



Genetic divergence studies for seed yield and its component traits in sesame (*Sesamum indicum* L.)

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Abstract

A field experiment comprising 45 sesame (*Sesamum indicum* L.) genotypes, including two checks (YLM-146 and TKG-22), was conducted during *rabi* 2025-26 at the dryland farm of Sri Venkateswara Agricultural College, Tirupati, Acharya N.G. Ranga Agricultural University, in a randomized block design with three replications. Genetic divergence among the genotypes was assessed for 14 seed yield and yield-attributing characters using Mahalanobis's D² statistic. Seed yield per plant (17.9%) contributed the maximum towards total divergence, followed by number of secondary branches per plant (17.1%), days to 50% flowering (13.2%) and 1000-seed weight (10.9%). Applying Tocher's method, the 45 genotypes were grouped into six non-overlapping clusters. Cluster I was the largest, comprising 28 genotypes, followed by cluster II with eight, cluster III with four and clusters IV and V with two genotypes each, while cluster VI, represented by the single genotype JCS-3993, indicated its distinct genetic constitution. The maximum inter-cluster distance was recorded between cluster III and cluster V (2803.64), followed by cluster V and cluster VI (2018.30) and cluster I and cluster V (1594.03), whereas the minimum inter-cluster distance occurred between cluster II and cluster IV (405.02). Cluster V recorded the highest mean values for number of capsules per plant and harvest index, while cluster II recorded the highest mean for seed yield per plant. As no single cluster combined all the desirable attributes, hybridization between genotypes drawn from the widely divergent clusters III, V, VI and I is suggested to generate superior transgressive segregants and to broaden the genetic base of cultivated sesame.

Keywords: Sesame, genetic divergence, Mahalanobis D², Tocher's method, cluster analysis, seed yield

Introduction

Sesame (*Sesamum indicum* L.), often referred to as the 'queen of oilseeds', is among the oldest domesticated oilseed crops and is prized for its exceptionally high oil content, which can reach up to 63%, along with a rich protein content and favourable fatty acid profile. Its seeds also contain unique lignans, namely sesamin, sesamol and sesamol, which confer strong antioxidant properties and are associated with cholesterol-lowering and antihypertensive effects (Majdalawieh and Mansour, 2019) [11]. Owing to these nutritional and industrial qualities, sesame oil finds wide application in the food, cosmetic and pharmaceutical sectors. Sesame is widely grown across Asia and Africa, with Asia harbouring greater diversity among cultivated forms and Africa among wild relatives (Kurdistani and Tohidinejad, 2011) [9].

In India, sesame is cultivated largely under rainfed and dryland conditions. During 2024 [7]-25, the crop occupied an area of about 1,576 thousand hectares with a production of 893 thousand tonnes and an average productivity of 567 kg ha⁻¹, with Uttar Pradesh, Madhya Pradesh, West Bengal, Rajasthan and Gujarat accounting for the major share of area, while West Bengal, Madhya Pradesh and Gujarat led in production (Indiastat, 2024 [7]-25). Despite its wide adaptability and low input requirement, national productivity continues to lag behind the potential of the crop, largely on account of a narrow genetic base, poor

harvest index and the limited availability of high-yielding varieties suited to specific agro-climatic conditions (Teklu *et al.*, 2021) [18].

Sustainable improvement in seed yield requires the identification and utilization of genetically diverse parental lines in hybridization programmes, since the magnitude of genetic variability available for seed yield and its component traits directly determines the scope for breeding progress (Kadvani *et al.*, 2020) [5]. Among the several biometrical tools available for quantifying genetic divergence, the Mahalanobis D² statistic has proved to be one of the most reliable, as it permits simultaneous consideration of multiple characters and enables grouping of genotypes into distinct, non-overlapping clusters through Tocher's method, and has long been recognized as an important tool in sesame breeding (Ashri, 1998) [1]. Genotypes drawn from widely divergent clusters, when hybridized, offer a greater probability of generating heterotic combinations and transgressive segregants than crosses made between genotypes of similar genetic background or geographic origin. Several earlier workers have studied genetic diversity in sesame to identify divergent genotypes for use in improvement programmes (Begum *et al.*, 2011; Jadhav and Mohrir, 2013; Tripathi *et al.*, 2013) [2, 8].

