628.47	485	847.22	573	807.29	936.11	529.2	683.60	0
Dicho *EW006-9-1	677.08	715	937.5	673	869.79	918.51	491.7	749.86	11
EW002 * Dicho -5-3	229.16	983	392.36	881	572.91	636.11	608.3	610.29	9
EW002 * Wama-10-2-1	631.94	610	857.63	742	828.12	895.83	704.2	747.46	10
EW002 *Obsa 21-1	552.08	550	798.61	952	724.10	948.14	730	745.23	10
EW006*BG006-2-1-1	555.55	785	798.61	825	734.37	936.11	704.2	756.93	12
EW023(2) *BG006-13-1-1	427.08	654	677.08	931	609.37	598.14	708.3	652.88	3
MTM-12 13 23 (2)	781.25	240	1045.13	556	901.04	992.59	1020.8	786.84	16
MTM-23 13 12 (3)	795.14	710	1086.8	675	921.87	688.88	520.8	766.67	13
Obsa*EW023(2)-2-1-1	1107.63	863	1152.7	1017	1057.29	909.25	741.7	971.83	43.8
Mean	620.17	487	846.64	898	785.47	836.16	836.16	722.36	
CV%	39.6	33.5	31.97	30.5	29.29	16.96	16.96		
LSD	402.61**	270.8*	443.78**	454.8ns	377.16**	235.09*	235.09*		

Key: McARC= Mechara Agricultural Research Center, Fedis= Agricultural Research Center, CV= coefficient of variation in percentage, LSD= least Signiant difference at 5 percent

3.2. AMMI Analysis

The AMMI model analysis of variance for grain yield showed highly significant differences ($P \leq 0.01$) for genotypes, environments and genotypes by environments interactions. Partitioning of the variance components indicated that 34.09% was due to environment, 5% due to replication, 7.15% due to genotype, and 21.5% due to GEI (Table 4). The large proportion of variance due to environment and low contribu-

tions of variance due to genotype and medium due to GEI. Great variation indicates the significant influence of environment in evaluation of sesame genotypes for yield performance. The present finding line is with [6], who found similar results in sesame.

The first IPCA captured 45.57%of the interaction sum of squares; similarly, the second IPCA explained 30.19% of the GEI sum of squares. The sum of squares for the first two IPCAs cumulatively contributed to 75.76 % of the total GEI.

Table 4. AMMI analysis of variance for grain yield tested at seven environments.

Source variation	DF	SS	MSS	% Explained SS
Total	377	34299202	90979	
Treatments	125	21536708	172294***	62.79.
Genotypes	17	2453684	144334***	7.15
Environments	6	11695900	1949317***	34.09
Replication	14	1737221	124087***	5
Interactions	102	7387124	72423**	21.5
IPCA1	22	3366452	153021**	45.57
IPCA2	20	2230268	111513***	30.19
Residuals	12	12871	1073	
Error	238	11025273	46325	

Note: d.f. = degree freedom, SS= Sum of square, MSS= Mean Sum of square, SS%= Percentage of sum of square, IPCA 1and 2= first and second principal component

3.3. AMMI Stability Value (ASV)

AMMI Stability Value (ASV): [11] indicated ASV as the distance from the coordinate point to the origin in a two dimensional scatter gram of IPCA1 scores against IPCA2 score should also see to decide the stability of genotypes. The genotypes with low stability value (ASV) is said to be stable and the breeder chose the stable genotypes, having grain yield above the grand mean yield. In this study genotype G14 showed lowest ASV followed by G16, G3, G1, G8 and G15 (Table 5) indicating these genotypes can be suitable for the studied environments. However, since stability in itself should not be the only parameter for selection, as the most stable genotype wouldn't necessarily give the best yield performance [10].

3.4. Genotype Stability Index (YSI)

Genotypes with the least genotype stability index (GSI) and high grain yield are considered as the most stable [8]. Genotypes with lowest estimated value are desirable and considered as the most stable. Based on genotype stability index (GSI), G15 and G16 had the lowest GSI values and high mean yield over average yield and showed stable performance over the testing sites. Therefore, these genotypes are wide adaptation.

Table 5. AMMI stability value with IPCA 1 and IPCA 2 scores for yield and yield stability index.

