



Genetic divergence for yield and quality traits in sesame: Implications for parental selection

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Abstract

Genetic diversity among parental genotypes is a key determinant of success in any crop improvement programme. In the present study, hierarchical cluster analysis was employed to assess genetic divergence among 104 sesame (*Sesamum indicum* L.) genotypes based on yield and yield attributing traits. The genotypes were grouped into nine distinct clusters, irrespective of their geographical origin, indicating the absence of association between genetic divergence and geographical distribution. The maximum inter-cluster distance (6.46) was observed between clusters V and VI, followed by 6.37 (IV–V), 6.09 (II–IX), 5.65 (II–VIII), and 5.22 (II–VII), indicating substantial genetic diversity among these clusters. Cluster IX recorded the highest mean seed yield per plant (15.41 g), whereas Cluster V exhibited the highest oil content (49.44 %). Based on the large inter-cluster distances, crosses involving parents from highly divergent clusters, particularly V × VI, IV × V, II × IX, II × VIII, and II × VII, are expected to generate superior recombinants and transgressive segregants for yield, earliness, and oil-related traits. The progenies derived from these crosses may be effectively utilized in future breeding programmes for the development of high-yielding, nutritionally rich, and climate-resilient sesame varieties.

Keywords: Sesame, Genetic divergence, Hierarchical Cluster analysis Parental selection, Yield components, breeding

Sesame (*Sesamum indicum* L., $2n = 26$), a key member of the Pedaliaceae family, is one of the earliest domesticated oilseed crops and is renowned for its adaptability to stressful, low-input environments. Often described as the “queen of oilseeds,” sesame contains 40–63 % high-quality oil and is enriched with proteins, vitamins, minerals, and natural antioxidants such as sesamin, sesamol, and γ -tocopherol, which impart exceptional oxidative stability (Were *et al.*, 2006). Its consumption is associated with several health-promoting effects, including reduced blood pressure, decreased cholesterol levels, and lower cancer risk. Oil content in sesame is highest compared to other oil seed crops like groundnut, soybean, mustard and it has the important properties like pleasant flavor, resistance to oxidative deterioration and high unsaturated fatty acid content and can be used as active ingredient in antiseptics, bactericides, viricides and disinfectants etc. (Manasa *et al.*, 2023).

Despite its economic and nutritional importance, sesame productivity remains low in many countries including India. Globally, it is cultivated on 128.36 lakh ha with a production of 67.41 lakh tonnes and an average productivity of 525 kg ha⁻¹. India contributes 46.5 % of the global sesame acreage and ranks second in production after China. However, its average productivity (432 kg ha⁻¹) is substantially lower than that of China (1382 kg ha⁻¹) (Manasa *et al.*, 2025). In Andhra Pradesh, sesame is grown on 0.23 lakh ha and yields remain suboptimal at 287 kg ha⁻¹ (Indiastat, 2023–24), highlighting the urgent need for genetic improvement. A critical requirement for accelerating genetic gain in

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sesame breeding is a comprehensive understanding of the available genetic diversity (Ramprasad *et al.*, 2019). Sesame, being predominantly self-pollinated, exhibits a relatively narrow genetic base in cultivated germplasm, which restricts progress in improving yield and resilience traits. Genetic diversity studies enable the identification of genetically divergent parents that are more likely to produce heterotic or transgressive segregants, thereby enhancing the efficiency of recombination breeding (Bhatt, 1973). It provides insights into evolutionary

relationships, genetic differentiation and breeding potential of germplasm collections. Diversity not only brings about genetic variation but also brings new recombination of genes in gene pool. Moreover, assessing genetic divergence facilitates the strategic utilization of landraces, indigenous accessions, and wild relatives that harbour unique alleles for biotic and abiotic stress tolerance traits of increasing relevance under climate variability (Wei *et al.*, 2015; Pathak *et al.*, 2021).

