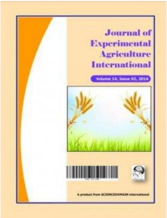

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Grain Yield Performance and Stability Analysis of Sesame *(Sesamum indicum* L.*)* Genotypes in Western Tigray, Ethiopia

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Authors' contributions

This work was carried out in collaboration between all authors. Author FB designed the study, performed the statistical analysis, wrote the protocol, and wrote the first draft of the manuscript. Authors YT and FA managed the analyses of the study. All authors read and approved the final manuscript.

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ABSTRACT

The experiment was carried out in three different locations (a total of 7 environments) of Western Tiray, Ethiopia from 2011-2013 cropping seasons and thirteen sesame genotypes were evaluated. The objective of this study was to estimate the stability of sesame genotypes and to determine the association of the stability parameters and sesame seed yield. The design was a randomized complete block design with three replications and a total plot size of $14m^2$. The Additive Main effects and Multiplicative Interaction (AMMI) model for grain yield noticed significant effects of the genotypes (37.3 % sum of squares (SS)), environments (29.5 % sum of squares) and Genotype x Environment interaction (25.9 % SS). The AMMI model extracted five significant interaction principal component analysis (IPCA) with a total of 96.9 % SS and 90.3% corresponding degrees of freedom. According to the total rank value (TR), G12, G11 and G4 were the furthermost stable and widely adapted genotypes respectively, where as G8 and G9 were the furthermost unstable genotypes.

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Grain yield was positively associated with all of the ranks of stability parameters at different significance levels. Grain yield (GY) had significant and positive correlations with YSI, Pi, S1 and CV. Regarding to the inter-parameter correlation coefficients, neither of the stability parameters were negatively correlated among each other. Environments E1, E2, and E4 were unfavorable environments; while E5, E6 and E7 were favorable environments and E3 was moderately favorable environment for most of the genotypes.

Keywords: AMMI; environment; GxE interaction; IPCA.

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) which belongs to the Pedaliaceae family is an annual oil crop. It is an erect herbaceous annual plant with either single stemmed or branched growth habits and two growth characteristics of determinate and indeterminate type, with a large tap root of reaching 90 cm and reaching up to 2m height [1]. Most of the sesame seeds which are rich in protein, fat, fibre, carbohydrates and some minerals are used for oil extraction and the rest are used for edible purposes [2]. Among the different varieties of sesame *Sesamum indicum* is the most usually cultivated variety all over the world. Sesame, which contains about 50-60% oil content mainly grown for its seeds. It is also rich in fat, protein, carbohydrates, fibre and some minerals [3].

About 7.8 million hectares of the total world crop area is under sesame cultivation with about 3.83 million tons of total production. Of the world production of sesame, Asia and Africa account for 2.29 and 1.38 million tons correspondingly. In Western Tigray of the Northern Ethiopia Sesame is the most important cash crop and it also uses for local oil extraction. Fiseha et al. [4] reported that there was a presence of a wide range of variation between the genotypes, years, locations and their interactions, that confirms the existence of significant GxE interaction in the finding. So to advance the production and productivity of sesame in Ethiopia evaluating different genotypes across different locations and years or the study of genotype x environment interaction (GxE interaction) might be important to estimate the stability of sesame genotypes so as to identify specific or widely adapted improved sesame varieties.

GxE interaction (genotype by environment interaction) is the deviation in performance of any traits of genotypes within the various growing environments. The existence of GxE interaction obscures the varietal selection process as it reduces the usefulness of genotypes by confounding their yield performance through minimizing the association between genotypic and phenotypic values [5]. Nevertheless, it is likely to develop genotypes with small GxE interaction via sub-division of heterogeneous area into smaller, more homogeneous sub-regions; and by selecting genotypes with a better stability across a wide range of locations and years [6]. Therefore, GxE interaction cab be accounted both as an opportunity and a challenge for breeders [7].

In multi-environment trials different researchers are using different stability parameters to select the stable genotype for its area of adaptability. Among which, AMMI Stability Value (ASV), Yield Stability Index (YSI), Sum of Interaction Principal Component (SIPC), Cultivar performance Measure (Pi), Wricke's Ecovalence (Wi), Francis and Kannenberg's Coefficient of Variability (CV) and Nassar and Hühn's Mean Absolute Rank Difference (S1) are the most common parameters to identify stable genotype.

