International Journal of Agriculture, Environment and Biotechnology
Citation: *IJAEB*: **19**(03): 105-114, September 2026
DOI: 10.30954/0974-1712.03.2026.1

ASSOCIATION FOR AGRICULTURE ENVIRONMENT AND BIOTECHNOLOGY

RESEARCH PAPER

Yield Stability and Adaptability of Elite Sesame (*Sesamum indicum* L.) Breeding Lines Across Environments Using AMMI and GGE Biplot Analysis

Anowar Hossain[1,2*], Maini Bhattacharjee[3], Tapash Dasgupta[1], Satyaki Nandan Maity[1] and Yendrembam Surjalata Devi[4]

[1]Department of Genetics and Plant Breeding, Ramakrishna Mission Vivekananda Educational and Research Institute, Narendrapur, Kolkata, West Bengal, India
[2]Crop Improvement Division, ICAR-Central Rice Research Institute, Cuttack, Odisha, India
[3]Reseach and Development Laboratory, Mali Agri Tech. Pvt. Limited, Ranaghat, Nadia, West Bengal, India
[4]Department of Sericulture, Raiganj University, Raiganj 733134, Uttar Dinajpur, West-Bengal, India

*Corresponding author: anwrhsn1999@gmail.com (**ORCID ID:** 0009-0009-2461-0210)

Paper No. 1243 **Received:** 17-06-2026 **Revised:** 24-08-2026 **Accepted:** 03-09-2026

ABSTRACT

Sesame (*Sesamum indicum L.*) is an important oilseed crop cultivated largely under rainfed and marginal environments where yield instability remains a major production constraint. The present study evaluated the yield performance and stability of elite sesame genotypes across three agro-ecological locations of West Bengal during the pre-*kharif* season. Pooled analysis of variance revealed significant effects of genotype, environment, and genotype × environment (G × E) interaction for seed yield per plant (SYPP), capsules per plant (CPP), and thousand-seed weight (TSW) indicating differential performance of genotypes across environments. The AMMI and GGE biplot identified G4, G5, G12, and G14 as promising breeding lines across the evaluated traits under the tested environments. White-seeded genotypes exhibited higher seed weight and oil content, with G12 recording the highest oil content (48.5%). However, as the evaluation was conducted over a single cropping season the observed stability patterns should be considered preliminary and require validation through multi-season and multi-location testing. These findings provide valuable information for selecting promising sesame breeding lines and parental materials for future genetic improvement.

HIGHLIGHTS

- Evaluation advanced breeding lines.
- Promising stable genotypes identified across environments.
- Multivariate stability model AMMI and GGE biplot used.
- White coated sesame seeds confer higher test weight and oil content.

Keywords: Sesame, genotype × environment interaction, yield stability, AMMI, GGE biplot, multi-environment trials

Sesame (*Sesamum indicum* L.) is one of the most ancient oilseed crops and belongs to the family Pedaliaceae, which comprises approximately 34 diploid and allotetraploid species. The cultivated species is diploid ($2n = 2x = 26$) with an estimated genome size of 309.4 Mb (Nayar 1970; Wang *et al.* 2022). According to Ramanujam and Joshi (1954), wild relatives such as *Sesamum capense* and *Sesamum schenkii* are distributed across Africa, Peninsular

How to cite this article: Hossain, A., Bhattacharjee, M., Dasgupta, T., Maity, S.N. and Devi, Y.S. (2026). Yield Stability and Adaptability of Elite Sesame (*Sesamum indicum* L.) Breeding Lines Across Environments Using AMMI and GGE Biplot Analysis. *Int. J. Ag. Env. Biotech.*, **19**(03): 105-114.

Source of Support: None; **Conflict of Interest:** None

India, and the East Indies regions considered primary centre of origin and diversity from which the crop subsequently spread to other parts of the world.

The term "sesame" derived from Arabic word semsen or simsin, with various colloquial names in India, including *til* (Hindi, Bengali), *tila* (Sanskrit) and *nuvvulu* (Telegu) (Candolle 1886). Although it is classified as a minor oilseed, sesame seeds contain 48-55% oil (Hegde 2012), primarily unsaturated fatty acids like oleic (18:1) and linoleic acid (18:2), reaching up to 38.84% and 46.26%, respectively (Nzikou 2010), hence the sobriquet "queen of oilseeds". The presence of antioxidants like sesamol and sesamolin promote oxidative stability and impart extended storage life (Budowski 1950).

India shares 11.82% of the world's total sesame production of 7.24 billion kg, standing second after Sudan and followed by Myanmar and China (FAOSTAT 2023). In India, the major producing state is Uttar Pradesh and Madhya Pradesh, with a contribution of 0.11 million tonnes and a highest productivity of 873 kg ha^{-1} from Bihar in 2025-26 year (DAFW 2025).

Despite its economic importance, sesame productivity remains low and unstable, primarily due to cultivation under rainfed conditions, poor soil fertility, high sensitivity to environmental fluctuations and intrinsic physiological traits such as capsule dehiscence and non-synchronous flowering (Ashri 1994). Yield instability caused by genotype × environment (G×E) interaction poses a major challenge to breeders, as genotypes that perform well in one environment may not exhibit similar performance in others. According to Singh *et al.* (1999), cross-over (qualitative) interactions revealed environment-specific adaptation and erratic ranking patterns, but non-cross-over (quantitative) interactions made it easier to identify extensively adapted genotypes (Gauch 2013). Understanding *G×E* interaction is crucial for identifying genotypes with either broad or specific adaptation. Multi-environment testing enables breeders to assess yield stability and adaptability, thereby facilitating the selection of genotypes that combine high yield potential with consistent performance.

Multivariate approaches including Additive Main Effects and Multiplicative Interaction (AMMI), Genotype Main Effect Plus Genotype-by-Environment Interaction (GGE) biplots provided precise partitioning of genotype, environment, and G × E effects separately and superior ability to identify stable genotypes and mega-environments (Fox 1997; Mohammadi 2021).

