

Original Research Article

<https://doi.org/10.20546/ijcmas.2026.1508.010>

Assessment of Distinctness, Uniformity and Stability (DUS) traits for Genetic Diversity in Sesame (*Sesamum indicum* L.)

S. Keerthana^{1*}, R. Dhanush², M. Dharanichselvan², M. Gokul², J. Hanesh²,
M. Harinadhan², S. Harish², V. Kalideeshwaran², K. Manikandan²,
K. Muthu Pandi² and V. K. Ohm Harini Vasam²

Imayam Institute of Agriculture & Technology, Thuraiyur, India

**Corresponding author*

ABSTRACT

Keywords

DUS traits, clustering, divergence, parental selection

Article Info

Received:

15 June 2026

Accepted:

20 July 2026

Available Online:

10 August 2026

The present study was undertaken to evaluate the Distinctness, Uniformity and Stability (DUS) characteristics and assess the genetic diversity of 20 sesame genotypes (*Sesamum indicum* L.), including one wild relative (*Sesamum alatum*). The experiment was conducted during kharif 2026 using a Randomized Block Design with three replications. Observation was recorded for five qualitative and seven quantitative traits. All the twenty genotypes were significant at 1% probability level except 1000 seed weight. Cluster analysis grouped the genotypes into four distinct clusters. Highest inter cluster distance was marked between the clusters I and II (99.8303). Therefore, the genotypes YLM 16 (Cluster II) and DS 5 (Cluster I) are recommended as parental materials for future sesame breeding programme to exploit maximum heterosis (hybrid vigour) and produce superior segregants in later generations

Introduction

The cultivation of sesame is a crucial component of worldwide agriculture, primarily occurring in tropical and subtropical areas. The worldwide market for sesame seeds is valued in the billions of dollars, with most exports directed towards China, Japan, South Korea, and the Middle East. India stands as a global leader in sesame production, allocating approximately 1.67 million hectares for its cultivation, resulting in an annual yield of around 7.47 lakh tonnes (Seay & Szczepanek *et al.*,

2024). Nevertheless, the national average productivity is comparatively low, at about 448 kg/ha, primarily due to dependence on rainfed agriculture, conventional broadcast sowing methods, and varieties that are prone to seed shattering (Madhu & Padmaja, 2025).

Sesame is the often-cross pollinating crop, the flowers are ideal (bisexual) and appear either individually or in small groups from the leaf axils (Pavani & Lal, 2020). The current study was undertaken to evaluate the DUS (distinctness, uniformity and stability) characters and

genetic diversity of sesame genotypes using standard DUS descriptors, identify distinct morphological characteristics, assess their uniformity and stability, and generate information useful for varietal identification, protection, conservation, and effective utilization of sesame genotypes in crop improvement programme.

Materials and Methods

Study details: The details of the genotypes along with their source and pedigree were recorded and maintained for further evaluation. The field experiment was conducted at the Departmental Farm of Imayam Institute of Agriculture and Technology, Thuraiyur during the year 2026 season of *Kharif*. The region is characterized by a semi-arid, tropical climate with an average annual rainfall of 626.4mm, and the soil of the field was Red Loamy soil in texture.

Genotype Details: The experiment included 20 treatments (T1-T20) and was laid out in three replications under field conditions. T1- TMV 7, T2- TMV 6, T3-TMV 5, T4- TMV 4, T5- TMV 3, T6- VRI 3, T7- VRI 4, T8-VRI 5, T9 -VRI (SV 1), T10 – VRI (SV 2), T11- CO 1, T12 – SVPR 1, T13 – YLM 16, T14 – YLM 17, T15 – DS 5, T16 – DSS 9, T17 – PYR 1, T18 – Kayamkulam 1, T19 – YLM 11, T20 – *Sesamum alatum*

Observation noted: Data were recorded for Qualitative traits for Petal colour, Stem hairiness, Growth Habit, Leaf lobe and Seed coat colour. Quantitative traits plant height (cm), Days to 50 percent flowering (days), No of capsules per plant, 1000 seed weight (gm), Single plant yield (gm), Oil content (%) and Protein content (%). Observations were recorded on prescribed DUS descriptors at different growth stages of the crop. The traits included qualitative, quantitative and diversity analysis characters. The sesame genotypes were evaluated based on the DUS (Distinctness, Uniformity and Stability) Test Guidelines prescribed by the Protection of Plant Varieties and Farmers' Rights Authority (PPV&FRA), Government of India.