2. MATERIALS AND METHODS

2.1 Experimental Materials and Methods

Plant Material and Methods: The study was carried out in seven environments that comprise location (three testing locations), genotypes (13 genotypes) and year. The soil and climatic description of the locations is given in Table 1. The 13 genotypes (see Table 2) were evaluated for three years in both Humera and Dansha (2011-2013) and for one more year in Sheraro (2013), All the field evaluation were undertaken under a rainfed condition and the environments were designated as E1 (Humera 2011), E2 (Humera 2012), E3 (Humera 2013), E4 (Dansha 2011), E5 (Dansha 2012), E6 (Dansha 2013) and E7 (Sheraro 2013). The thirteen sesame genotypes were sown using a randomized complete block design (RCBD) with three replications in a plot area of 14 m^2, Each experimental plot received the same rate of DAP (100kg/ha) and urea (50kg/ha).

Table 1. Climatic and soil characteristics of the experimental locations

Location		Humera	Sheraro	Dansha
Latitude (^{o}N)		14o15'	14o24'	13o36'
Longitude (^{o}E)		36o37'	37o45'	36o41'
Altitude (m)		609	1028	696
Anual RF (mm)		576.4	676.7	888.4
Min - Max Temp (^{o}c)		18.8-37.6	18.8-34.9	28.7(mean)
Soil texture	Clay (%)	35.6	21	-
	Silt (%)	25.6	27.3	-
	Sand (%)	38.6	51.7	-

Table 2. Designation and description of the sesame genotypes

Genotype name	Genotype code	Seed source	Status of the genotype	Sesame seed color
Acc#031	G1	WARC	Advanced line	White
Oro (9-1)	G2	WARC	Advanced line	White
NN-0079-1	G3	WARC	Advanced line	White
Acc-034	G4	WARC	Advanced line	White
Abi-Doctor	G5	WARC	Advanced line	White
Serkamo	G6	WARC	Released	Brown
Acc-051-020sel-14	G7	WARC	Advanced line	Brown
Tate	G8	WARC	Released	Brown
Acc-051-02sel-13	G9	WARC	Advanced line	White
Adi	G10	WARC	Released	White
Hirhir	G11	HuARC	Farmers seed (local check)	White
Setit-1	G12	HuARC	Released (standard check)	White
Humera-1	G13	HuARC	Released (standard check)	White

WARC-Werer Agricultural Research Center, HuARC-Humera Agricultural Research Center

2.2 Statistical Analysis

About six stability statistics currently in use are examined in this study. Bartlet's test [8] was used for combined analysis over locations in each year as well as over locations and years (for the combined data) and the homogeneity of residual variances was tested preceding to a combined analysis. Accordingly, the data collected were homogenous and all data showed normal distribution.

2.3 AMMI Model Analysis

AMMI analysis combines analysis of variance (ANOVA) with additive and multiplicative parameters in to a single model [9] and accordingly the grain yield data were subjected to AMMI analysis. After combining the data and after removing the replicate effect, the genotypes and environments observations portioned in to two sources: The first one is additive main effects for genotypes and environments; and the second one is non-additive effects due to genotype by environment interaction.

2.4 Stability Analysis Using the AMMI Model

- Wricke's [10] ecovalence and Francis & Kannenberg's [11] Coefficient of variability were performed using the SAS program developed by Hussein et al. [12].
- Lin & Binns's [13] cultivar superiority performance and Nassar & Hühn's [14] absolute rank difference were also carried out using the GenStat 16th edition [15].
- AMMI stability value (ASV) was calculated using the formula developed by Purchase et al. [16]:
- $\mathrm{ASV} = \sqrt{\left[\frac{\mathrm{SS_{IPCA1}}}{\mathrm{SS_{IPCA2}}}(\mathrm{IPCA1_{score}})\right]^2 + (\mathrm{IPCA2_{score}})^2}$

  Where: SS is sum of squares; IPCA1 is interaction of principal component axis one; and IPCA2 is interaction of principal component axis two.
- Sum of interaction principal component (SIPC) was also calculated using the formula developed by Sneller et al. [17]:

$$\mathrm{SIPC} = \sum_{n=0}^{N} \left|\lambda^{05}{}_{n}\gamma_{in}\right|$$

Where: $\lambda^{05}{}_{n}\gamma_{in}$ is the interaction principal component (IPC) scores for the i^{th} genotype; n is number of IPC; and N is number of significant IPC retained in the model via F-test.