In eastern India, particularly in West Bengal, sesame is grown across diverse agro-climatic zones characterized by variation in rainfall, temperature, and soil type. However, systematic information on the stability and adaptability of elite sesame genotypes in this region remains limited. The present investigation was therefore undertaken to evaluate elite sesame genotypes across multiple environments in West Bengal and to identify stable, high-yielding genotypes suitable for wide or specific adaptation.

MATERIALS AND METHODS

Description of the Study Area

The field experiment was conducted at three geographically distinct locations in the Eastern Zone (EZ) of India, namely the Agricultural Experimental Farm, Narendrapur (South 24 Parganas district, West Bengal), the Mali Agri-Tech Experimental Farm, Ranaghat (Nadia district, West Bengal), and the State Agricultural Adaptive Farm, Malda (Malda district, West Bengal), during the pre-*kharif* season (March-May 2022). The overall agro-climatic characteristics and prevailing environmental conditions of the experimental sites are presented in Table 1.

Plant Materials and Experimental Design

A total of 19 advanced breeding lines of different generations along with six check varieties were evaluated in this study. Pedigree of all the genotypes used are provided in Table 2. The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications at each experimental location. Each plot measured 2 m × 6 m with 1.5 m spacing between blocks and 1.0 m between adjacent plots. Seeds were manually sown at a spacing of 40 cm between rows and 15 cm between plants within each row. Standard agronomic practices including recommended fertilizer application, timely irrigation, and manual weed management

Table 1: Agro-ecological characteristics of experimental site in cropping season 2022

Location	Code	Latitude	Longitude	Elevation	Soil type	Av. Temp.	Av. Rainfall
Narendrapur	E1	22.44^0 N	88.4^0 E	9 m	Alluvial	30^{o}C	159.60 mm
Ranaghat	E2	23.17^0 N	88.56^0 E	8 m	New alluvial	30.68^{o}C	163.20 mm
Malda	E3	25.01^0 N	88.14^0 E	17 m	New Gangetic alluvial	29.64^{o}C	249.50 mm

Table 2: Pedigree and description of experimental materials of sesame.

No.	Breeding line	Pedigree	Generation	Seed Color
1	G1	EC 90 X Savitri	F8	Beige
2	G2	EC 90 X Savitri	F8	Beige
3	G3	EC 90 X Savitri	F8	Dark brown
4	G4	EC 90 X Savitri	F8	Red brown
5	G5	EC 90 X Savitri	F8	Black
6	G6	AT 238 X Suprava	F4	Beige
7	G7	AT 238 X Suprava	F4	White
8	G8	AT 238 X Suprava	F4	White
9	G9	AT 238 X Suprava	F4	Beige
10	G10	AT 238 X Suprava	F4	Beige
11	G11	AT 238 X Suprava	F4	Red brown
12	G12	AT 238 X Suprava	F4	White
13	G13	AT 238 X Suprava	F4	White
14	G14	AT 238 X Suprava	F4	White
15	G15	AT 238 X Suprava	F4	White
16	G16	Suprava X CUHY57	F3	Dark brown
17	G17	JLT 408 X EC 90	F3	Red brown
18	G18	Suprava X RT 351	F3	Black
19	G19	JLT 408 X EC 90	F3	White
20	G20 (Savitri)	Selection from germplasm SWB32	Released, 2008	Light brown
21	G21 (CUHY 57)	Uma x TKG 352	CVRC,2018	brown
22	G22 (Rama)	Selection from 'Khosla' local	Released, 1989	Red brown
23	G23 (Prachi)	Mutant of B67	Released, 2004	Black
24	G24 (GT-10)	Selection from TNAU17	Released,2002	Black
25	G25 (Suprava)	Mutant of IC 625735	CVRC,2018	Dark brown

were uniformly followed across all experimental locations.

Data Collection

For each trait, observations were recorded from three randomly selected competitive plants per plot in each replication, excluding border rows. Capsules per plant (CPP) were recorded at plant maturity whereas seed yield per plant (SYPP) and thousand-seed weight (TSW) were measured after harvesting, threshing, and drying the seeds collected from individual plants at physiological maturity. Oil content (%) was determined using seed samples collected from the Ranaghat (E2) location. Oil extraction was performed following the cold hexane extraction method described by Latif and Anwar (2011).

Statistical Analysis

Statistical analyses were performed using R software version 4.2.2 (R Core Team, 2022). Genotype × environment interaction and phenotypic stability were evaluated using the Additive Main Effects and Multiplicative Interaction (AMMI) model and Genotype plus Genotype × Environment (GGE)

biplot model in the "metan" package (Olivoto and Lúcio 2020).

RESULTS AND DISCUSSION

Variability Observed Among Selected Lines

Substantial phenotypic variation was observed during field evaluation and all recorded traits conformed to the DUS descriptors for sesame as prescribed under PPV&FRA (2019). Considerable variability in capsule length was recorded ranging from short to long (1.5-2.8 cm). Differences in capsule arrangement were evident, including alternate, opposite, zigzag types. In addition, marked variation was observed in the number of locules per capsule, which ranged from 4 to 8. Distinct floral color namely light purple and white noted while lobing pattern and leaf size varied in respect to leaf morphology (Supplementary figure S1). Post-harvest assessment revealed noticeable variation in seed and oil-related traits. Differences in seed coat color were observed among genotypes and during oil extraction color ranged from white to light yellow indicating genotypic differences in seed composition.

To ensure phenotypic consistency, harvested plants were reconfirmed by matching the seed coat color of the harvested seeds with that of originally sown seeds thereby minimizing the possibility of admixture or misclassification (Supplementary figure S2).