Genotype code	Grain yield	RMYD	IPCA1	IPCA2	ASV	RASV	GSI	RGSI
G15	893.58	1	-4.13	-3.94	4.44	5	6	1
G6	778.37	2	-4.5	1.21	6.36	9	11	4
G11	775.99	3	-17.94	-5.63	24.65	17	20	9
G17	751.64	4	5.64	-9.96	11.1	14	18	7
G16	722.68	5	0.93	1.5	1.718	2	7	2
G3	718.58	6	1.13	-8.12	8.15	11	17	6
G8	709.52	7	2.09	3.22	3.73	4	11	4
G18	709.25	8	-2.26	-13.11	13.19	15	23	11
G14	708.53	9	0.49	-0.44	0.95	1	10	3
G12	697.28	10	-5.66	9.08	9.1	12	22	10

Genotype code	Grain yield	RMYD	IPCA1	IPCA2	ASV	RASV	GSI	RGSI
G13	697.28	11	-7.6	4.54	4.9	8	19	8
G1	668.05	12	-2.1	2.01	2.92	3	15	5
G5	667.11	13	8.09	-3.14	10.66	13	26	13
G9	633.13	14	3.17	-5.58	6.22	10	24	12
G10	617.98	15	21.26	4.57	31.61	18	34	15
G2	603.9	16	3.33	3.48	4.8	7	23	11
G7	600.11	17	-4.19	16.3	16.56	16	33	14
G4	521.94	18	2.22	4.02	4.45	6	24	12

Key: ASV= AMMI stability value, RASV=Rank of AMMI stability value, RMYD=Rank of mean yield, GSI=Genotypic selection index, RGSI= Rank of Genotypic selection index

3.5. GGE-Biplot

GGE bi-plot analysis is a multivariate analytical technique that graphically displays a two way table and allows visualizing the relation among genotypes, environments and their interactions. It is necessary to construct GGE bi-plot for visual observation in order to understand which genotypes best performed in which environment, or which genotypes were stable and unstable as well as to visualize the discriminating ability and representativeness of the environments.

According to [16], discriminating ability and representativeness view of the GGE- biplot is the important measure of test environments, which provide valuable and unbiased information about the tested genotypes. Environments with longer vectors had the more discriminating ability of the genotypes, whereas environments with very short vectors had little or no information on the genotype difference.
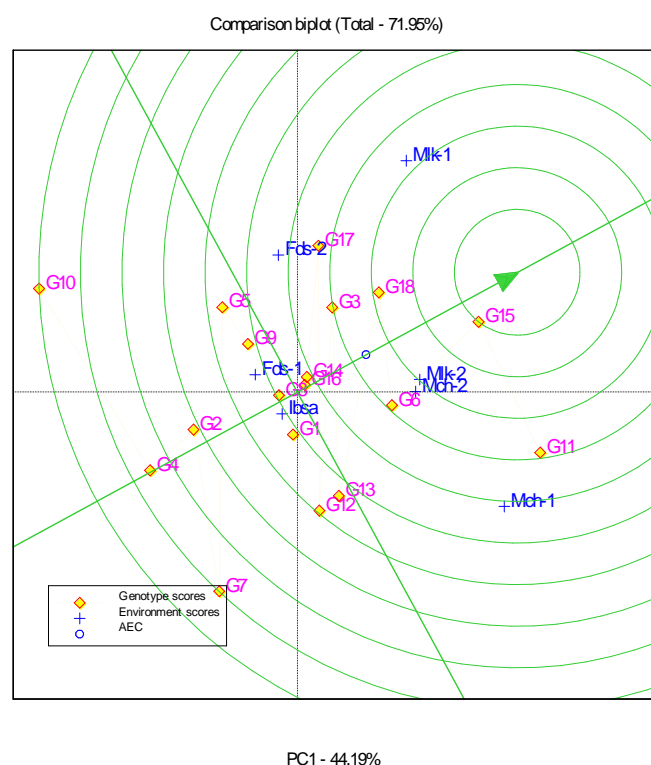

Figure 1. GGE-bi-plot showing a comparison of all sesame genotypes with in good performing ideal genotypes for grain yields.