- Similarly yield stability index (YSI) was also computed by summing up the ranks from mean grain yield and ASV:
  YSI= RGY + RASV;
  Where: RGY is rank of mean grain yield and RASV is rank of AMMI stability value

To statistically compare the seven stability analysis procedures used in the study, the Spearman's rank correlation coefficient (r_s) Steel and Torrie [8] was estimated using SPSS version 16 statistical software.

3. RESULTS AND DISCUSSION

3.1 Stability Measures from Additive Main Effects and Multiplicative Interaction (AMMI) Model

The AMMI model for grain yield showed significant variation ($p<0.001$) for both the main and interaction effects confirming the presence of a wide range of variation between the genotypes, years (seasons), locations and their interactions (Table 3). Genotypes had a lion's share in grain yield variation and accounted about 37.3% of the total sum of squares reflecting that the major source of variation for grain yield among the genotypes were mainly the intrinsic genetic constituent of the evaluated genotypes. Similar result were reported in sesame [18]. Environments and interaction effects took 29.5% and 25.9% contribution for the total sum of squares correspondingly. The AMMI model take out five significant ($p<0.001$) IPCAs from the interaction component (Table 3). These five IPCAs accounted 96.9% of the interaction sum of squares with 90.3% corresponding degrees of freedom with a remaining 3.1% assumed as noise (Table 3). Knowing that the degree of information decreases from the first to the last IPCAs the extracted IPCAs are capable of providing an information on the interaction effect. According to Zobel et al. [19] the first two IPCAs could best explain the interaction sum of squares. Accordingly, in this finding the first two IPCA's with a total of 57.6% sum of squares and 44.4% of corresponding degrees of freedom used to explain the interaction effect.

The IPCA scores of the genotypes is presented in Table 4. Genotypes scoring a larger IPCA score are the more reactive genotypes for the interaction effect and the more explicitly adapted genotypes to a specific growing season or growing area. On the other hand, the genotypes scoring smaller IPCA scores are with minor interaction effect and are believed to be widely adapted genotypes. Consequently genotypes with higher magnitude of IPCA1 like G7 (13.7), G8 (9.2), and G5 (5.7), were the more reactive and attributed highly to the interaction component and may be considered as a specifically adapted genotypes. In contrast to this, G12 (0.57) followed by G9 (0.68) and G3 (2.3) were the genotype with lower share to the interaction component as they are with lower IPCA reflecting their wider adaptability or stability in different growing seasons and locations (see Table 4).

Table 3. Combined AMMI analysis of variance for grain yield of Sesame genotypes

Source of variation	DF	TSS	TSS (%)	GXE explained (%)	Cumulative (%)	MS
Genotypes	12	2500959	37.3			208413***
Environments	6	1979243	29.5			329874***
Block (within Env)	14	90120	1.3			6437ns
Interactions	72	1738701	25.9			24149***
IPCA1	17	583954		33.6	33.6	34350***
IPCA2	15	416566		24	57.6	27771***
IPCA3	13	260364		15	72.6	20028***
IPCA4	11	240543		13.8	86.4	21868***
IPCA5	9	181706		10.5	96.9	20190***
Residuals	7	55568				7938
Error	168	398652				2373
Total	272	6707676				24661

****highly significant at (P<0.001), ns= non-significant*

3.1.1 AMMI Stability Value (ASV) Analysis

ASV is the distance from the coordinate point to the origin in a two-dimensional scatter gram of IPCA1 scores against IPCA2 scores in the AMMI model [16]. The genotypes with larger IPCA score, be it negative or positive, are the more specifically adapted to specific years and locations and those with least IPCA scores indicate a more stable genotype in different growing seasons and locations. Consequently, G3 with least ASV (3.9) followed by G11(4.5) and G12 (4.8) were the most stable genotypes; whereas, G7(19.9) followed by G8 (13.8) (Table 4) were ranked as less stable and more sensitive genotypes to environmental change.