AMMI Variance Components Analysis

The AMMI analysis of variance revealed highly significant ($P < 0.001$) effects of genotype, environment, and genotype × environment ($G \times E$) interaction for all three evaluated traits. In addition, the first two interaction principal component axes (IPCA1 and IPCA2) were also highly significant (Table 3). Replication effects within the environment were non-significant at $P > 0.05$, reflecting little variability among the replications and also manifesting uniform field conditions and low experimental error. The environment accounted for the largest proportion of variation in SYPP (49.2%) while the interaction between genotype and environment contributed the highest variation to CPP (59.64%). In contrast, TSW exhibited significantly lower G × E interaction (14.14%), which indicates that the trait was under stronger genetic control and less susceptible to environmental variation. The Interaction of two PC axes cumulatively captured 100% of the $G \times E$ interaction due to limited environmental degrees of freedom. Considering seed yield, it was observed that 58.6% of this was explained by PC1 and the remaining 41.4% by PC2. This trend was equally exhibited in the other traits. This suggests clear interaction patterns and structured genotype behavior across environments. These findings are in agreement with Esan *et al.* (2023) who reported in AMMI model first two principal components are sufficient to displayed existing variability.

AMMI I Biplot

Interpretations of both AMMI1 and AMMI2 biplots were performed following the methods described by Gauch *et al.* (1997). The AMMI I biplot depicts the relationship between mean value of genotypes

Table 3: AMMI analysis of variance for SYPP, CPP and TSW

		Seed Yield Per Plant (SYPP)			Capsule Per Plant (CPP)			Thousand Seed Wt. (TSW)		
Source	**df**	**MS**	**TSS%**	**G x E Explained %**	**MS**	**TSS%**	**G x E Explained %**	**MS**	**TSS%**	**G x E Explained %**
ENV	2	656.51***	49.28		22540.31***	17.22		0.430***	3.72	
REP(ENV)	6	0.809			23.88			0.002		
GEN	24	28.30***	25.49		2483.44***	23.14		0.777***	82.14	
GEN: ENV	48	14.01***	25.24		3176.47***	59.64		0.067***	14.14	
PC1	25	15.81***		58.6	4690.23***		76.9	0.087***		67
PC2	23	12.15***		41.4	1531.07***		23.1	0.046***		33
Residuals	143	1.07			37.99			0.004		
Total	271	12.90			1526.61			0.098		

*df-Degrees of freedom, MS- Mean square, TSS- Total sum of square, G- Genotypes, E- Environment, *** 0.01 % level of significance.*

across environments on x-axis and scores of PC1 on y-axis. The performance of genotypes falling on the right side of the grand mean was superior while those that were positioned closer zero to the PC1 line were more stable. For SYPP, Fig. 1A shows that G15 had the closest value to the overall mean value of 12.63 g. The genotypes G21, G10, G12, G8, and G5 expressed more than average value for seed yield. In case of CPP (Fig. 1B), the genotypes G6, G22, G19, G18, and G8 recorded more than 133 capsules per plant. Among them, G4 was found to be highly stable and widely adaptive. For TSW (Fig. 1C), G14 was the most stable with the highest value of 3.66 g followed by G13, G15, G7, and G12. Accordingly, E1 and E2 were favorable for superior performance of seed yield and thousand-seed weight.

AMMI II Biplot Interpretation

The AMMI II biplot (Fig. 2) illustrates the distribution of genotypes based on their PC1 and PC2 scores. The genotypes closest to the origin were considered stable while those near specific environment vectors exhibited particular adaptability to that zone. For seed yield per plant (SYPP) (Fig. 2A) identified G24, G5, G12, and G2 as the most stable genotypes across environments. Genotypes G15 and G1 showed specific adaptation to E1 whereas G17, G16, G12, and G11 were better adapted to E2. For capsules per plant (CPP), the AMMI II biplot (Fig. 2B) indicated that G4, G21 and G16 were relatively stable across environments while G9 and G1 exhibited specific adaptation to E2. Fig. 2C illustrates the TSW biplot where PC1 and PC2 accounted for 67% and 33% of the interaction variation. While G18, G8 and G24 identified as the most stable genotypes.

GGE Biplot: Which-Won-Where Pattern

The GGE biplot graph including which-won-where, means and stability, discriminativeness and representativeness were interpreted following method described by Yan and Tinker (2005). This biplot grouped the test environments into mega-environments and identified winning genotypes. For SYPP (Fig. 3A), the genotypes G1, G19, G14, G21 and G18 positioned vertices of polygon indicating their strong responsiveness. G18 performed superior in E1 while G21 performed best in E2 which describe environment-specific superiority. In case of CPP, Fig. 3B showed that E2 and E3 belonged to one mega-environment while E1 represented