Multivariate statistical approaches, particularly hierarchical Euclidean cluster analysis based on Ward's method (Ward, 1963), provide a robust framework for quantifying genetic divergence across multiple traits simultaneously. Such analyses are instrumental in detecting redundancy within germplasm collections, optimizing the composition of core and mini-core sets, and identifying diverse parental groups for designing high-efficiency crossing blocks. Consequently, genetic diversity studies represent a foundational step for broadening the genetic base, sustaining long-term genetic improvement, and developing high-yielding, nutritionally superior, and climate-resilient sesame varieties.

The study was conducted during *rabi* 2023–24 using 100 sesame genotypes along with four check varieties obtained from the Regional Agricultural Research Station, Tirupati, Andhra Pradesh. The experiment was laid out in an unreplicated Augmented Block Design (ABD) (Federer, 1961). Each genotype was sown in two rows of 4 m row at a spacing of 30 cm × 15 cm, while checks were repeated across blocks for adjustment of block effects. All recommended agronomic practices were followed throughout the cropping season.

Data were recorded from five randomly selected plants on key twelve yield and yield-attributing traits, including

days to 50% flowering, days to maturity, plant height, number of primary branches, number of secondary branches, plant height to first capsule, number of capsules per plant, number of seeds per capsules, capsule length, 1000 seed weight, seed yield per plant and seed oil content. Adjusted means were generated using Augmented Block Design procedures. Hierarchical cluster analysis was performed using standardized trait values, with Euclidean distance as the dissimilarity measure. Clustering was carried out using Ward's minimum variance method (Ward.D2) in R software. The resulting dendrogram grouped the 104 sesame genotypes into nine distinct clusters. Inter- and intra-cluster distances and cluster mean values were used to quantify genetic divergence and identify diverse parental combinations. All statistical analyses were carried out using R and SPSS software.

Cluster analysis

The diversity analysis grouped the 104 genotypes into nine distinct clusters, reflecting considerable genetic variation among the materials studied (**Table 1 & Fig.1**). Among the clusters, cluster VI was the largest, containing 19 genotypes, followed by cluster IX (17 genotypes), cluster IV (16 genotypes), cluster II (13 genotypes), cluster V (11 genotypes), cluster VII (9 genotypes), cluster I (8 genotypes), cluster VIII (6 genotypes), and cluster III (5 genotypes). A similar result was also observed in sesame by Bharathi *et al.* (2023) and Manasa *et al.* (2025) to identify the potential parents in the hybridization programme. Their findings revealed that the genotypes were distributed into distinct clusters showing the presence of measurable genetic divergence within the evaluated germplasm, independent of geographical origin, underscoring the potential of these clusters to serve as sources of elite, genetically diverse parental lines for future breeding programmes.

Table 1. Cluster composition of 104 sesamum genotypes using hierarchical cluster analysis method

Cluster number	Number of genotypes	Name of the genotypes
I	8	VZM-2, GT-10, IC-205036, YLM-66, MT-107, VZM-3, VZM-4, TKG-501
II	13	IC-376996, IC-204830, IC-205219, VS-16-009, SKL-8, IC-205381, YLM-146, YLM-11, YLM-17, Madhavi, IIOS-3101, SKL-2, IC-204682
III	5	IC-557273, RMT-253, IC-205228, IC-205470, RT-46
IV	16	IC-205258, VSP-16, SKL-6, PT-10, RMT-204, IC-205284, RT-69, IC-205283, IC-205317, MT-11-1-13, JCS-DT-26, SKL-3, IC-205318, IC-397379, SKL-5, IC-567285
V	11	VSP-1, IC-205077, IC-205201, IC-204411, EC-376997, SI-17, RT-183, SI-199-2-84, IC-205499, IC-204383, IC-205391
VI	19	RMT-176, IC-413229, SI-772, RT-176, RMT-187, IC-205591, RT-68, RMT-132, IC-205402, RT-311, RT-204, IC-205372, SKL-4, IC-413247, IC-204528, RMT-202, RT-289, RMT-130, IC-2557251
VII	9	IC-205383, RMT-236, Gouri, IIOS-1102, IC-557252, RT -54, IC-205027, Chandana, IC-205188
VIII	6	LT-210, IC-326984, DS-18-46, RMT-175, IC-326777, IC-204667
IX	17	IC-204400, IC-204402, IC-205321, IC-376984, Rajeshwari, JCS-1020, IC-204503, IC-204647, IC-204725, TKG-22(C2), JTS-8, IC-205354, IC-205362, VSP-2, IC-557271, JCS RF 4, IC-205091