3.1.2 Yield Stability Index (YSI) Analysis

Yield stability index (YSI) is suggested to be as one of the measures of stability for genotypes, which is calculated by summing the rank of mean grain yield across locations and growing seasons and rank of ASV of genotypes [20]. The genotypes with lowest value of YSI are desirable genotypes with high mean yield and stability. Henceforth, YSI identified G12 and G11 as the most stable genotypes correspondingly; whereas G9 was recognized as the least stable genotype. Hagos and Fetien [21] also used theses ASV and YSI to designate stability of sesame genotypes in Northern Ethiopia.

3.1.3 Sum of Interaction Principal Component (SIPC)

Sum of interaction principal component (SIPC) developed by Sneller et al. [17] is also another stability statistics from AMMI model. It is the summation of the absolute value of IPC scores (SIPC) of the genotypes that were retained in the AMMI model via F-tests. The genotypes with lower SIPC are recognized as the most stable and adapted across different seasons and locations (widely adapted) otherwise adapted to a certain growing areas or season (specifically adapted). Accordingly, G12 (with 8.3 SIPC) was the most stable genotype and considered as a widely adapted; and G8 (with 27.9 SIPC) and G7 (with 27.2 SIPC) as unstable genotypes with a highly inconstant performance across environments. Zali et al. [22] reported a similar finding using SIPC in his study conducted in chick pea.

3.2 Univariate Stability Analysis Methods

Irrespective of how a stability parameter is measured, one of the most critical question is whether it is inherent or not. If the characteristic measured by the parameter is non-genetic, it is inheritable and thus selection for such parameter is fruitless. However, Farshadfar et al. [23], have proved that stability indices are genetic and hence heritable. The above discussions confirmed the ranking order of grain yield and other traits of the genotypes was varying from environment to environment. Hence, for better selection and further adaptation of high yielding and stable genotypes for the locations distinguishing their stability is critically important and the stability of the genotypes based on different measures is depicted in Table 4.

3.2.1 Cultivar performance Measure (Pi)

Lin and Binns [13] defined the performance measure (Pi) of the i^{th} test genotype as the distance mean square between the cultivar's response and the maximum response over locations. In this stability measure pair-wise genotype by environment interaction computation is performed between each cultivar and the maximum yield at each location. Hence, the less is the distance of the genotype with maximum yield the smaller the value of Pi and the more stable is the genotype. The genotype coded as G4 was the most stable as to the Pi stability parameter. The Pi based ranking of the genotypes was very similar with that of the mean yield ranking (with few exceptions) and often considered as a measure of performance than a measure of stability [24].

3.2.2 Wricke's Ecovalence (Wi)

According to Wrick [10] genotypes with a low Wi value have smaller deviations from the overall mean across environments and are thus more stable. According to the meaning of ecovalence, the stable genotype possesses a low ecovalence. Hence, G7 followed by G9, which possessed high ecovalence, was marked as the least stable genotypes.

3.2.3Francis and Kannenberg's Coefficient of Variability (CV)

This stability parameter developed by Francis and Kannenberg [11] measures the performance and coefficient of variation (CV) for each genotype over all environments and the genotype that provides a high yield performance and consistent low coefficient of variation is considered to be stable genotype. Therefore, G9 was recognized as the unstable genotype.