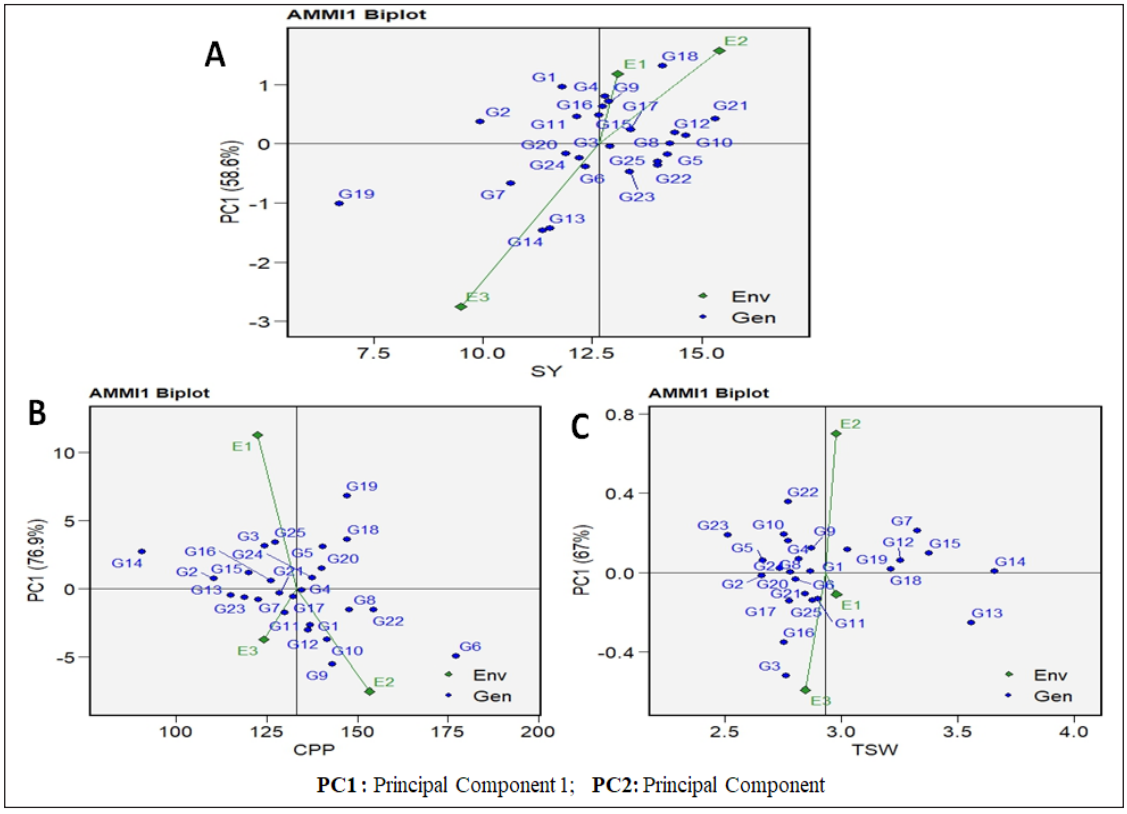


Fig. 1: AMMI 1 biplot for PC1 interaction with seed yield **(A)** capsules for plant **(B)** and thousand seed weight **(C)**

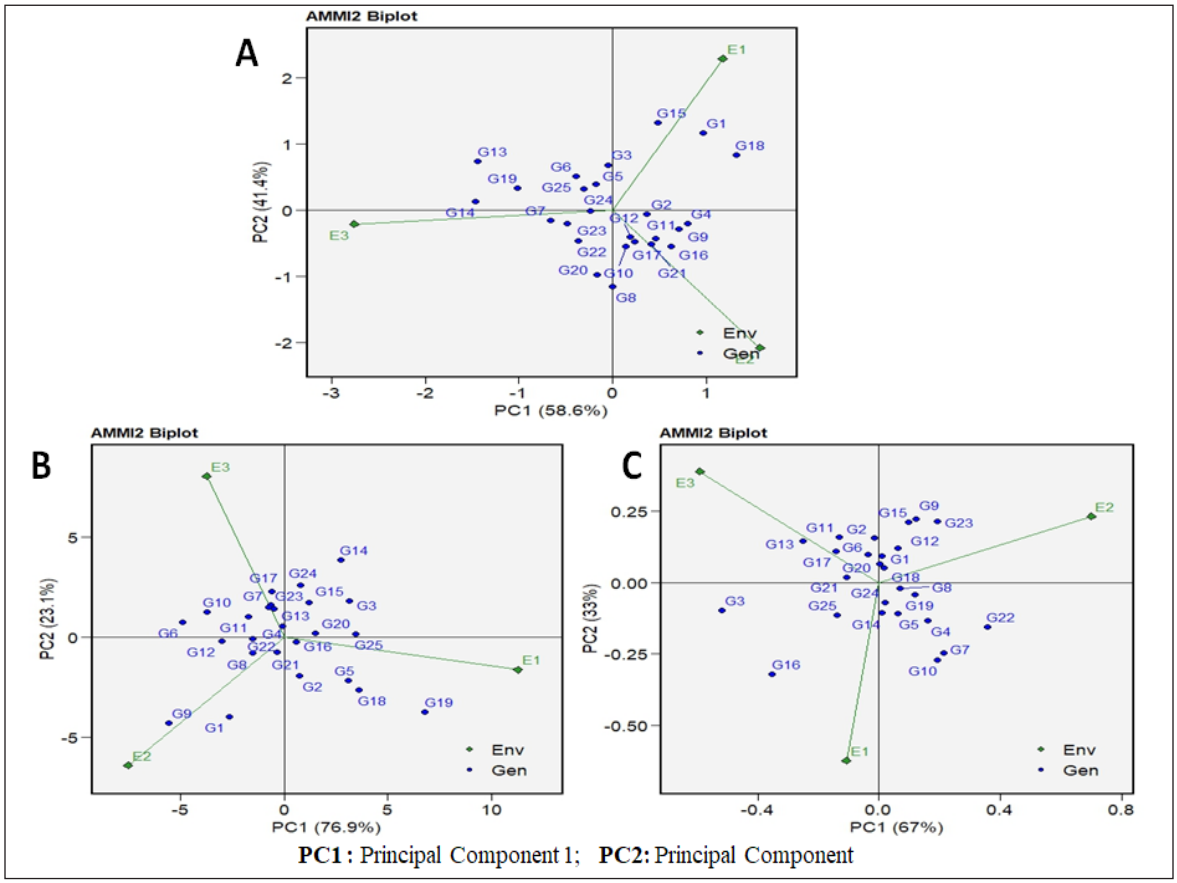


Fig. 2: AMMI 2 biplot for seed yield **(A)** capsules per plant **(B)** and thousand seed weight **(C)** based on PC1 and PC2 Gen. × Env. interaction

