



Asian Journal of Plant Sciences

ISSN 1682-3974

science
alert

ANSI*net*
an open access publisher
<http://ansinet.com>

RESEARCH ARTICLE

OPEN ACCESS

DOI: 10.3923/ajps.2014.178.183

AMMI Analysis of Genotype×Environment Interaction and Stability of Sesame Genotypes in Northern Ethiopia

¹Fiseha Baraki, ²Yemane Tsehaye and ²Fetien Abay

¹Crop Research Core Process, Humera Agricultural Research Center, Ethiopia

²Department of Crop and Horticultural Science, Mekelle University, Ethiopia

ARTICLE INFO

Article History:

Received: December 20, 2014

Accepted: February 18, 2015

Corresponding Author:

Fiseha Baraki,

Crop Research Core Process,

Humera Agricultural Research Center,

Ethiopia

ABSTRACT

The study was carried out in three locations (a total of 7 environments) of Northern Ethiopia from 2011-2013 cropping seasons and thirteen sesame genotypes were evaluated. The objective of this study was to determine the magnitude of G×E interaction and stability of sesame genotypes. The experiment was laid out in randomized complete block design with three replications and a total plot size of 14 m². The Additive Main effects and Multiplicative Interaction (AMMI) model for grain yield detected significant effects of the genotypes (37.3% Sum of Squares (SS)), environments (29.5% Sum of Squares) and Genotype×Environment interaction (25.9% SS). The model also extracted five significant Interaction Principal Component Analysis (IPCA) with a total of 96.9% SS and 90.3% corresponding degrees of freedom. Acc-034 (G4) (926.8 kg ha⁻¹) followed by Acc # 031 (G1) (895.1 kg ha⁻¹) had the highest average yield which was much greater than the grand mean (742.9 kg ha⁻¹) and declared as area specific adapted genotypes. Based on the magnitude of the IPCA1, Yield Stability Index (YSI) and Sum of Interaction Principal Component (SIPC), Setit-1 (G12) with greater yield (832.7 kg ha⁻¹) than the grand mean was declared as widely adapted genotype. 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 sesame genotypes.

Key words: AMMI, G×E interaction, IPCA, stability

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an annual plant that belongs to the Pedaliaceae family. It is an erect herbaceous annual plant with either single stemmed or branched growth habits and two growth characteristics of indeterminate and determinate, reaching up to 2 m height and with a large tap root of 90 cm (Pham *et al.*, 2010). Most of the sesame seeds which are rich in fat, protein, carbohydrates, fibre and some minerals are used for oil extraction and the rest are used for edible purposes (El Khier *et al.*, 2008). Among the different varieties of sesame *Sesamum indicum* is the most usually cultivated variety all over the world. Sesame which is grown for its seeds contains about 50-60% oil content is also rich in fat, protein, carbohydrates, fibre and some minerals (Caliskan *et al.*, 2004).

About 7.8 million hectares of the total world crop area is under sesame cultivation with about 3.83 million metric tons of total production. Of the world production of sesame, Asia and Africa account for 2.29 and 1.38 million tons, respectively. Ethiopia is the Sixth largest sesame producer in the world and third in Africa next to Tanzania and Uganda, respectively (FAOSTAT., 2012). In Northern Ethiopia Sesame is the most important cash crop and it also uses for local oil extraction. So, to improve the production and productivity of sesame in Ethiopia evaluating different genotypes across different environments or the G×E interaction study might be important for supplying area specific or widely adapted improved seeds.

G×E interaction (genotype by environment interaction) refers to the deviation in performance of any attributes of genotypes within the various growing environments

(across locations and years). The presence of G×E interaction complicates 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 (Farshadfar *et al.*, 2012). However, it is possible to develop genotypes with low G×E 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 environments (Farshadfar *et al.*, 2011b). So, G×E interaction may be considered both as an opportunity and a challenge for breeders. AMMI is important to analyze multi-environment trials data and it interprets the effect of the Genotype (G) and Environments (E) as additive effects and the G×E as a multiplicative component (which are sources of variation) and submits it to principal component analysis. The AMMI procedure has been shown to increase estimation accuracy since it fits additive main effects for genotypes and environments by an ordinary ANOVA procedure and then applies PCA to the matrix of residuals of that remain after the fitting of main effects (Gauch, 1988). In AMMI model the interaction (GE_{ij}) and the residual (ϵ_{ij}) can be decomposed into several Interaction Principal Component Axes (IPCA) using PCA.