Table 4. Mean grain yield (GY), various stability measures and their ranking order

Gen	GY	R	IPCA1	IPCA2	ASV	R	YSI	R	Pi	R	S1	R	SIPC	R	CV	R	Wi	R	TR
G1	895.1	2	-5.71	1.81	7.0	6	8	3	4433	2	1.8	3	23.2	9	14.7	7	39728.3	7	37
G2	638.1	12	3.31	5.29	8.3	9	21	8	55022	11	2.7	7	17.4	4	14.2	6	28506.8	3	48
G3	740.4	6	-5.22	8.69	3.9	1	7	2	27403	6	3.5	12	22.3	6	13.9	5	38856.6	6	38
G4	926.8	1	-13.70	-5.22	11.4	10	11	4	1239	1	0.6	1	22.9	7	6.5	1	48249.6	9	33
G5	662.6	10	0.68	-12.13	8.2	8	18	7	48904	10	3.1	8	23.2	10	17.9	8	52922.5	10	61
G6	711.5	7	3.53	3.94	7.6	7	14	6	38459	8	1.9	4	16.6	3	20.4	9	31195.4	5	42
G7	687.5	9	2.78	2.24	19.9	13	22	9	43319	9	3.5	11	27.2	12	21.6	11	100929.4	13	78
G8	655.2	11	4.00	-0.69	13.8	12	23	10	56649	12	3.1	9	27.9	13	25.0	12	66710.4	11	79
G9	614.3	13	2.28	2.24	12.2	11	24	11	70599	13	3.3	10	23.1	9	31.2	13	68370.6	12	79
G10	697.6	8	-5.53	-2.84	6.3	5	13	5	36750	7	4.0	13	24.0	11	20.6	10	45063.7	8	59
G11	791.5	5	4.88	-3.34	4.5	2	7	2	19282	4	2.7	6	16.0	2	13.1	4	18713.3	2	22
G12	832.7	3	-0.57	4.77	4.8	3	6	1	9525	3	1.3	2	8.3	1	7.5	2	10063.2	1	13
G13	805.1	4	9.25	-4.77	5.7	4	8	3	20244	5	2.0	5	17.9	5	12.9	3	30245.5	4	29

Where: GY= grain yield (kg/ha); ASV = AMMI stability value; YSI= yield stability index; Pi = Lin & Binns's cultivar superiority performance; S1= Nassar & Hühn's absolute rank difference; SIPCA= Sum of interaction principal component; CV = Francis & Kannenberg's Coefficient of variability; Wi = Wricke's ecovalence; TR= total rank; R= Rank

3.2.4 Nassar and Hühn's Mean Absolute Rank Difference (S1)

Nassar and Hühn [14] described non-parametric measures of stability based on ranks of the genotypes across locations and provide a viable alternative to existing parametric analyses. The mean absolute rank difference (S1) estimates are all possible pair wise rank differences across locations for each genotype. This gives equal weight to each location or environment and genotypes with less change in rank are expected to be more stable. According to this S1 stability parameter G4 was identified as the most stable genotype and G10 and G3 identified as unstable genotypes.

Despite the lack of consistency among the stability measures, G12, G11 and G4 were the most stable and widely adapted genotypes respectively, whereas G8 and G9 were the most unstable genotypes equally according to total rank value (TR).

3.3 Associations between Grain Yield and the Stability Parameters

Spearman's coefficient of rank correlation Steel and Torie [8] was executed for possible pair wise comparisons of the ranks of different stability parameters and yield ranks (Table 5). The correlation between mean grain yield (GY) and the seven stability parameters varied considerably. Grain yield was positively associated with all of the ranks of stability parameters at different significance levels. Grain yield (GY) had significant and positive correlations with YSI, Pi, S1 and CV, but its association with ASV, SIPC and Wi was non-significant although it was positively associated. Grain yield was highly and positively correlated (at p<0.01) with Pi (r = 0.98) as the rank-correlation coefficient was near to unity (Table 5). This indicates that choosing a genotype based on Pi stability parameter could lead to selecting a genotype with highest grain yield. As reported by Issa [25], the association between GY and Wi was positive but weak.

The inter-parameter correlation coefficients indicated that neither of the stability parameters were negatively correlated among each other (table 5). The highest positive correlation among the parameters (at p<0.01) were recorded between Wi and SIPC (r = 0.894), ASV and YSI (r = 0.890), and Pi and YSI (r=0.85). This also partially concurred with the findings of Farshadfar [6]. On the other side, the weakest correlation was observed between YSI and S1 (r=0.12) indicating that the genotypes selected according to the ranking order of these parameters may be quite different.