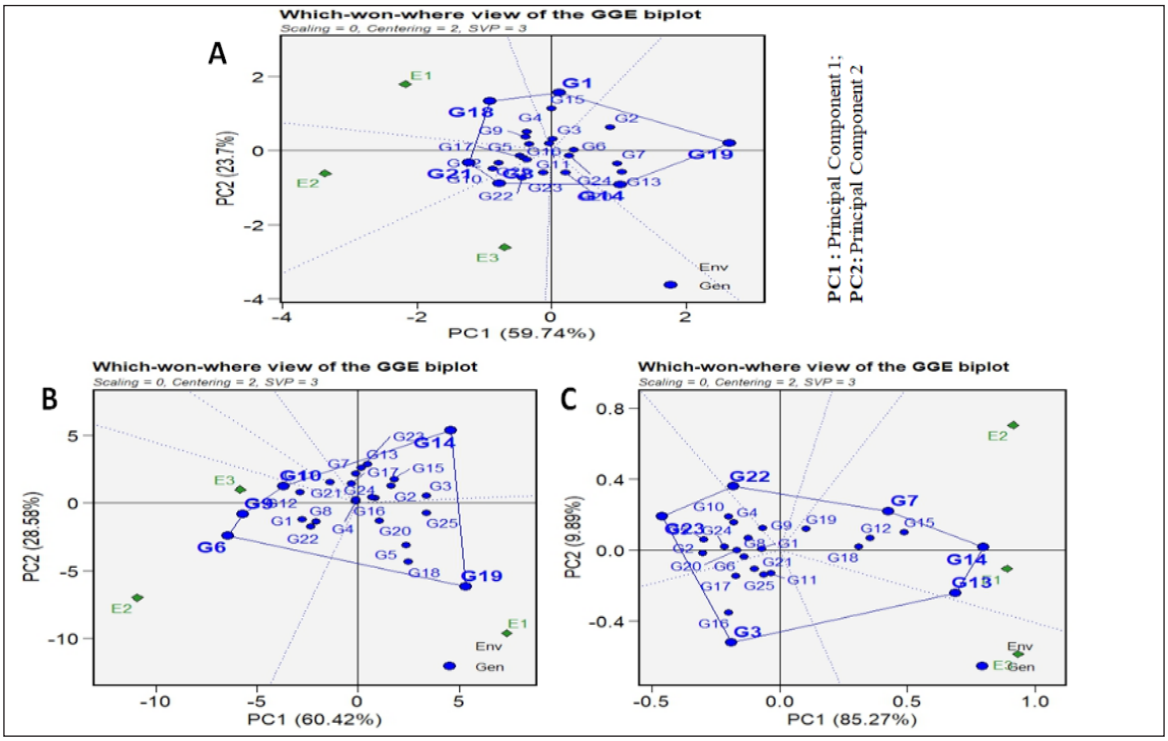


Fig. 3: Polygon view of SGGE biplot for which-won where pattern of seed yield **(A)**, capsules per plant **(B)** and thousand seed weight **(C)**

another mega-environment. The genotypes G9, G6 and G10 were the best performers in E2 + E3 while G19 was the best performer in E1. For TSW (Fig. 3C), the G7, G14 and G13 performed best in E1 + E2 while E3 represented a different environment.

Means and Stability Biplot

The means versus stability biplot (Fig. 4) ranked genotypes using the Average Environment Coordination (AEC) axis. Genotypes placed towards to the arrow of the AEC abscissa side had above average means while the shorter projections towards the ordinate which showed higher stability. For SYPP Fig. 4A, G21, G5, G10, G12 and G25 were stable and higher the grand mean value. For CPP (Fig. 4B), G6> G9> G22> G1> G19>G18>Grand Mean, however G4 and G8 were the most stable. For TSW (Fig. 4C), G14, G13, G15, G7, G12, and G18 were outperformed the average value whereas G14, G12, G18 and G15 showing the greatest consistency across environments.

Discriminativeness vs. Representativeness

The biplot (Fig. 5) of the environment comparison identified the most discriminative and representative tested trial site. Vector length denotes discriminative ability while vector angle relative to the AEC abscissa is related to representativeness. E2 considered as best discriminativeness and representativeness environment for both SYPP and CPP. On the other hand, E1 was the most representative environment for TSW. Consequently, E1 and E2 were ideal for selection and breeding trials.

Oil Content

Oil content in the 25 genotypes ranged from a low of 29.16% to a high of 48.50%, with an overall mean of 39.31%. The genotypes G12 (48.50%), G22 (46.61%), and G14 (46.59%) were the topmost for their oil levels (Fig. 6). Other promising genotypes, such as G13, G15, and G8, neared the 45% level and thus showed promise for oil improvement breeding.

Overall, advanced sesame breeding lines exhibited significant variation across tested environments for CPP and SYPP, while TSW showed relatively low environmental influence indicating strong genetic determination of this trait. Similar findings were reported by Baraki and Berhe (2019) and Azon *et al.* (2023). The AMMI model effectively partitioned G × E interaction into two principal interaction axes

