International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(8): 562-566
www.biochemjournal.com
Received: 13-06-2025
Accepted: 16-07-2025

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Genetic diversity study in Sesame germplasm (*Sesamum indicum* L.)

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DOI: https://www.doi.org/10.33545/26174693.2025.v9.i8Si.5209

Abstract
The current study set out to identify the kind and degree of genetic variability among the variables influencing seed production. Using a Randomised Block Design with two replications, 40 sesame genotypes were assessed for nine different characteristics at the Agriculture Research farm, College of Agriculture, Dhule, in the summer of 2024. The genotypes were divided into six clusters based on the D^2 value. In addition to providing options for improving the base population and achieving a high heterotic impact, intercrossing them would restore suitable transgressive segregants and a broad spectrum of diversity in succeeding generations.
The JLSG-1659 genotype is superior in terms of earliness in terms of days to 50% flowering and days to maturity when taking into consideration inter-cluster distances, cluster mean, per se performance, and divergence class as demonstrated in the current study. Plant height, protein content, and seed yield per plant were determined to be superior for genotype TKG-377. In terms of 1000 seed weight, number of primary branches per plant, and number of capsules per plant, genotype NIC-790 is superior. Plant height is greater for genotype TNAU-64-3. By intercrossing these genotypes, more variety can be created in sesame and beneficial heterosis can be obtained.

Keywords: Genetic diversity, sesame, cluster, genotypes, D^2 value

1. Introduction
Sesame, an annual flowering plant in the *Pedaliaceae* family, is one of the earliest oilseed crops cultivated by humans. Originating in tropical and subtropical Asia and Africa, it is native to India and East Africa. The plant grows between 60 to 120 cm tall, with a quadrangular stem and a well- developed root system. Its strong taproot and deep lateral extensions help it withstand drought conditions.
The leaves of sesame are simple and vary widely in shape and arrangement depending on the plant's growth stage. Lower leaves tend to be broad and lobed, while upper leaves are narrower and lance- shaped. Sesame flowers are tubular, bisexual, and zygomorphic (bilaterally symmetrical), usually borne singly or in pairs in the axils of the upper leaves. They are typically white, pink, or pale purple in color and open early in the morning, lasting only one day. Although sesame is mostly self-pollinated, insect activity may cause some cross-pollination.
The fruit is a dehiscent capsule, 2-5 cm long, which splits open at maturity to release numerous small, flat seeds. These seeds vary in color- from white, yellow, brown, red, to black- depending on the genotype and are the main economic product of the plant.
Sesame has a relatively short growth cycle ranging from 75 to 120 days, depending on the variety and environmental conditions. The growth stages include germination, vegetative development, flowering, pod formation, and maturation. Flowering generally begins 35-45 days after sowing and may continue over several weeks. Fertilization follows pollination and seed capsules mature within another 30-40 days. A significant challenge in sesame cultivation is seed shattering, which leads to losses during harvest, especially if harvesting is delayed beyond the point of physiological maturity.
Sesame is well-adapted to hot, dry climates and performs best under temperatures of 25-35°C. It is highly sensitive to frost, waterlogging and heavy rainfall, particularly during flowering and seed development. Sesame grows optimally in well-drained, sandy loam soils with a neutral to slightly acidic pH (6.0-7.5), but it can tolerate relatively poor and marginal soils due to its hardy nature. Rainfall requirements are modest, typically between 500 to 650

mm, but the crop benefits from well- distributed moisture during the initial growth phase followed by dry conditions.

2. Materials and Methods.

In this study, 40 sesamum germplasm were used as a trial material. The statistical analysis utilized the averages of observations on a variety of features (besides days to 50% flowering and days to maturity) recorded for five competing plants per genotype in each replication, which were chosen at random. The seeds from the five observational plants for each genotype were combined and these seeds were used for protein and oil analysis. The oil and protein content was determined using NIR Spectrometer equipment at the College of Engineering and Technology, M. P. K.V., Rahuri, Aannasaheb Shinde.