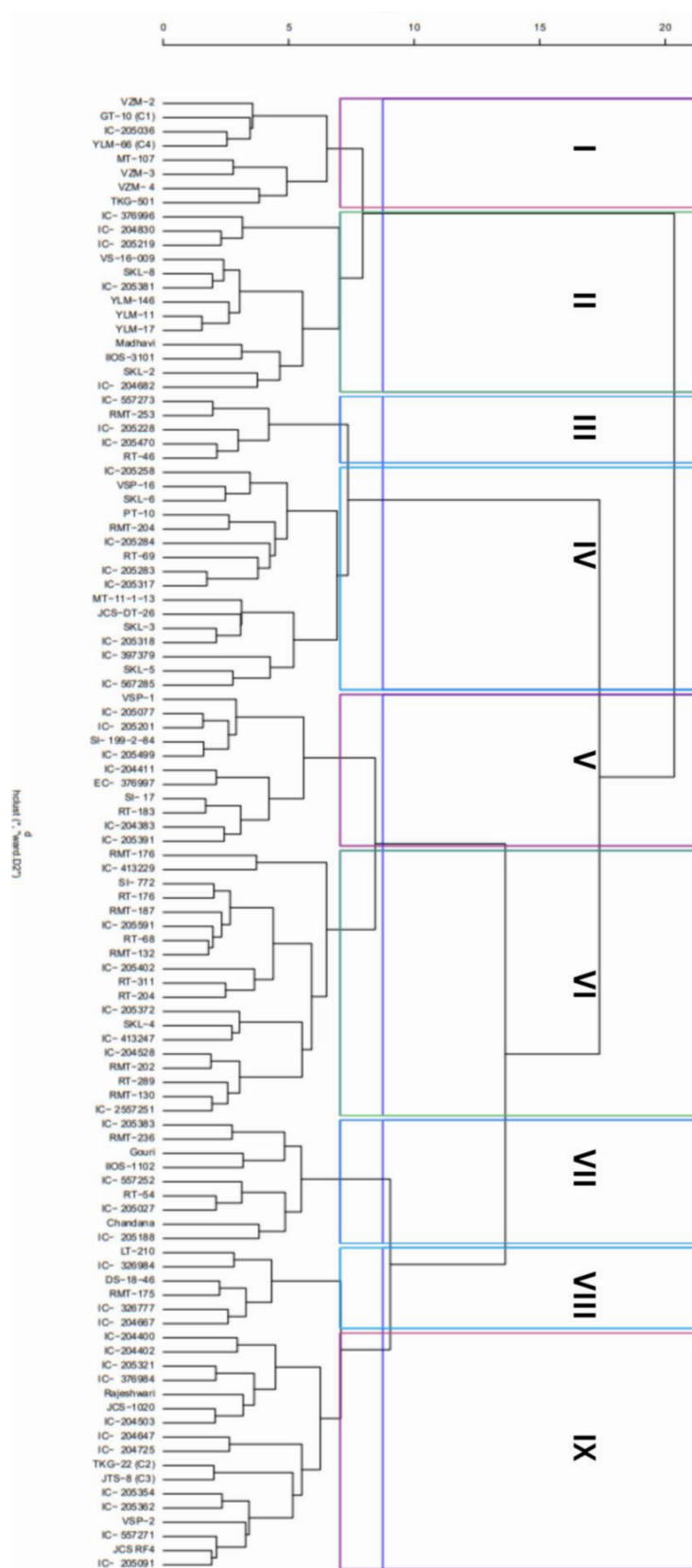


Fig. 1. Hierarchical cluster dendrogram of 104 sesame genotypes generated using Ward.D2 clustering based on euclidean distance