MATERIALS AND METHODS

Experimental material and method: The experiments were conducted for three growing seasons (2011-2013) in Humera and Dansha and in a single year (2013 cropping season) in Sheraro (total seven environments) under rain fed condition where: E1, E2, E3 are 2011, 2012, 2013 growing seasons respectively in Humera; E4, E5, E6 are 2011, 2012, 2013

growing seasons respectively in Dansha and E7 is 2013 growing season in Sheraro. Edaphic and climatic description of the study areas as well as description of the genotypes is listed in Table 1 and 2, respectively. Thirteen sesame genotypes were sown in RCBD with three replications and evaluated for their grain yield. Each genotype was randomly assigned and sown in a plot area of 2.8 m by 5 m with 1m between plots and 1.5 m between blocks keeping inter and intra row spacing of 40 and 10 cm, respectively.

AMMI model analysis: The grain yield data were subjected to AMMI analysis which combines analysis of variance (ANOVA) with additive and multiplicative parameters in to a single model (Gauch, 1988). After removing the replicate effect when combining the data, the genotypes and environments observations are portioned in to two sources: Additive main effects for genotypes and environments and non additive effects due to genotype by environment interaction.

The AMMI model is:

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

where, $I = 1, 2, \dots, 13$, $j = 1, 2, \dots, 7$, 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. Ordinarily the number n is judged on the basis of empirical consideration of F-test of significance.

Table 1: Agro-climatic and soil characteristics of the experimental sites

Location	Latitude (°N)	Longitude (°E)	Altitude (m)	Annual RF (mm)	Min-max temp (°C)	Soil texture (%)		
						Clay	Silt	Sand
Humera	14°15'	36°37'	609	576.4	18.8-37.6	35.6	25.6	38.6
Sheraro	14°24'	37°45'	1028	676.7	18.8-34.9	21.0	27.3	51.7
Dansha	13°36'	36°41'	696	888.4	28.7 (mean)	-	-	-

Source for Soil texture: Bereket and Yirgalem (2012)

Table 2: Description of the sesame genotypes

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

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

Stability analysis using the AMMI Model:

- AMMI Stability Value (ASV) was calculated in the excel spread sheet using the formula developed by Purchase (1997):

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

where, SS_{IPCA1} is Sum of squares of interaction principal component analysis 1, SS_{IPCA2} is Sum of squares of interaction principal component analysis 2, $IPCA1$ is interaction principal component analysis one and $IPCA2$ is interaction principal component analysis two

- SIPC (Sum of interaction principal component) was also calculated in the excel spread sheet using the formula developed by Sneller *et al.* (1997):

$$SIPC_i = \sum_{n=1}^N |\lambda_n^{0.5} \gamma_{in}| \text{ OR } SIPC_i = |IPCAN_1 + IPCAN_2 + \dots + IPCAN_i|$$

where, SIPC is Sum of interaction principal component, $I = 1, 2, \dots, 13$, $\lambda_n^{0.5} \gamma_{in}$ is the Interaction Principal Component Analysis (IPCA) scores for the i th genotype, n is number of IPCA and N is number of significant IPCA retained in the model via F-test

- Similarly Yield Stability Index (YSI) was also computed by summing up the ranks from ASV and mean grain yield (Farshadfar *et al.*, 2011a):

$$YSI_i = RASV_i + RGY_i$$

where, $RASV_i$ is rank of AMMI stability value of the i th genotype and RGY_i is rank of mean grain yield of the i th genotype.

Statistical analysis: Homogeneity of residual variances was tested prior to a combined analysis over locations in each

year as well as over locations and years using Bartlett's test (Steel *et al.*, 1996). Result are significant at $p < 0.001$. Accordingly, the data collected were homogenous and all data showed normal distribution.