3.4 Environmental Performance and Stability

The environments had different mean grain yields (table 6) which indicates that the different environments were not similarly favorable/advantageous or unfavorable for the genotypes grown in these environments. Based on the environmental index (EI) Environments often categorized as favorable and unfavorable; where environments with a negative environmental index considered as unfavorable and those with positive environmental index regarded as favorable [26]. Hence, E1 with a negative environmental index (-113.4), was classified as the least favorable environment while E6 with highest and positive environmental index (149.2) considered as the most favorable environment (Table 6). Generaly, E1, E2, and E4 both with negative environmental index and below average mean yield considered as unfavorable environments. Whereas, E5, E6 and E7 with positive and significant environmental index and above average mean yield performance classified as favorable

Table 5. Spearmen rank correlation among ranks of grain yield and other stability parameters

	GY	ASV	YSI	Pi	S1	SIPC	CV	Wi
GY	_							
ASV	0.522^{ns}	_						
YSI	0.818^{**}	0.890^{**}	_					
Pi	0.984^{**}	0.560^{*}	0.846^{**}	_				
S1	0.670^{*}	0.121^{ns}	0.419^{ns}	0.626^{*}	_			
SIPC	0.41^{ns}	0.630^{*}	0.641^{*}	0.432^{ns}	0.569^{*}	-		
CV	0.775^{**}	0.588^{*}	0.807^{**}	0.797^{**}	0.654^{*}	0.682^{*}	_	
Wi	0.44^{ns}	0.764^{**}	0.741^{**}	0.478^{ns}	0.473^{ns}	0.894^{**}	0.698^{**}	_

*ns= non-significant, *significant (P<0.05), ** highly significant (P<0.01)*

Table 6. IPCA scores, Environmental Index (EI), and AMMI stability value of seven environments

Env.	Env. code	Env. Mean	IPCA1	IPCA2	EI	ASV
Humera-2011	E1	629.5	-15.705	2.69668	-113.44**	22.2
Humera-2012	E2	658.6	2.1842	12.9542	-84.343**	13.3
Humera-2013	E3	737.3	-5.3562	-4.7389	-5.6429^{ns}	8.9
Dansha-2011	E4	695.5	11.7269	2.10177	-47.443**	16.6
Dansha-2012	E5	770.9	0.54909	-7.0447	27.9571**	7.1
Dansha-2013	E6	892.2	4.16373	-10.169	149.257**	11.7
Sheraro-2013	E7	816.6	2.43698	4.19989	73.6571**	5.4

***significant at (P<0.01), ns= non-significant*

environments. Remarkably, E3 with a negative but non-significant environmental index was considered as moderately favorable environment for most of the sesame genotypes.

Based on the ASV the environments were also designated for their stability. Hence, E1(22.2) and E4 (16.6) with largest ASV were the least stable environments; whereas E7(5.4) followed by E5(7.1) with smallest ASV were stable environments and these environments may be representative and better for further breeding program.

4. CONCLUSION AND RECOMMENDATION

The AMMI model, that detected significant variation (p<0.001) for both the main and interaction effects, extracted five significant (p<0.001) IPCAs from the interaction component. The existence of such significant GxE interaction in varietal development may be both a challenge and an opportunity for breeding program and breeders in different crops. According to total rank value (TR) genotypes G12, G11 and G4 were the most stable and widely adapted genotypes respectively, whereas G8 and G9 were the most unstable genotypes.

Grain yield was positively associated with all of the ranks of stability parameters at different significance levels: Grain yield (GY) had significant and positive correlations with YSI, Pi, S1 and CV, although it was non significantly and positively associated with ASV, SIPC and Wi. Regarding the inter-parameter correlation coefficients, neither of the stability parameters were negatively correlated among each other. The highest positive correlation among the parameters (at p<0.01) were recorded between Wi and SIPC (r = 0.894), ASV and YSI (r = 0.890), Pi and YSI (r=0.85).

With respect to the environments E1, E2, and E4 were considered as unfavorable environments; while E5, E6 and E7 were considered as favorable environments. Remarkably, E3 with a negative but non-significant environmental index was considered as moderately favorable environment for most of the sesame genotypes.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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