Intra and inter cluster euclidean distances

Inter- and intra-cluster Euclidean distances provide important metrics for understanding the magnitude of genetic divergence and the results are represented in **Table 2**. In this study, inter-cluster distances were consistently higher than intra-cluster distances, confirming the presence of meaningful differentiation among the clusters.

The highest inter-cluster distance was recorded between Cluster V and Cluster VI (6.46), followed by Cluster IV and Cluster V (6.37), Cluster II and Cluster IX (6.09), and Cluster II and Cluster V (5.95). These large distances indicate that genotypes belonging to these cluster pairs are genetically most dissimilar and therefore offer the greatest potential for producing heterotic or transgressive segregants in hybridization programmes (Singh and Chaudhary, 1981). In contrast, the lowest inter cluster distances observed between Cluster IV and VI (3.83), Cluster VII and IX (3.90), Cluster IV and Cluster VII (4.10), and Cluster VI and Cluster VII (4.13) indicate close genetic relationships among the genotypes in these groups. Such clusters may be less valuable for generating broad variability but may serve as useful sources for stabilizing specific traits.

Intra cluster distances further confirmed variability patterns. Cluster III exhibited the lowest intra-cluster distance (2.92), reflecting homogeneity among its genotypes, while Cluster V recorded the highest (4.07), indicating considerable internal variability. These findings align with previous reports of substantial inter-cluster divergence and variable intra-cluster heterogeneity in sesame (Kumhar *et al.*, 2013; Bharathi *et al.*, 2023 and Habite and Sendekie, 2023; Jadhav and Mohrir, 2013).

Cluster mean performance for quantitative traits

The cluster mean values for twelve quantitative traits are presented in **Table 3**, revealing substantial variation among the nine clusters and highlighting the polygenic nature of yield and its component traits in sesame. Considerable differences among clusters indicate the presence of exploitable genetic diversity for simultaneous improvement of multiple traits.

Clusters V (33.25 days) and IX (33.44 days) recorded the lowest mean values for days to 50% flowering, followed by Clusters VII (34.38 days) and VIII (34.38 days), indicating their suitability as sources of earliness. The earliest maturity was observed in Cluster IV (80.86 days), followed by Cluster I (81.07 days) and Cluster VI (81.85 days). Plant height ranged from 73.26 cm in Cluster I to 96.78 cm in Cluster II, providing opportunities for selection according to breeding objectives such as lodging resistance or plant architecture.

Cluster III recorded the highest number of primary (5.99) and secondary (5.16) branches per plant, followed by Cluster II (5.14 and 3.06, respectively). The highest number of capsules per plant was observed in Cluster III (128.02), followed by Cluster IX (104.52), Cluster VIII (96.68) and Cluster II (90.75). Cluster V recorded the highest number of seeds per capsule (87.62) along with a relatively longer capsule length (2.63 cm), whereas the maximum capsule length was recorded in Cluster VII (2.70 cm).

Higher thousand-seed weight was recorded in Cluster V (3.82 g), followed by Cluster VI (3.73 g), Cluster IX (3.50 g), Cluster VII (3.40 g) and Cluster II (3.33 g). Oil content varied from 40.26 % in Cluster IV to 49.44 % in Cluster V, while Clusters VI (47.79 %), VII (47.23 %), VIII (46.41 %), I (46.14 %) and IX (45.87 %) also recorded values above the general mean (45.75%). The highest seed yield per plant was recorded in Cluster IX (15.41 g), followed by Cluster III (12.44 g), Cluster II (12.41 g), Cluster VIII (10.56 g) and Cluster VII (10.25 g), indicating their potential utility in yield improvement programmes.