According to Rao (1952) [19], the D2 Statistic of Mahalnobis (1936) [13] was used to analyse divergence. To determine the significance between the genotypes, analysis of variance for each of the various characters under study was calculated using RBD. Only the characters with notable changes were utilised for additional D2 analysis. Character pair covariance analysis was performed using plot averages (Cochran and Cox, 1957) [27]. The analysis of variance was carried out using the Panse and Sukhatmate (1995) [26] methodology. RBD was used to do the analysis of variance for each character under study in order to determine the relevance of the genotypes. Divergence was analysed using the D2 Statistic of Mahalnobis (1936) [13], as discussed by Rao (1952) [19], and clusters were created using Tocher's method, as explained by Rao (1952) [19]. We calculated the possible paternal divergence boundaries where heterosis was likely to occur, following Arunachalam and Bandopadhyaya (1984) [2]. The crucial condensation approach was used to transform. The first row of the reduced matrix was divided by the square root of the two identical pivotal condensation elements to determine the transformation's coefficients.

3. Results and Discussion

The analysis of variance for nine quantitative characters is given in Table 1. In the present study, analysis of variance revealed highly significant differences among the genotypes for all the characters except no. of primary branches and no. of capsule per plant indicating the presence of considerable variability among the genotypes for the characters studied. However, the difference due to replications were non-significant indicating that land selected for experiment was homogenous. Six clusters were formed from the forty genotypes (Table 4). Cluster I contained the most genotypes (20), followed by cluster III (10), cluster II (7), and cluster IV, V, and VI, which all had only one genotype. This shows how selection pressure increases the genetic diversity.

These clusters were therefore unique in terms of multivariate composition. The group constellation pattern demonstrated that there was a considerable degree of variation among the genotypes under study. The genotypes included in cluster IV may have a completely different genetic structure than those included in cluster V, as indicated by the highest inter-cluster distance (9.03) between cluster IV and V in the current study, which is shown in Table 2 and Fig. 1. This suggests that the genotypes in these clusters have a significant degree of genetic divergence. Manivannan and Ganesan (2000) [14], Solanki and Gupta (2002) [21], Narayanan and Murugan (2013) [16], and Mohammed and Firew (2015) [15] have all observed similar findings. Followed by cluster III and V (D^2 = 8.05), cluster III and IV (D^2 = 7.84), II and V (D^2 = 7.79), cluster V and VI (D^2 = 7.75). This showed that, these genotypes having the maximum genetical variation.

The lowest genetic divergence (D^2 = 5.50) was recorded between clusters I and II, indicating a close genotypic similarity among the genotypes in these groups. Conversely, the highest level of intra-cluster divergence was observed in cluster III (D^2 = 5.07), followed by cluster II (D^2 = 4.66), suggesting considerable genetic variability within these clusters. Such diversity highlights their potential value as parental lines in hybridization efforts. Based on the cluster means for nine evaluated traits (Table 3), cluster VI showed the highest average seed yield per plant (10.58 g), while cluster II, consisting of seven genotypes, had the lowest yield, averaging 4.21 g per plant.

Table 2 presents the average inter- and intra-cluster genetic divergences. The inter-cluster D^2 values ranged from 5.50 to 9.03, with the greatest divergence observed between clusters IV and V (D^2 = 9.03). This was followed by divergence between clusters III and V (D^2 = 8.05), III and IV (D^2 = 7.84), II and V (D^2 = 7.79), and V and VI (D^2 = 7.75). In contrast, the lowest inter-cluster divergence was recorded between clusters I and II (D^2 = 5.50), followed by I and III (D^2 = 5.52), II and IV (D^2 = 5.79), and IV and VI (D^2 = 5.97). In terms of intra-cluster divergence, values ranged from 0.00 to 5.07. The highest intra-cluster divergence was found within cluster III (D^2 = 5.07), followed by cluster II (D^2 = 4.66). Clusters IV, V, and VI exhibited no intra-cluster divergence, indicating that these clusters were composed of genetically identical (monogenetic) genotypes.