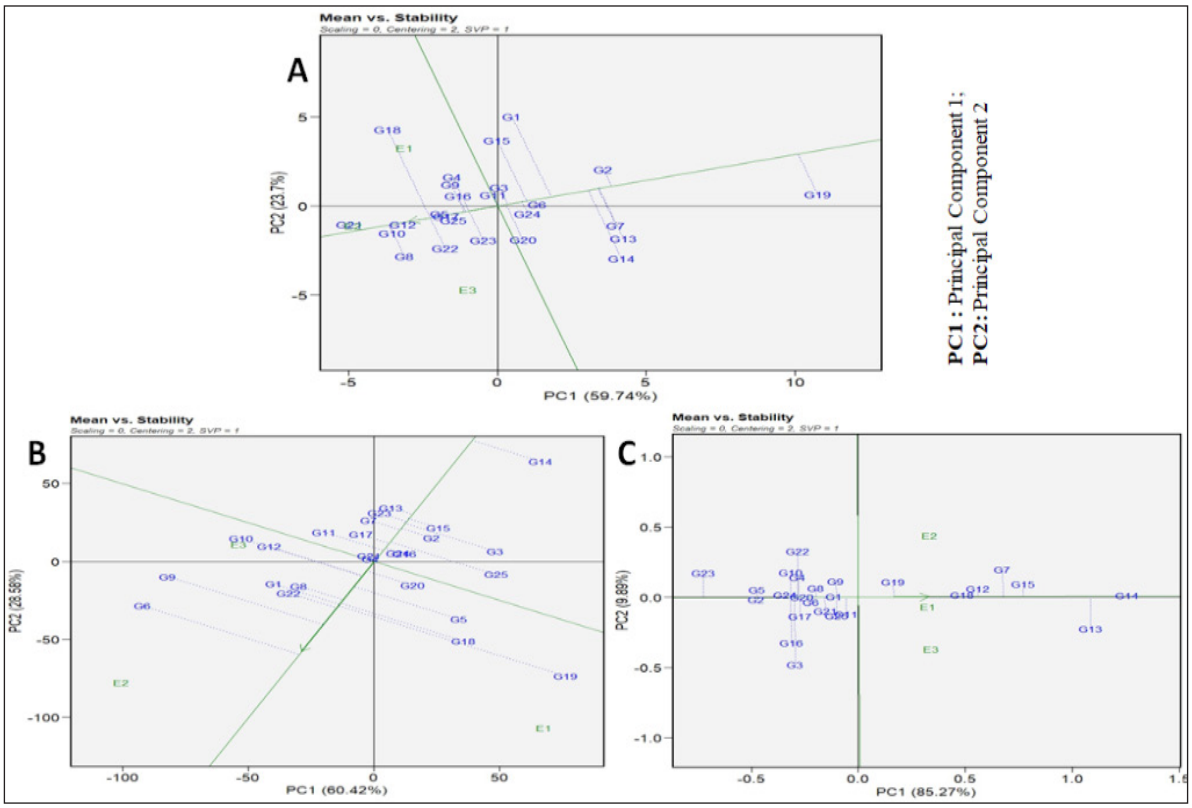


Fig. 4: Mean and stability biplot for seed yield (A), capsules per plant (B) and thousand seed weight (C)

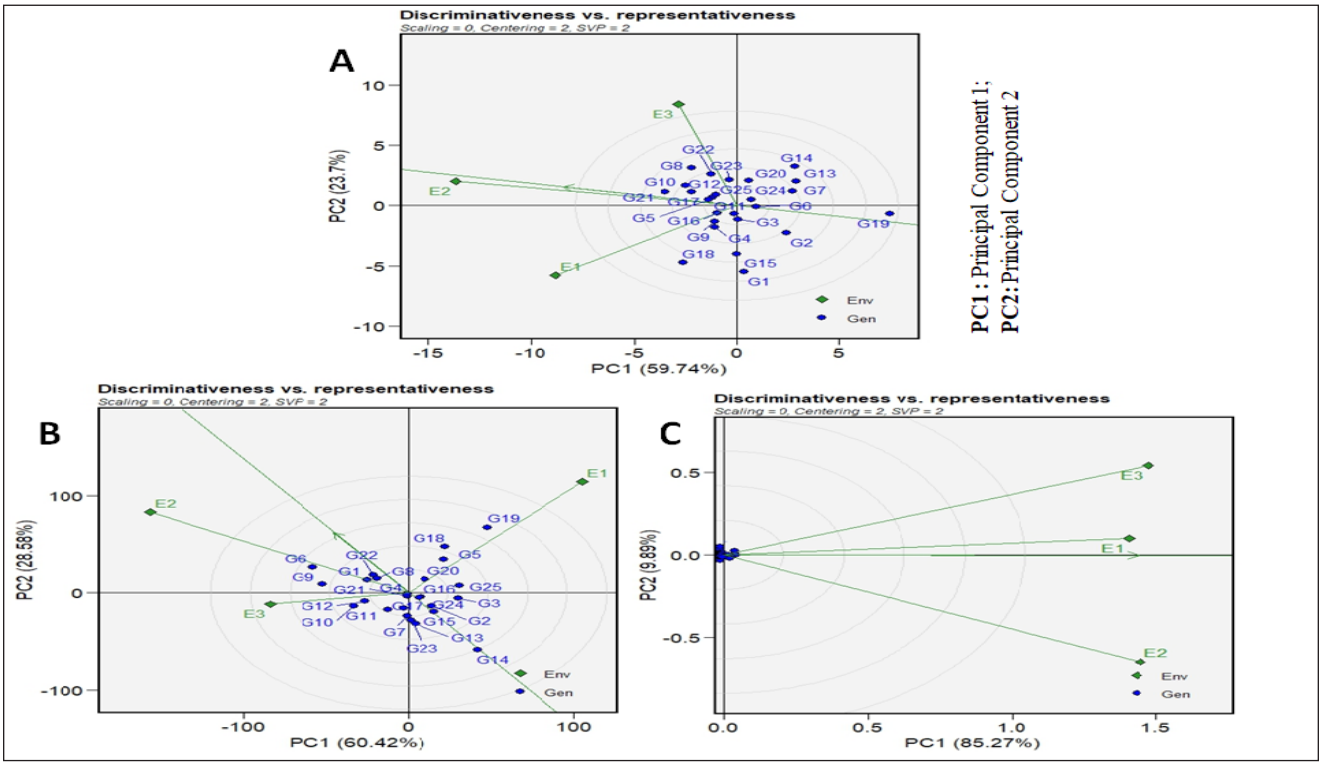


Fig. 5: Discriminativeness and representativeness GGE biplot for seed yield **(A)**, capsules per plat **(B)** and thousand seed weight **(C)**