RESULTS AND DISCUSSION**Additive Main effects and Multiplicative Interaction (AMMI) analysis:**

The AMMI model for grain yield detected significant variation ($p < 0.001$) for both the main and interaction effects indicating the existence 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 indicating that the greatest source of variation for grain yield among the genotypes were mainly the inherent genetic component. Similar results were reported in sesame (Zenebe and Hussien, 2009). Environments and interaction effects had 29.5 and 25.9% contribution for the total sum of squares respectively. The AMMI model extracted five significant ($p < 0.001$) IPCAs from the interaction component (Table 3). These five IPCAs accounted a total 96.9% of the interaction sum of squares with 90.3% corresponding degrees of freedom with a remaining 3.1% considered as noise (Table 3). The extracted IPCAs are capable of providing an information on the interaction effect although their degree decreases from the first to the last IPCAs. However, the first two IPCAs could best explain the interaction sum of squares (Zobel *et al.*, 1988). Accordingly, 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.

Genotypes adaptability and stability analysis: As depicted in Table 4 below the average grain yield of the tested sesame genotypes over the seven environments was 742.9 kg ha^{-1} . The G4 (926.8 kg ha^{-1}) had the highest average yield followed by G1 (895.1 kg ha^{-1}) and G12 (832.7 kg ha^{-1}) while G9 (614.3 kg ha^{-1}) was the poorly yielding genotype). The magnitude (absolute value) of the IPCA scores of the genotypes is presented in Table 4. Genotypes with a greater IPCA score are the more responsive ones for the interaction

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

Source of variation	df	TSS	TSS (%)	G×E 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		24.0	57.6	27771****
IPCA3	13	260364		15.0	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

Table 4: IPCA scores and stability parameters from AMMI model

Genotype	Gen code	YLD (kg)	Rnk	IPCA1	IPCA2	ASV	Rnk	YSI	Rnk	SIPC	Rnk
Acc#031	1	895.10 ^b	2	-5.71	1.81	7	6	8	3	23.2	9
Oro (9-1)	2	638.10 ^{hi}	12	3.31	5.29	8.3	9	21	8	17.4	4
NN-0079-1	3	740.40 ^a	6	-5.22	8.69	3.9	1	7	2	22.3	6
Acc-034	4	926.80 ^a	1	-13.70	-5.22	11.4	10	11	4	22.9	7
Abi-Doctor	5	662.60 ^{sh}	10	0.68	-12.13	8.2	8	18	7	23.2	10
Serkamo	6	711.50 ^{af}	7	3.53	3.94	7.6	7	14	6	16.6	3
Acc-051-020 sel-14	7	687.50 ^{fg}	9	2.78	2.24	19.9	13	22	9	27.2	12
Tate	8	655.20 ^{sh}	11	4.00	-0.69	13.8	12	23	10	27.9	13
Acc-051-02 sel-13	9	614.30 ⁱ	13	2.28	2.24	12.2	11	24	11	23.1	9
Adi	10	697.60 ^f	8	-5.53	-2.84	6.3	5	13	5	24.0	11
Hirhir	11	791.50 ^d	5	4.88	-3.34	4.5	2	7	2	16.0	2
Setit-1	12	832.70 ^e	3	-0.57	4.77	4.8	3	6	1	8.3	1
Humera-1	13	805.10 ^{ed}	4	9.25	-4.77	5.7	4	8	3	17.9	5
Mean		742.90									
LSD		83.83									
CV (%)		7									

effect and the more specifically adapted genotypes to a certain environment or location. In contrast to this, the genotypes with smaller IPCA scores are with lower interaction and are considered as widely adapted genotypes. Genotypes with greater magnitude of IPCA1 such as G7 (13.7), G8 (9.2) and G5 (5.7), were the more responsive and contributed largely to the interaction component and may be considered as a specifically adapted genotypes. On the other hand, G12 (0.57) followed by G9 (0.68) and G3 (2.3) were the genotype with least contribution to the interaction component as they are with lower IPCA1 and mapped near to the bi-plot origin indicating their wider adaptability or stability (Table 4) which was also similar to YSI and SIPC stability ranks.