The variability among cluster means offers insights into the relative significance of individual traits in contributing to genetic divergence. As shown in Table 5, oil content emerged as the most influential trait, accounting for 35.90% of the total divergence. This was followed by 1000-seed weight (21.03%), days to 50% flowering (11.92%), days to maturity (8.08%), protein content (6.54%), plant height (6.03%), seed yield per plant (5.90%), number of primary branches (2.31%), and number of capsules per plant (2.31%). Previous studies have also highlighted similar trends: Sudhakar (2003) [22] reported significant contributions from days to 50% flowering and number of capsules per plant; Gangadharao (2004) [8] identified key roles for number of capsules per plant, 1000-seed weight, and seed yield; Parameshwarappa *et al.* (2010) [17] emphasized the importance of 1000-seed weight, number of capsules per plant, and seed yield; Narayanan and Murugan (2013) [16] highlighted seed yield per plant, number of capsules, and days to 50% flowering; while Chandra (2014) and Mohammed and Firew (2015) [15] also underscored the significance of seed yield and 1000-seed weight. Keeping in the view all the above aspects, the following genotypes in the present investigation, deserve to be considered as potent parent for future crossing programme for improvement of seed yield and yield contributing characters.

1	TKG-377	6 RT-377
2	NIC-790	7 TLT-09
3	G-23-2 (W)	8 SI-772
4	JLSG-1659	9 JL-SEL-07-23
5	TNAU-64-3	

Based on inter-cluster genetic divergence, cluster means, individual genotype performance, and divergence classification, the identified genotypes hold strong potential for use in future breeding programs. Their selection could contribute to the generation of a broad range of variability for key yield-contributing traits. This, in turn, would facilitate the development of superior genotypes that combine multiple desirable characteristics and allow for the simultaneous improvement of more than one trait.

Table 1: Analysis of variance for different characters in sesame.

Sr. No.	Characters	Replications	Mean sum of square Genotypes	Error
1	Days to 50% flowering	51.2	4.9179**	0.6102
2	Days to maturity	72.2	14.8961*	2.6358
3	Plant height	0.001	59.4891*	13.1466
4	Number of branches /	0.4205	0.4281	0.1712
5	Number of capsules /	0.9702	62.5561	34.6887
6	1000 seed weight	0.0594	0.4834**	0.0501
7	Seed yield / plant	3.8465	3.7621	0.9656
8	Oil content	1.7552	15.7365**	1.0720
8	Protein content	0.2030	5.9381*	1.1345

*, ** Indicates significance at 5% and 1% level, respectively

Table 2: Average intra and inter-cluster distance (D2) value for nine characters in sesame

Cluster	I	II	III	IV	V	VI
I	4.21	5.5	5.52	6.81	6.51	6.09
II		4.66	7.31	5.79	7.79	6.24
III			5.07	7.84	8.05	7.05
IV				0	9.03	5.97
V					0	7.75
VI						0

Table 3: Cluster mean of forty sesame genotypes

Sr. No.	Characters	Days to 50% flowering	Days to maturity	Plant height	No. of primary branches/ plant	No. of seeds/ capsule	1000 Seed wt.	Seed yield/ plant	Oil content (%)	Protein content (%)
1.	I	39.88	89.58	61.17	1.78	27.54	4.05	4.54	48.82	21.25
2.	II	39.29	86.36	57.34	2.17	29.77	3.94	4.21	52.03	21.86
3.	III	42.2	89.85	63.53	1.94	32.18	3.57	4.83	47.75	21.65
4.	IV	37.5	85	59.8	1.9	32.5	2.65	4.62	53.49	19.47
5.	V	37.5	86	61	3	38.2	4.16	5.41	42.76	19.4
6.	VI	38.5	85.5	64.9	1.9	33.2	3.5	10.58	50.22	23.58

Table 4: Grouping of forty genotypes in different clusters.