Statistical Approach: In the present experiment, Randomized Block Design (RBD) was adopted, provided a simple and effective layout where treatments are assigned to experimental units entirely at random. For the statistical analysis of the data obtained under RBD, AGRISTAT software was employed. This software facilitates precise computation of various statistical parameters, analysis of variance (ANOVA) and

comparison of treatments means, Mahalanobis D^2 values thereby enabling accurate interpretation of the experimental result.

Result and Discussion

Analysis of variance: The mean square values of seven quantitative traits are mentioned in table 1. The Analysis of Variance (ANOVA) revealed varying mean square values across the evaluated quantitative traits. The calculated mean squares were 315.61 for plant height, 84.30 for days to 50 percent flowering, 14,740.58 for the number of capsules per plant, 0.53 for 1000-seed weight, 26.88 for single plant yield, 138.20 for oil content, and 6.91 for protein content. Among these traits, the number of capsules per plant exhibited the maximum square value (14,740.58), whereas the 1000-seed weight recorded the lowest (0.53).

The result of ANOVA revealed a significant treatment effect, indicating that the differences among the treatment means were not due to experimental error but rather to the actual influence of treatments. This suggested that at least one treatment meant differed significantly from the others. It is inferred that the treatments imposed in the experiment had a measurable and meaningful impact on the response variable (Teklu & Abbas, *et al.*, 2025). The result of ANOVA revealed a significant treatment effect, indicating that the differences among the treatment means were not due to experimental error but rather to the actual influence of treatments.

Mean performance of genotypes: The mean performance of genotypes evaluates for qualitative traits and quantitative traits were represented in table 1.

Qualitative traits: Among the 20 genotypes evaluated, variations were observed across five qualitative traits, which are detailed in Table 3. Petal color distribution included white with pink shading (10 genotypes), pure white (5), white with slight purple coloration (4), and dark purple or reddish pink (1). For stem hairiness, the genotypes were classified as absent (7), sparse (6), sparse-to-moderate (4), dense (2), or glabrous (1). Leaf lobe shapes varied from deeply lobed (8) to slightly lobed (3), trilobed (3), heart-shaped (1), non-lobed (1), and distinct lobed (1). The growth habit was predominantly erect with moderate branching (8) or branched erect (5), followed by bushy with profuse branching (2), profuse branching (2), mono-stem (1), and

top-branched (1). Finally, seed coat color was identified as brown (8), white (5), dark brown (3), reddish-brown (1), black (1), and light brown (1). The characterization of qualitative traits for twenty sesame genotypes is represented in table 2.

Quantitative traits: In respective of all traits, DUS character for 20 genotypes. the maximum value was recorded in T12 – SVPR 1 (127.28 cm) for plant height, Days to 50% flowering (T20-*Sesamum alatum* (46.13 days), number of capsule per plant (T20 - *Sesamum alatum* (366.50), 1000 seed weight (T2 – TMV 6 (3.84g)), single plant yield (T13- YLM 16 (14.27g)), oil content (T2 – TMV 6 (52.83%) and protein content (T16 – DSS 9 (27.50%). Least score for plant height (T8 – VRI 5 (86.57 cm)), Days to 50 % flowering(T12 – SVPR 1 (25.97 days)), number of capsules per plant (T16 – DSS 9 (38.57)), 1000 seed weight (T20 - *Sesamum alatum* (2.03g)), single plant yield (T1 – TMV 7 (6.30g)), protein content (T1 – TMV 7 (23.50%)), oil content (T1 – TMV 7(48.37 %)). The mean performance for quantitative traits was represented in table 3.