With this background, the present investigation was undertaken to assess the extent and pattern of genetic divergence among 45 sesame genotypes for seed yield and

its component traits, to identify the characters contributing most to divergence and to suggest genetically diverse parental combinations that could be exploited in future sesame breeding programmes.

Materials and methods

The experimental material comprised 45 sesame genotypes, including two checks (YLM-146 and TKG-22), evaluated during rabi 2025-26 at the dryland farm of Sri Venkateswara Agricultural College, Tirupati, Acharya N.G. Ranga Agricultural University, Andhra Pradesh. The trial was laid out in a randomized block design with three replications and recommended agronomic practices were followed. Observations were recorded on five randomly selected plants per genotype in each replication for 12 quantitative characters, namely SPAD chlorophyll meter reading (SCMR), specific leaf area ($\text{cm}^2 \text{g}^{-1}$), plant height (cm), first capsule axis height (cm), number of primary branches per plant, number of secondary branches per plant, number of capsules per plant, capsule length (cm), 1000-seed weight (g), harvest index, oil content (%) and seed yield per plant (g), while days to 50% flowering and days to maturity were recorded on plot basis.

Mean data for the 14 characters were subjected to multivariate analysis following Mahalanobis's D^2 statistic (Mahalanobis, 1936) ^[10] to estimate the magnitude of genetic divergence among genotype pairs. The generalized distances were computed for all possible pairwise combinations of the 45 genotypes $[(45 \times 44)/2 = 990 \text{ pairs}]$ after transforming the mean values into standardized, uncorrelated variates through pivotal condensation. The genotypes were subsequently grouped into non-overlapping clusters following Tocher's method as described by Rao (1952) ^[15]. The relative contribution of each character towards total divergence was estimated based on the number of times a character was ranked first in pairwise comparisons.

Results and discussion

Analysis of variance revealed significant differences among the 45 genotypes for all 14 characters studied, confirming the presence of adequate variability in the experimental material and justifying its use for divergence analysis based on Mahalanobis's D^2 statistic.

Contribution of Characters towards Genetic Divergence

The per cent contribution of individual characters towards total genetic divergence is presented in Table 1 and Fig 1. Seed yield per plant (17.9%) contributed the maximum towards divergence, being ranked first in 177 of the 990 pairwise comparisons, followed closely by number of secondary branches per plant (17.1%, ranked first 169 times). Days to 50% flowering (13.2%) and 1000-seed weight (10.9%) also contributed appreciably to overall divergence, while number of capsules per plant (9.4%) and oil content (7.3%) made a moderate contribution. In contrast, number of primary branches per plant (0.1%) and capsule length (1.0%) contributed the least towards divergence, indicating a comparatively narrow range of variation for these two traits among the genotypes studied. These results suggest that seed yield, branching pattern, flowering duration and test weight should be given priority while choosing parents for hybridization aimed at broadening genetic variability in sesame.

Table 1: Per cent contribution of characters towards genetic divergence in sesame

S. No.	Character	Times ranked first	Per cent contribution
1	Days to 50% flowering	131	13.2
2	Days to maturity	64	6.5
3	SPAD chlorophyll meter reading (SCMR)	28	2.8
4	Specific leaf area ($\text{cm}^2 \text{g}^{-1}$)	21	2.1
5	Plant height (cm)	28	2.8
6	First capsule axis height (cm)	56	5.6
7	Number of primary branches per plant	1	0.1
8	Number of secondary branches per plant	169	17.1
9	Number of capsules per plant	93	9.4
10	Capsule length (cm)	10	1.0
11	1000 seed weight (g)	108	10.9
12	Harvest index	32	3.2
13	Oil content (%)	73	7.3
14	Seed yield per plant (g)	177	17.9