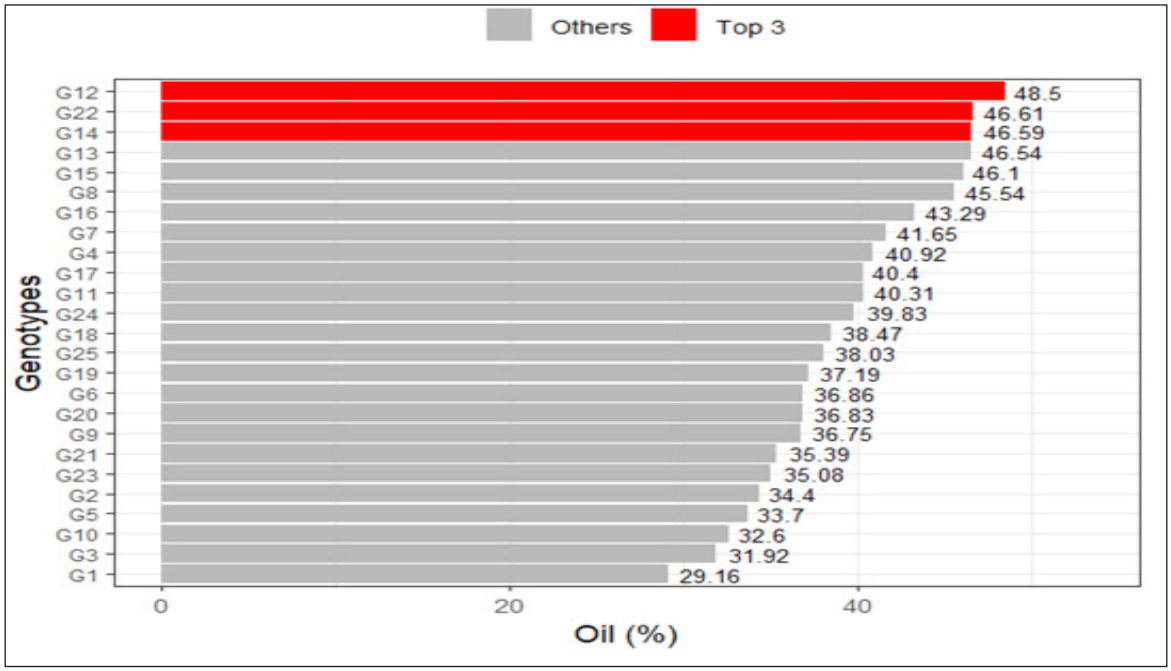


Fig. 6: Percentage of oil content in 25 sesame genotypes

explaining nearly 100% of interaction variation. Whereas the GGE model explained 83.44% for SYPP, 89% for CPP, and 95.16% for TSW. Comparisons between the both multivariate AMMI and GGE biplot models showed that G5 and G12 had strong overall evidence of high seed yield and broad adaptation for seed yield per plant (SYPP). While G10 showed high mean SYPP and favorable performance in the GGE analysis, indicates that it should not be classified as broadly stable across all three locations. In contrast, genotypes G12, G14 and G18 exhibited stable 1000-seed weight (TSW) across

environments. While G4 and G8 demonstrated stable performance for capsules per plant (CPP). Azon *et al.* (2023) evaluated 19 sesame accessions across eight environments in Benin using AMMI and GGE biplot analysis and reported consistent identification of stable genotypes and suitable test environments. Comparable findings were previously observed by Daba *et al.* (2015) and Shim *et al.* (2015).

At the E2 (Ranaghat) location, oil-content observations showed an apparent association with seed coat color and thousand-seed weight. however, because oil content was evaluated in only one environment, this relationship should be interpreted as descriptive rather than as evidence of a stable association. White-seeded genotypes (G12, G14, G13, G15) showed the highest oil content (46-48.5%) and heavier seeds (3.25-3.56 g) which were higher than grand mean value. Genotypes with oil content below 37% correspondingly exhibited lower seed weight (< 2.93 g), whereas those with higher oil content displayed proportionally greater seed weight. These results are consistent with earlier reported Paroha *et al.* (2014) that white whole and decorticated seeds contained 47.5% and 51% oil respectively, exceeding other seed-coat color. Dossa *et al.* (2018), using near-infrared reflectance spectroscopy on diverse global germplasm also found that light-colored seeds particularly white and light brown had higher protein, oil, and linoleic acid content than dark-seeded samples. Thousand-seed weight is positively related to seed yield, oil content, and major yield attributes while seed yield itself is positively correlated with plant height, number of seeds per capsule, thousand-seed weight, and oil content at genotypic and phenotypic levels (Babu *et al.* 2004; Kante *et al.* 2022). In soybean, loci controlling both seed weight and oil content were identified through genomic and transcriptomic association studies and showed a strong positive relationship between the two traits (Yuan 2024).

Based on the combined evidence from these analyses, genotypes G4 and G5, currently at the F_8 generation have been prioritized for further multi-location evaluation as advanced recombinant inbred lines. Likewise, G12 and G14, currently at the F_4 generation were identified as promising white-seeded breeding lines to fulfil prevailing market demands for premium white sesame seed characterized by elevated oil content, addressing a critical regional deficit in locally adapted white-seeded germplasm.

CONCLUSION

This study demonstrated significant genotypic and genotype × environment interaction effects for seed yield and its associated traits in sesame across three test environments. The AMMI and GGE biplot models identified G4, G5, G12, and G14 as promising breeding lines with favorable performance and stability under the tested environments. Ranaghat (E2) was identified as the discriminative and representative testing environment for genotype evaluation. However, as the experiment was conducted over a single cropping season, these findings should be considered preliminary. Therefore, the selected breeding lines should be subjected to further multi-location and multi-season evaluation before being considered for varietal release.

ACKNOWLEDGEMENTS

The authors gratefully thankful to Ramakrishna Mission Vivekananda Educational and Research Institute (RKMVERI) for providing support and facilities during the course of this research work.

GENERATIVE AI DECLARATION

The author(s) confirm that there was no use of artificial intelligence (AI)-assisted technology for assisting in the writing or editing of the manuscript, and no images were manipulated using AI. The authors developed and verified all scientific content, data analysis, interpretation of results, and conclusions. The authors take full responsibility for the accuracy, integrity, and originality of the work presented, and no AI tool was listed as an author.

REFERENCES

Ashri, A. 1994. Genetic resources of sesame: Present and future perspectives. *In:* Arora, R.K. and Riley, K.W. (eds). *Sesame Biodiversity in Asia- Conservation, Evaluation and Improvement*, IPGRI Office for South Asia, New Delhi, India, pp. 25-39.