Sr. No.	Cluster	No. of genotype	Name of genotypes
1.	I	20	RT-54, IC-20396, SI-1147, KMS-5-373, EC-370540, RT-377, RMT-496, JCS-1860, IC-413248, VRI (SV2), JR-22, NIC-7913, G-1-2, TLF-13-1, RMT-504, SI- 2123, KMR-24, EC-231-2-84, PKVNT-11, KT-183
2.	II	7	TLT-09, JL.SEL.07-09, JLT-510, JMLS-07-23, JLS-414-7, IC-41329, GS-10
3.	III	10	G-13-3 (W), TNAU-64-3, DS-19, MT-210-23-3, SI-3315-5, KMR-13, RSS-106, G-23-2 (W), SI-772, KMR-77-1
4.	IV	1	JLSG-1659
5.	V	1	NIC-790
6.	VI	1	TKG-377

Table 5: Relative per cent contribution of different characters towards total genetic divergence in sesamum.

Sr. No.	Characters	Times ranked 1st	% contribution
1	Days to 50% flowering	93	11.92%
2	Days to maturity	63	8.085%
3	Plant height (cm)	47	6.03%
4	Number of branches per plant	18	2.31%
5	Number of capsules per plant	18	2.31%
6	1000 seed weight (g)	164	21.03%
7	Seed yield per plant (g)	46	5.90%
8	Oil content (%)	280	35.90%
9	Protein content (%)	51	6.54%
	Total	780	100%