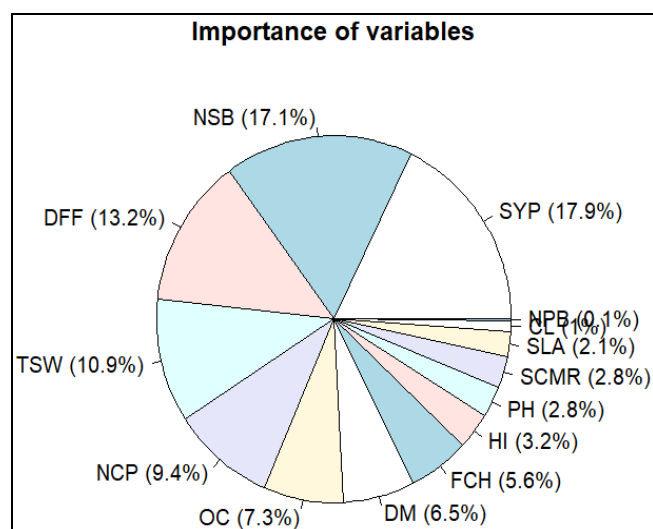


Fig 1: Pie chart representing the percentage distribution of genotypes according to characters.

DFF: Days to 50% flowering; **DM:** Days to maturity; **SCMR:** SPAD chlorophyll meter reading; **SLA:** Specific leaf area ($\text{cm}^2 \text{g}^{-1}$); **PH:** Plant height (cm); **FCH:** First capsule axis height (cm); **NPB:** Number of primary branches per plant; **NSB:** Number of secondary branches per plant; **NCP:** Number of capsules per plant; **CL:** Capsule length (cm); **TSW:** 1000-seed weight (g); **HI:** Harvest index; **OC:** Oil content (%); **SYP:** Seed yield per plant (g).

Clustering Pattern

Based on the D^2 values, the 45 sesame genotypes were grouped into six non-overlapping clusters using Tocher's method (Table 2). Cluster I was the largest, comprising 28 genotypes, indicating a comparatively narrow genetic base and close genetic relatedness among the majority of the test entries, which may be attributed to a common ancestry or similar selection history. Cluster II, with eight genotypes, formed the second-largest group, followed by cluster III with four genotypes and clusters IV and V with two genotypes each. Cluster VI, represented solely by the genotype JCS-3993, was monogenotypic, reflecting its unique genetic constitution and pronounced divergence

from all other genotypes evaluated. The distribution of genotypes across clusters did not correspond to their geographic or pedigree origin, corroborating earlier reports that genetic drift and differential selection pressure, rather than geographic distance, are the principal drivers of

divergence in self-pollinated crops such as sesame (Murty and Arunachalam, 1966) [12]. Similar clustering patterns, largely independent of geographical origin, have also been reported in sesame germplasm by Patil and Sheriff (1994), Hika *et al.* (2015) and Shwetha Yadav *et al.* (2022) [6, 14, 17].

Table 2: Clustering pattern of 45 sesame genotypes based on Tocher's method

Cluster No.	No. of genotypes	Genotypes
I	28	TPTS-18, YLM-171, TPTS-66, TPTS-152, VS-20-008, MT-2019-3, YLM-146(c), GT-10, JCS-3287, VS-20-001, JCS-4021, TPTS-95, VS-21-060, TPTS-80, DS-97, TPTS-45, EC-362447, TPTS-129, VS-21-008, TPTS-67, JCS-4024, VS-21-078, TPTS-69, CUS-101, TPTS-235, KMR-35, TPTS-83, NIC-16386
II	8	TKG-22(c), PCU-23-1, TPTS-64, IC-205595, RMT-677, KMR-42, RMT-586, JTS-8
III	4	TPTS-243, VS-19-036, RT-372, RMT-631
IV	2	TPTS-244, TPTS-144
V	2	TPTS-94, TPTS-128
VI	1	JCS-3993

Intra and Inter-Cluster Distances

The intra and inter-cluster distances among the six clusters are presented in Table 3 and Fig 2. Inter-cluster distances were consistently higher than intra-cluster distances, confirming greater divergence between clusters than within them. Among the intra-cluster distances, the maximum was recorded in cluster V (337.17), followed by cluster III (245.62) and cluster I (236.34), indicating the presence of some residual variability even within these groups, whereas cluster VI, being monogenotypic, recorded a nil intra-cluster distance.