Based on inter-cluster distances and cluster mean performance, the genotypes IC-397379 (Cluster IV), IC-204411 and EC-376997 (Cluster V), RT-289 (Cluster VI), IC-204830, IIOS-3101, SKL-2, IC-205219, IC-204682 (Cluster II), and IC-376984 (Cluster IX) were identified as promising parents for hybridization to develop high-yielding, early-maturing sesame varieties with enhanced oil content. Crosses involving parents from highly divergent clusters, particularly V × VI, IV × V, and II ×

Table 2. Intra and inter cluster distances among 104 sesame genotypes

Clusters	C1	C2	C3	C4	C5	C6	C7	C8	C9
C1	3.63	5.6	5.23	5.44	4.46	5.65	4.43	4.49	4.81
C2		3.82	4.15	4.82	5.95	4.21	5.22	5.65	6.09
C3			2.92	4.56	5.94	4.13	4.89	4.67	5.51
C4				3.42	6.37	3.83	4.1	4.95	4.3
C5					4.07	6.46	5.48	5.4	5.68
C6						2.95	4.13	4.98	4.94
C7							3.48	4.38	3.9
C8								3.87	4.39
C9									3.09

Table 3. Cluster mean value for 12 traits among 104 sesame genotypes

Cluster	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Plant height to first capsule (cm)	Number of capsules per plant	Number of seeds per capsule	Capsule length (cm)	Thousand seed weight (g)	Oil content (%)	Seed yield per plant (g)
I	34.71	81.07	73.26	4.08	0.80	21.85	54.47	68.86	2.44	3.00	46.14	6.35
II	36.41	88.00	96.78	5.14	3.06	32.10	90.75	70.39	2.48	3.33	45.42	12.41
III	35.95	83.30	95.17	5.99	5.16	28.82	128.02	68.07	2.43	2.94	43.23	12.44
IV	34.86	80.86	86.71	4.19	1.64	25.68	70.20	66.68	2.28	3.13	40.26	7.03
V	33.25	82.50	88.75	3.95	0.30	23.11	54.85	87.62	2.63	3.82	49.44	7.35
VI	34.71	81.85	86.31	3.65	0.80	24.18	58.38	72.44	2.54	3.73	47.79	8.58
VII	34.38	86.23	95.42	4.16	1.30	28.30	70.98	75.04	2.70	3.40	47.23	10.25
VIII	34.38	84.49	91.46	3.72	1.57	22.09	96.68	75.31	2.45	3.04	46.41	10.56
IX	33.44	85.66	94.66	4.57	2.50	26.05	104.52	77.87	2.60	3.50	45.87	15.41
General mean	34.68	83.77	89.84	4.38	1.90	25.80	80.98	73.59	2.51	3.32	45.75	10.04

IX, are expected to generate superior recombinants and transgressive segregants for yield, earliness and oil content. These findings are in agreement with earlier reports emphasizing the importance of selecting genetically divergent parents for maximizing heterosis and broadening the genetic base in sesame (Bisht *et al.*, 1998; Pandey *et al.*, 2018; Durge *et al.*, 2022).

The integration of inter-cluster divergence with trait-specific mean performance proved effective in identifying genetically diverse and agronomically superior parents for sesame improvement. The substantial genetic variability observed among the clusters, along with the identification of highly divergent genotype pairs, provides a strong foundation for designing strategic hybridization programmes. Crosses involving parents from the divergent clusters V × VI, IV × V, and II × IX are expected to throw desirable recombinants and transgressive segregants for key traits such as earliness, seed yield, and oil content. Future breeding efforts should prioritize the utilization of these genetically diverse gene pools to broaden the crop's genetic base and develop early-maturing, high-yielding, and nutritionally enhanced sesame cultivars. Such an approach will contribute to strengthening the adaptability, resilience and overall productivity of sesame under diverse agro-climatic conditions.

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