Key: Environments (Milk-1=Milkaye year -1, Milk-2=Milkaye year -2, Mch-1=Mechara year-1, Mch-2=Mechara year-2, Fds-1=Fedis year-1, Fds-2=Fedis year-2 and Ibsa-1=Ibsa year-1

An ideal genotype is defined as a genotype with the greatest PC1 score (mean performance) and with zero GEI, as represented by an arrow pointing to it. Genotype is located closer to the ideal genotype; it becomes more desirable than other genotypes which are located far away from the ideal genotype. Therefore, concentric circles were drawn around the central circle which contains the ideal genotype in order to visualize the distance between each genotype and the ideal genotype. From the present investigation (Figure 1) G15 was laid on small concentric circle so it is "ideal" genotype, with the highest mean grain yield, followed by G18 located closer to the ideal genotype and was considered as desirable genotype. Similar result was reported by [13, 1].
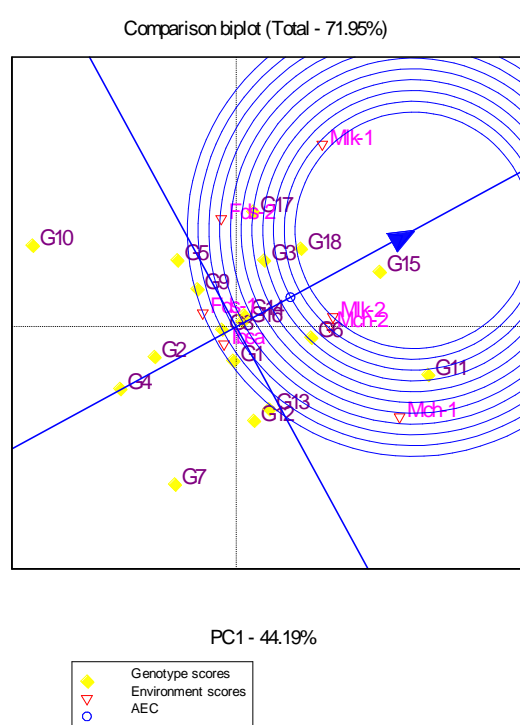

Figure 2. *GGE-bi-plot based on environment-focused scaling for comparison of the environments with the ideal environment.*

Key: Environments (Milk-1=Milkaye year -1, Milk-2=Milkaye year -2, Mch-1=Mechara year-1, Mch-2=Mechara year-2, Fds-1=Fedis year-1, Fds-2=Fedis year-2 and Ibsa-1=Ibsa year-1

The ideal test environment should have large PC1 scores (more power to discriminate genotypes in terms of the genotypic main effect) and small (absolute) PC2 scores (more representative of the overall environments). Such an ideal environment was represented by an arrow pointing to it (Figure 2). Actually, such an ideal environment may not exist, but it can be used as an indication for genotype selection in the METs. An environment is more desirable if it is located closer to the ideal environment. Therefore, using the ideal environment as the center, concentric circles were drawn to help visualize the distance between each environment and

the ideal environment [16]. Accordingly, Milk year -2, which fell on concentric circle, followed by Milk year -1 and Mch year -2 near to concentric circle an ideal test environment in terms of being the most representative of the overall environments and powerful to discriminate genotypes (Figure 2). Similar result was reported by [14] on common bean have used GGE bi-plot to identify the best desirable testing environment.

4. Conclusion and Recommendation

AMMI analysis of variance result showed 75.67% of the total variation accounted due to environment (34.09%), genotype (7.15%) and G x E interaction (21.5%) contributed to the observed variations among genotypes for yield. Genotype G15(972kgha^{-1}) showed the best yield performance across the test environment with 46.67% yield advantage over average yield, the most stable among tested genotypes across environments. Milkaye site was identified as high yielding and best desirable testing environment for sesame production. Therefore, genotype G15 was proposed as candidate variety for verification trial and possible release and it can be used as parent material in the future breeding program.

Abbreviations

AMMI	Additive Main Effects and Multiplicative Interaction
AEC	Average Environment Coordinate
ANOVA	Analysis of Variance
ASV	Ammi Stability Value
CSA	Central Statistical Authority
G	Genotype
GEI	Genotype by Environmental Interaction
GSI	Genotype Stability Index
IPCA	Interaction Principal Component Axis
MET	Multi Environmental Trial
PCA	Principal Component Analysis
rASV	Rank of Ammi Stability Value
rYLD	Rank of Yield

Acknowledgments

Author Contributions

Shanene Hail: Conceptualization, Data curation, Formal Analysis, Funding acquisition, Investigation, Methodology, Software, Supervision, Validation, Visualization, Writing - original draft, Writing - review & editing

Ahmed Muhamad: Data curation, Investigation, Methodology, Software, Supervision

Firaol Adugna: Data curation, Formal Analysis, Investigation, Methodology, Supervision

Conflicts of Interest

The authors declare no conflicts of interest.

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