AMMI Stability Value (ASV) analysis: The 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 (Purchase, 1997). The genotypes with larger IPCA score, either negative or positive, are the more specifically adapted to certain environments and those with smaller IPCA scores indicate a more stable genotype across environments. Accordingly, G3 with lowest 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.

Yield Stability Index (YSI) analysis: Yield Stability Index (YSI) Farshadfar *et al.* (2011a) which is similar to genotype selection index developed by Farshadfar (2008) is recommended as a measure of stability which is calculated by summing the rank of mean grain yield across environments and rank of AMMI stability value of genotypes. The genotypes with lowest value of this parameter are desirable genotypes with high mean yield and stability. Hence, YSI identified G12 and G11 as the most stable genotypes respectively whereas G9 was identified as the least stable

genotype. Both ASV and YSI were also used by Tadesse and Abay (2011) to describe stability of sesame genotypes in Northern Ethiopia.

Sum of Interaction Principal Component (SIPC): Sum of Interaction Principal Component (SIPC) is another stability statistics from AMMI model developed by Sneller *et al.* (1997). It is sums of the absolute value of IPC scores (SIPC) of the genotypes that were retained in the AMMI model via F-tests. The genotypes with smaller SIPC are considered as the most stable and widely adapted otherwise specifically adapted. With respect to SIPC G12 (8.3) was the most stable genotype and considered as a widely adapted and G8 (27.9) and G7 (27.2) as unstable genotypes with a highly variable performance across environments. Similar report has been made by Zali *et al.* (2012) in chick pea using SIPC.

Environmental performance and stability: The environments had different mean grain yields (Table 5) and this indicates that the different environments were not equally favorable or unfavorable for the genotypes grown under them. Environments often classified as favorable and unfavorable ones based on the Environmental Index (EI) where environments with a negative index considered as unfavorable and those with positive regarded as favorable (Farshadfar, 2008). Accordingly, E1 had a negative environmental index (-113.4) and was classified as the least favorable environment while E6 had the highest positive environmental index (149.2) and considered as the most favorable environment (Table 5). In general E1, E2 and E4 both with negative environmental index had below average mean yield and considered as unfavorable environments. Whereas, E5, E6 and E7 with positive and significant environmental index had above average mean yield performance and classified as favorable environments. Exceptionally, E3 which had negative but non-significant EI was considered as moderately favorable environment for most of the genotypes.

Table 5: IPCA scores, Environmental Index (EI) and AMMI stability value of seven environments

Environment	Environment code	Environment mean	IPCA1	IPCA2	EI	ASV
Humera-2011	E1	629.5	-15.70500	2.69668	-113.4400***	22.2
Humera-2012	E2	658.6	2.18420	12.95420	-84.3430***	13.3
Humera-2013	E3	737.3	-5.35620	-4.73890	-5.6429**	8.9
Dansha-2011	E4	695.5	11.72690	2.10177	-47.4430***	16.6
Dansha-2012	E5	770.9	0.54909	-7.04470	27.9571***	7.1
Dansha-2013	E6	892.2	4.16373	-10.16900	149.2570***	11.7
Sheraro-2013	E7	816.6	2.43698	4.19989	73.6571***	5.4

***Significant at (p<0.01), ns: Non significant

The environments were also described for their stability based on their ASV. Hence, E1 (22.2) and E4 (16.6) with highest ASV were the least stable environments, whereas E7 (5.4) followed by E5 (7.1) were stable environments and which may be better for further breeding program.

CONCLUSION

The AMMI model for grain yield detected significant variation (p<0.001) for both the main and interaction effects indicating the existence of a wide range of variation between the genotypes, years (seasons), locations and their interactions which confirms the presence of significant G×E interaction in the study. The existence of such significant G×E interaction in varietal selection may be both a challenge and an opportunity for plant breeders and breeding program. Furthermore, the model extracted five significant (p<0.001) IPCAs from the interaction component which accounted a total 96.9% of the interaction sum of squares with 90.3% corresponding degrees of freedom.

Despite of their instability G4 (926.8 kg ha⁻¹) followed by G1 (895.1 kg ha⁻¹) had the highest average yield which was much greater than the grand mean (742.9 kg ha⁻¹) and declared as area specific adapted genotypes. On the other hand, based on the magnitude of the IPCA1, YSI and SIPC G12 with greater yield (832.7 kg ha⁻¹) than the grand mean was declared as the most stable genotype over all environments.