Apart from the genotypes, superior performance across all the seven DUS character traits in those, TMV 7 shows superiority in days to 50 percent flowering and TMV 6 in 1000 seed weight, DS 5 genotype in protein content and oil content and TMV 6 genotype in oil content. The assessment of DUS traits among the evaluated sesame genotypes revealed significant phenotypic diversity, which is essential for future crop improvement programs. The wild relative, *Sesamum alatum*, prioritized a high volume of reproductive structures, achieving the highest capsule density, while maintaining smaller seed weights. This behaviour reflects an evolutionary survival mechanism where extended vegetative phases allow for maximized photo-assimilate accumulation. Conversely, cultivated lines demonstrated the results of human selection, favouring superior seed weight and rapid flowering at the expense of total capsule numbers.

Diversity analysis

Cluster constellation: Dendrogram and tabulation was depicted (Figure 1 & Table 4) to show the genetic relationships and clustering pattern of 20 sesame genotypes grouped into four distinct clusters based on DUS traits, primarily driven by the evolutionary divergence between cultivated varieties and wild crop relatives. Cluster I emerged as the largest group,

containing 14 genotypes (TMV 7, TMV 6, TMV 5, TMV 4, TMV 3, VRI 3, VRI 5, VRI(SV1), VRI(SV2), CO1, SVPR 1, YLM 16, YLM 17, and DS 5). This high concentration of varieties suggests a narrow genetic base among mainstream cultivated lines, likely due to shared ancestry and parallel selection pressures during regional breeding programs. Cluster II (DSS9, PYR 1, Kayamkulam 1) and Cluster III (YLM 11, VRI 4) represent intermediate clusters with moderate genetic distances, indicating unique adaptive traits or distinct parentage that set them apart from the primary cultivated pool (Baydar, H. 2005). Grouping of twenty sesame genotypes is presented in table 4.

The most prominent finding is the isolation of *Sesamum alatum* as a single-genotype group in Cluster IV. This mono-cluster status underlines its profound genetic divergence from all other evaluated germplasm. As a wild relative, its unique genetic architecture prevents it from clustering with domesticated lines, making it an invaluable genetic resource. The distinct separation of Cluster IV confirms that *Sesamum alatum* possesses unique alleles for yield, phenology, and seed quality traits. Breeders can strategically exploit this divergence by using Cluster IV as a donor parent in hybridization programs with Cluster I genotypes to maximize heterosis, break current yield plateaus, and broaden the genetic diversity of cultivated sesame (Arya & Vishwakarma, 2026)

Intra and inter-cluster distance: The divergent patterns of intra- and inter-cluster distances reveal a highly structured genetic landscape among the 20 evaluated sesame genotypes. Cluster III recorded the maximum intra-cluster distance (12.344), indicating significant genetic variation among its component lines (YLM 11 and VRI 4). This suggests that although grouped together, these genotypes possess distinct individual trait combinations that could be exploited for specific selection criteria. Conversely, Cluster IV exhibited the lowest intra-cluster distance (0.000), which is expected due to its mono-cluster nature. The cluster distance is shown in table 5.

Regarding inter-cluster relationships, the maximum distance was identified between Cluster I and Cluster II (99.830). This substantial distance highlights a profound genetic dissimilarity between the primary cultivated variety pool (Cluster I) and the group containing DSS9, PYR 1, and Kayamkulam 1 (Cluster II).

Table.1 Analysis of variance (ANOVA) for quantitative characters of Sesame

Source of variation	df	Plant height (cm)	Days to 50 percent flower	No. of capsules per plant	1000 seed weight (gm)	Protein content (%)	Oil content (%)	Single plant yield (g/plant)
Replication	2	163.24	0.30	825.35	0.005	3.27	0.57	1.32
Treatment	19	315.61**	84.30**	14.58**	0.53*	6.91**	138.20**	26.88**
Error	38	2.95	0.48	0.05	0.02	0.95	0.76	0.41