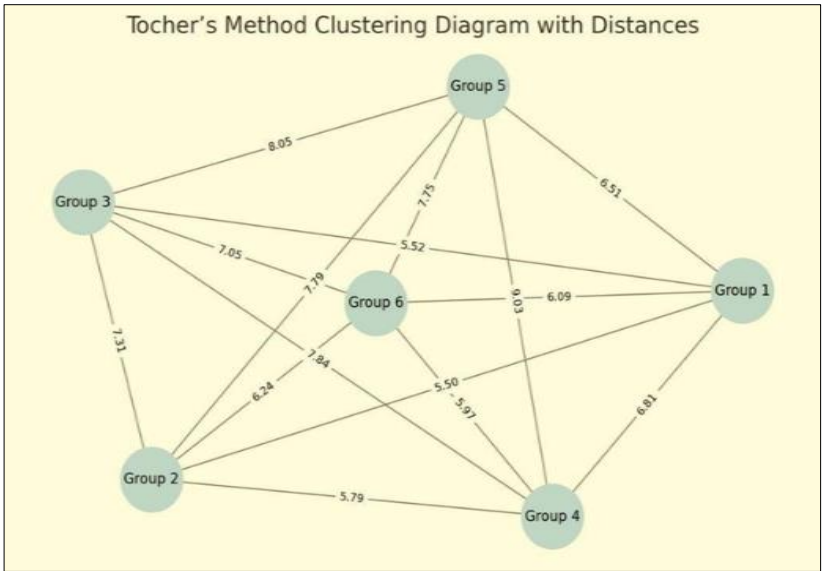

Fig 1: Cluster diagram of forty Sesame Genotype

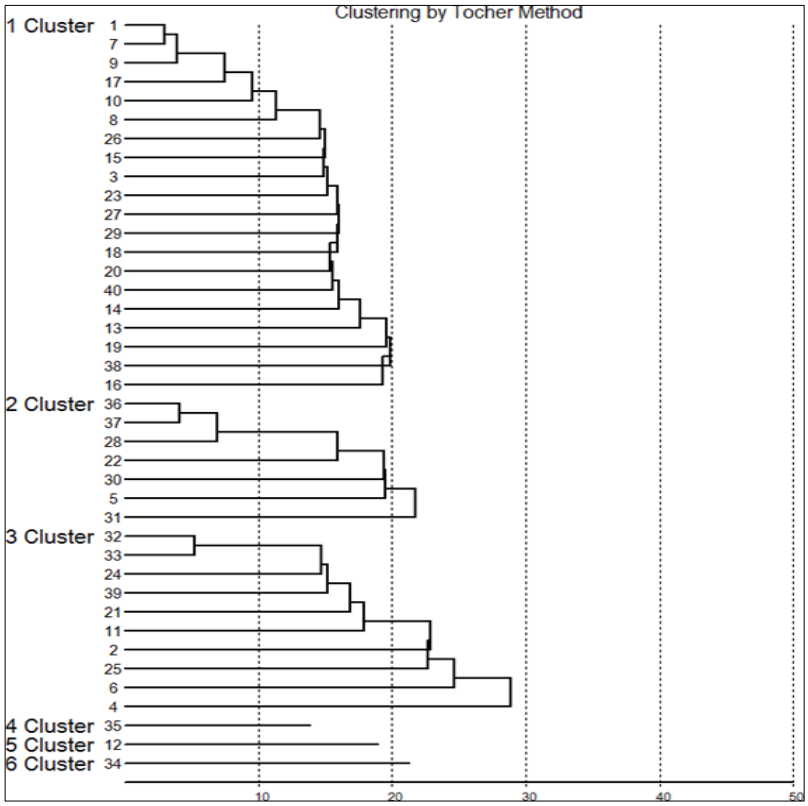

Fig 2: Cluster formation of Sesame genotype by Tocher method

Table 6: Tentative suggested crossing programme in future

	Characters to be improved	Cluster combination with inter- cluster distance	Genotypes possible	Crosses
1	50% flowering, days to maturity (Earliness)	IV x V = 9.03	JLSG-1659, NIC-790	JLSG-1659 x NIC- 790
2	Plant height (tall)	I x III = 5.52	RT-54, TNAU-64- 3	RT-54 x TNAU-64-3
3	Number of primary branches (maximum)	II x III = 7.31	TLT-09, TNAU- 64-3	TLT-09 x TNAU- 64-3
4	Number of capsules per plant (maximum)	V x VI = 7.75	NIC-790, TKG- 377	NIC-790 x TKG-377
5	1000 seed weight (g)	I x V = 6.51	RT-54, NIC-790,	RT-54 x NIC- 790
	(maximum)		TLT-09	RT-54 x TLT-09
6	Oil content (%) (maximum)	IV x VI = 5.97	JLSG-1659, TKG- 377	JLSG-1659 x TKG- 377
7	Protein content (%) (maximum)	II x III = 12.73	TLT-09, DS-19	DS-19 x TLT-09 DS-19 x JL-SEL-07-23
8	Seed yield per plant (g)	V x VI =7.75 III x VI = 7.05	NIC-790, TKG- 377, SI-772	NIC-790 x TKG- 377 SI-772 x
	(maximum)			TKG-377

4. Summary and Conclusion

Analysis of variance revealed significant differences among genotypes for all studied traits. Based on D^2 statistics, the genotypes were grouped into six distinct clusters, indicating a considerable level of genetic diversity within the sesame germplasm. Cluster I was the largest, comprising 20 genotypes, followed by cluster III with 10 genotypes and cluster II with 7. In contrast, clusters IV, V, and VI were each represented by a single, distinct genotype, highlighting their uniqueness within the collection.

Clusters I and II exhibited the smallest genetic divergence (D^2 = 5.5), while the greatest inter-cluster distance was observed between clusters IV and V (D^2 = 9.03). Among the clusters, cluster III showed the highest intra-cluster divergence (D^2 = 5.07). Cluster VI recorded the highest average seed yield per plant, measuring 10.58 g. In this study, the genotype JLSG-1659 stood out for its earliness, showing superior performance in days to 50% flowering and days to maturity, based on inter-cluster divergence, cluster means, and individual performance. The genotype TKG-377 excelled in plant height, protein content, and seed yield per plant. NIC-790 was notable for its higher 1000-seed weight, number of primary branches, and number of capsules per plant. At maturity, genotype TNAU-64-3 was identified as the tallest. Hybridization among these genotypes is likely to generate heterotic combinations, facilitating the development of improved sesame varieties.

Disclaimer (Artificial Intelligence)

The author(s) hereby declare that no generative AI technologies, including but not limited to Large Language Models (e.g., ChatGPT, GitHub Copilot) or text-to-image generation tools, were used in the writing, editing, or preparation of this manuscript

Acknowledgement

The authors express their sincere gratitude to the Department of Agricultural Botany, College of Agriculture, Dhule, for providing the necessary facilities and support to conduct this research. All authors contributed equally to the work.

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