Azon, C.F., Hotegni, V.N.F., Sogbohossou, D.E.O., Gnangle, L.S., Bodjrenou, G., Adje, C.O. ... Achigan-Dako, E.G. 2023. Genotype× environment interaction and stability analysis for seed yield and yield components in sesame (*Sesamum indicum* L.) in Benin Republic using AMMI, GGE biplot and MTSI. *Heliyon,* **9**(11).

Babu, J.S., Reddy, C.D. and R. Reddy, N.S. 2004. Character association and path coefficient analysis in a set of white seeded genotypes of sesame (*Sesamum indicum* L.). *Annals of Agriculture Biology Research*, **19**: 13-18.

Baraki, F. and Berhe, M. 2019. Evaluating performance of sesame (*Sesamum indicum* L.) genotypes in different growing seasons in northern Ethiopia. *International Journal of Agronomy*, **2019**(1): 7804621.

Budowski, P., Menezes, F.G.T. and Dollear, F.G. 1950. Sesame oil. V. The stability of sesame oil. *Journal of the American Oil Chemists Society*, **27**(10): 377-380.

Daba, C., Ayana, A., Zeleke, H. and Wakjira, A. 2015. "Genotype x Environment interactions for seed yield in Sesame in western Ethiopia." *East African Journal of Sciences*, **9**(2): 85-96.

De, Candolle, A. 1886. *Origin of cultivated plants*., Kegan Paul, French Co, London. Reprinted by Noble Offset Printers, New York, 1959.

Department of Agriculture and Farmers Welfare. 2025. Unified Portal for Agricultural Statistics (UPAg), Government of India. https://upag.gov.in/.

Dossa, K., Wei, X. and Niang, M. *et al*. 2018. Near-infrared reflectance spectroscopy reveals wide variation in major components of sesame seeds from Africa and Asia. *The Crop Journal*, **6**(2): 202-206.

Esan, V.I., Oke, G.O., Ogunbode, T.O. and Obisesan, A. 2023. AMMI and GGE biplot analyses of Bambara groundnut [*Vigna subterranea* (L.) Verdc.] for agronomic performances under three environmental conditions. *Frontiers in Plant Science*, **13***:* 997429.

FAOSTAT. 2023. FAOSTAT statistical database, Food and Agriculture Organization of the United Nations. https://www.fao.org/faostat/en/.

Fox, P.N., Crossa, J. and Romagosa, I. 1997. Multi-environment testing and genotype× environment interaction. *In Statistical methods for plant variety evaluation.*, Dordrecht: Springer Netherlands, pp. 117-138.

Gauch, H. and Jr, G. 2013. A simple protocol for AMMI analysis of yield trials. *Crop Science*, **53**(5): 1860-1869.

Gauch, H., Jr, G. and Zobel, RW. 1997. Identifying mega-environments and targeting genotypes. *Crop Science*, **37**(2): 311-326.

Guidelines for the Conduct of Test for Distinctiveness, Uniformity and Stability on Sesame (*Sesamum indicum* L). 2019. *Protection of Plant Varieties and Farmers Right Authority (PPV&FRA).*, Government of India. https://plantauthority.gov.in/crop-dus-guidelines

Hegde, D.M. 2012. Sesame. *In Handbook of herbs and spices.*, Woodhead Publishing, pp. 449-486.

Kante, S., Wadikar, P.B., Sargar, P.R. and Patil, S.S. 2022. Correlation analysis for seed yield and its related attributes in genotypes of sesame (*Sesame indicum* L.). *International Journal of Plant and Environment*, **8**(01): 87-90.

Latif, S. and Anwar, F. 2011. Aqueous enzymatic sesame oil and protein extraction. *Food Chemistry*, **125**(2): 679-684.

Mohammadi, R., Sadeghzadeh, B., Poursiahbidi, M.M. and Ahmadi, M.M. 2021. Integrating univariate and multivariate statistical models to investigate genotype × environment interaction in durum wheat. *Annals of Applied Biology*, **178**(3): 450-465.

Nayar, N.M. and Mehra, K.L. 1970. Sesame: Its uses, botany, cytogenetics, and origin. *Economic Botany*, pp. 20-31.

Nzikou, J.M., Mvoula, Tsiéri. M. and Ndangui, C.B. 2010. Characterization of seeds and oil of sesame (*Sesamum indicum* L.) and the kinetics of degradation of the oil during heating. *Research Journal of Applied Sciences, Engineering and Technology*, **2**(3): 227-232.

Paroha, S., Bhargav, A., Tripathi, A., Garg, S., Kawreti, V. and Ranganatha, A.R.G. 2014. Biochemical composition of whole seed, decorticated seed and seed coat in sesame (*Sesamum indicum* L.) of different seed coat colours. *The Indian Society of Oilseeds Research.*, **126**.

Ramanujam, S. and Joshi, AB. 1954. Identity and taxonomical study of Sesamum ekambaramii Naidu. *Journal of the Bombay Natural History Society*, **52**: 657.

Olivoto. and Lucio. 2020. R-statistical software using "metan" package.

Shim, K., B., Shin., S.H., Shon, J.Y., Kang, S.G., Yang, W.H. and Heu, S.G. 2015. Interpretation of genotype × environment interaction of sesame yield using GGE biplot analysis. *The Korean Journal of Crop Science*, **60**(3): 349-354.

Singh, M., Ceccarelli, S. and Grando, S. 1999. Genotype × environment interaction of crossover type: detecting its presence and estimating the crossover point. *Theoretical and Applied Genetics*, **99**(6): 988-995.

Wang, M., Huang, J., Liu, S., Liu, X., Li, R., Luo, J. and Fu, Z. 2022. Improved assembly and annotation of the sesame genome. *DNA Research*, **29**(6): dsac041.

Yan, W. and Tinker, N.A. 2005. An integrated biplot analysis system for displaying, interpreting, and exploring genotype × environment interaction. *Crop Science*, **45**(3): 1004-1016.

Yuan, X., Jiang, X. and Zhang, M. *et al*. 2024. Integrative omics analysis elucidates the genetic basis underlying seed weight and oil content in soybean. *The Plant Cell*, **36**(6): 2160-2175.