The maximum inter-cluster distance was observed between cluster III and cluster V (2803.64), followed by cluster V and cluster VI (2018.30) and cluster I and cluster V

(1594.03), indicating that genotypes drawn from these cluster combinations are genetically the most divergent and would be expected to yield superior heterotic combinations and transgressive segregants on hybridization. Conversely, the minimum inter-cluster distance was recorded between cluster II and cluster IV (405.02), suggesting closer genetic affinity between the genotypes of these two clusters and consequently limited scope for their use as divergent parental combinations. Wide inter-cluster distances coupled with comparatively narrow intra-cluster distances, similar to those observed in the present study, have also been reported in other self-pollinated crops (Sheriff and Shivashankar, 1992) [16].

Table 3: Intra (diagonal) and inter-cluster average D^2 values of sesame genotypes (D values in parentheses)

Cluster	I	II	III	IV	V	VI
I	236.34 (15.37)	546.97 (23.39)	438.47 (20.94)	558.07 (23.62)	1594.03 (39.92)	520.93 (22.82)
II	-	202.33 (14.22)	1215.51 (34.86)	405.02 (20.12)	711.20 (26.67)	1019.89 (31.93)
III	-	-	245.62 (15.67)	1210.57 (34.79)	2803.64 (52.95)	592.90 (24.35)
IV	-	-	-	217.17 (14.74)	852.62 (29.20)	1232.43 (35.11)
V	-	-	-	-	337.17 (18.36)	2018.30 (44.92)
VI	-	-	-	-	-	0.00 (0.00)

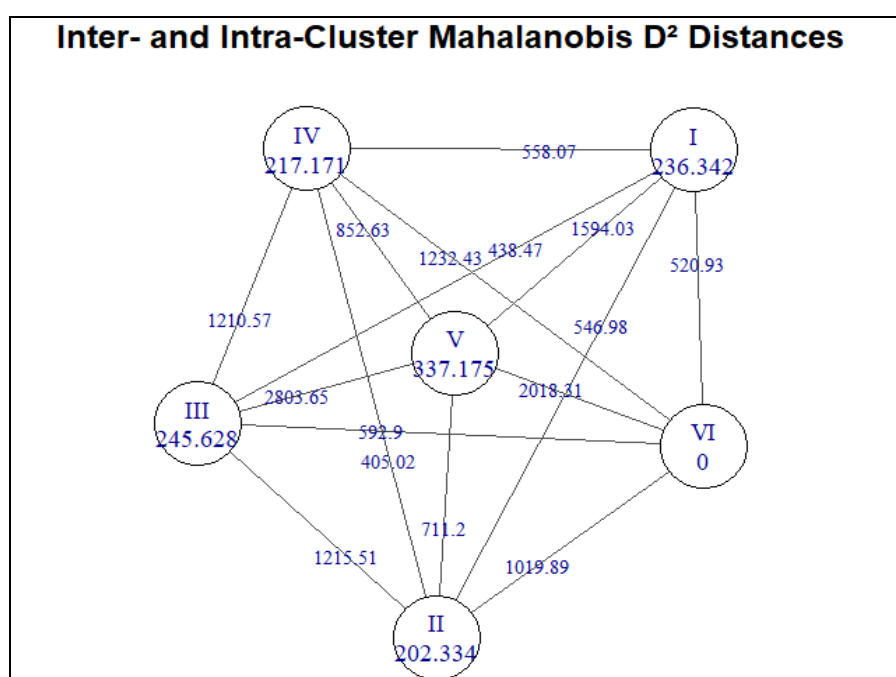


Fig 2: Intra (D^2) and Inter (D^2) cluster distances representation by Tocher's diagram

Cluster Means

The cluster mean values for the 14 characters studied are presented in Table 4 and reveal considerable differences among clusters. Cluster II recorded the highest mean for seed yield per plant (12.73 g), plant height (110.89 cm) and first capsule axis height (40.00 cm), whereas cluster V exhibited the highest mean for number of capsules per plant (150.15) and harvest index (40.19%).