With respect to the environments E1, E2 and E4 both with negative EI had below average mean yield and considered as unfavorable environments while E5, E6 and E7 with positive and significant EI had above average mean yield performance and classified as favorable environments. Exceptionally, E3 which had negative but non-significant EI was considered as moderately favorable environment for most of the genotypes.

ACKNOWLEDGMENT

The first author would like to sincerely acknowledge for research members of crop department in Humera Agricultural Research Center and Public and Private Partnership Organization project (PPPO) for financial support.

REFERENCES

- Bereket, H. and W. Yirgalem, 2012. Status survey of total plant and total DTPA Extractable soil Copper, Zinc, Iron and Manganese in different agro ecological zones, soils and districts of Tigray, Ethiopia. Tigray Agricultural Research Institute, Mekelle, Ethiopia.
- Caliskan, S., M. Arslan, H. Arioglu and N. Isler, 2004. Effect of planting method and plant population on growth and yield of sesame (*Sesamum indicum* L.) in a Mediterranean type of environment. Asian J. Plant Sci., 3: 610-613.
- El Khier, M.K.S., K.E.A. Ishag and A.E.A. Yagoub, 2008. Chemical composition and oil characteristics of sesame seed cultivars grown in Sudan. Res. J. Agric. Biol. Sci., 4: 761-766.
- FAOSTAT., 2012. Food and agriculture organization of the United Nations. FAOSTAT, Rome, Italy. <http://faostat.fao.org/>
- Farshadfar, E., 2008. Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat. Pak. J. Biol. Sci., 11: 1791-1796.
- Farshadfar, E., M. Geravandi and Z. Vaisi, 2012. Chromosomal localization of QTLs controlling genotype×environment interactions in barley. Int. J. Agric. Crop Sci., 4: 317-324.
- Farshadfar, E., N. Mahmodi and A. Yaghotipoor, 2011a. AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.). Aust. J. Crop Sci., 5: 1837-1844.
- Farshadfar, E., Z. Vaisi and A. Yaghotipoor, 2011b. Non parametric estimation of phenotypic stability in wheat-barley disomic addition lines. Ann. Biol. Res., 2: 586-598.
- Gauch, Jr. H.G., 1988. Model selection and validation for yield trials with interaction. Biometrics, 44: 705-715.
- Pham, T.D., T.D.T. Nguyen, T., A.S. Carlsson and T.M. Bui, 2010. Morphological evaluation of sesame (*Sesamum indicum* L.) varieties from different origins. Aust. J. Crop Sci., 4: 498-504.
- Purchase, J.L., 1997. Parametric analysis to describe genotype×environment interaction and yield stability in winter wheat. Ph.D. Thesis, University of the Orange Free State, Bloemfontein, South Africa.
- Sneller, C.H., L.K. Norquest and D. Dombek, 1997. Repeatability of yield stability statistics in soybean. Crop Sci., 37: 383-390.

- Steel, R.G.D., J.H. Torrie and D.A. Dickey, 1996. Principles and Procedures of Statistics: A Biometrical Approach. 3rd Edn., McGraw-Hill Companies, New York, USA., ISBN-13: 978-0070610286, pp: 471-472.
- Tadesse, H. and F. Abay, 2011. Additive main effects and multiplicative interactions analysis of yield performance of sesame genotypes across environments in Northern Ethiopia. *J. Drylands*, 4: 259-266.
- Zali, H., E. Farshadfar, S.H. Sabaghpour and R. Karimizadeh, 2012. Evaluation of genotype×environment interaction in chickpea using measures of stability from AMMI model. *Ann. Biol. Res.*, 3: 3126-3136.
- Zenebe, M. and M. Hussien, 2009. Study on genotype×environment interaction of yield in sesame (*Sesamum indicum* L.). *J. Phytol.*, 1: 199-205.
- Zobel, R.W., M.J. Wright and H.G. Gauch, 1988. Statistical analysis of a yield trial. *Agron. J.*, 80: 388-393.