Cluster III recorded the highest mean for 1000-seed weight (3.61 g) and oil content (52.04%). Cluster VI, on the other hand, recorded the lowest mean values for most yield-contributing traits, including number of capsules per plant (53.42), seed yield per plant (8.19 g) and oil content (41.52%), but was also the earliest to flower (35.33 days) and mature (75.00 days) and hence could be of value as an early-maturing donor parent.

Table 4: Cluster means for seed yield and yield component traits in sesame

Cluster	DFF	DM	SCMR	SLA	PH	FCH	NPB	NSB	NCP	CL	TSW	HI	OC	SYP
I	39.56	79.81	48.54	148.88	106.58	38.75	3.18	0.63	89.12	2.85	3.06	27.15	49.87	10.12
II	40.00	78.25	49.21	143.20	110.89	40.00	3.79	0.68	107.52	2.94	3.34	30.99	48.52	12.73
III	36.17	77.58	48.55	146.60	96.35	31.06	3.13	0.66	105.32	3.03	3.61	30.36	52.04	11.33
IV	39.17	78.33	48.18	131.58	84.73	29.47	3.60	0.56	75.37	2.76	3.38	29.78	43.86	9.26
V	36.67	75.67	49.42	130.16	94.83	33.37	3.87	0.67	150.15	2.88	3.06	40.19	47.81	11.73
VI	35.33	75.00	46.91	138.02	97.34	30.27	3.80	0.58	53.42	2.77	3.10	29.93	41.52	8.19
Mean	37.81	77.44	48.47	139.74	98.45	33.82	3.56	0.63	89.31	2.87	3.26	31.40	47.27	10.56

DFF: Days to 50% flowering; **DM:** Days to maturity; **SCMR:** SPAD chlorophyll meter reading; **SLA:** Specific leaf area ($\text{cm}^2 \text{g}^{-1}$); **PH:** Plant height (cm); **FCH:** First capsule axis height (cm); **NPB:** Number of primary branches per plant; **NSB:** Number of secondary branches per plant; **NCP:** Number of capsules per plant; **CL:** Capsule length (cm); **TSW:** 1000-seed weight (g); **HI:** Harvest index; **OC:** Oil content (%); **SYP:** Seed yield per plant (g).

The cluster means indicated that no single cluster combined all the economically desirable traits, which rules out the possibility of directly selecting an all-round superior cluster for release. Hybridization between the widely divergent clusters III and V, V and VI, and I and V is therefore recommended, as it would permit the combination of high seed yield and capsule number (cluster V), high test weight and oil content (cluster III), and earliness (cluster VI) into common recombinant progeny. Genotypes TPTS-94 and TPTS-128 of cluster V, despite modest per se performance, occupy a genetically distinct position and along with the divergent genotypes of clusters III (TPTS-243, VS-19-036, RT-372, RMT-631) and the monogenotypic cluster VI (JCS-3993), represent valuable donors for broadening the genetic base of sesame through planned hybridization. Considerable variation in cluster mean performance for yield and its component traits, and the effectiveness of exploiting maximally divergent clusters for parent selection, have similarly been documented in sesame germplasm collections (Parameshwarappa *et al.*, 2010).

Conclusion

The present study revealed considerable genetic divergence among 45 sesame genotypes evaluated for 14 seed yield and yield component traits. Seed yield per plant, number of secondary branches per plant, days to 50% flowering and 1000-seed weight were identified as the major contributors to genetic divergence and merit priority consideration while selecting parents in sesame improvement programmes. The genotypes were grouped into six clusters by Tocher's method, with cluster I being the largest and cluster VI (JCS-3993) remaining monogenotypic and distinctly divergent. Since no cluster possessed all the desirable trait combinations, hybridization between genotypes from the maximally divergent clusters, particularly III $\times$ V, V $\times$ VI and I $\times$ V, is recommended to obtain wider recombination

and superior transgressive segregants for future sesame breeding programmes.

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