* & ** indicates significance @ 5% and 1% probability level respectively

Table.2 Characterization of qualitative traits across twenty genotypes of sesame

Treatments	Genotypes	Petal Colour	Stem Hairiness	Growth Habit	Leaf Lobe	Seed Coat Colour
T1	TMV 7	White petal with purple coloration	Sparse	Branched erect	Deeply lobed	Brown
T2	TMV 6	White to pale pink colour	Sparse to moderate	Erect with moderate branched	Distinct lobed	Brown
T3	TMV 5	White	Sparse	Erect with moderate branched	Non lobed	Brown
T4	TMV 4	Pure white	Absent	Bushy with profuse branched	Deeply lobed	Brown
T5	TMV 3	Plain white	Sparse	Bushy with profuse branched	Deeply lobed	Dark brown
T6	VRI 3	White with deep pink shading	Sparse	Branched	Deeply lobed	White
T7	VRI 4	White with pink shading	Completely absent	Branched	Absent	Brown
T8	VRI 5	White with pink shading	Dense	Mono stem	Absent	White
T9	VRI (SV 1)	White	Sparse	Erect with profuse branched	Deeply lobed	Brown
T10	VRI (SV 2)	White petal with pink shading	Sparse	Profuse branched	Deeply lobed	Reddish brown
T11	CO 1	Light pink	Medium to sparse	Profuse branched	Trilobed to deeply lobed	Almost black
T12	SVPR 1	White with pink	Absent	Erect with moderate branched	Absent	White
T13	YLM 16	White with pink wash	Absent	Branched	Heart shaped lobe	Light brown
T14	YLM 17	White petal with pink or light purple wash	Absent	Erect with moderate branched	Trilobed upper leaves	Dark brown
T15	DS 5	White flower with light purple shading	Spare medium to	Erect to semi-erect	Slightly lobed	White
T16	DSS 9	Pale pink to light purple	Dense	Erect to branched	Slightly lobed	White
T17	PYR 1	White petal	Absent	Top branched	Deeply lobed	Black
T18	Kayamkulam 1	White with pink shading	Sparse to intermediate	Medium branched	Trilobed	Brown
T19	YLM 11	White with pink wash	Absent	Branched	Slightly lobed	Brown
T20	<i>Sesamum alatum</i>	Dark purple or reddish pink	Glabrous	Erect with branched	Deeply lobed	Dark brown

Table.3 Characterization of quantitative traits across twenty genotypes of sesame

Genotypes	Plant height (cm)	Days to 50 percent flower	No. of capsules per plant	1000 seed weight (gm)	Protein content (%)	Oil content (%)	Single plant yield (g/plant)
TMV 7	104.73	25.97	52.20	3.51	23.50	48.37	6.30
TMV 6	100.17	32.20	64.67	3.84	22.57	52.83	9.60
TMV 5	109.63	32.13	101.57	3.15	22.63	49.23	6.67
TMV 4	105.37	38.10	128.47	3.20	21.13	47.73	8.33
TMV 3	100.40	30.33	67.53	3.05	22.47	48.53	7.07
VRI 3	122.27	35.40	72.77	2.66	22.27	47.67	8.83
VRI 4	109.47	34.63	72.07	3.33	21.83	47.67	9.67
VRI 5	86.57	27.87	43.17	3.59	22.40	49.50	6.63
VRI (SV 1)	101.20	33.17	55.40	2.93	23.13	48.50	7.03
VRI (SV 2)	109.27	34.00	72.37	3.46	22.60	49.50	4.60
CO 1	118.03	30.97	56.20	2.89	23.73	38.67	7.00
SVPR 1	127.27	26.07	116.50	3.32	23.60	51.27	10.80
YLM 16	111.23	30.63	99.87	3.04	24.07	48.53	14.27
YLM 17	103.77	41.13	100.80	3.05	23.70	44.30	12.27
DS 5	117.80	42.17	88.80	3.57	24.63	49.37	6.70
DSS 9	86.73	39.40	38.57	2.78	27.50	49.03	4.24
PYR 1	106.50	32.60	57.27	3.37	22.37	43.00	4.30
Kayamkulam 1	100.70	33.77	41.20	3.79	20.50	48.37	3.27
YLM 11	108.10	37.63	73.10	3.08	22.50	49.70	6.87
<i>Sesamum alatum</i>	115.37	46.13	86.50	2.03	22.83	20.80	10.50
General Mean	107.23	34.21	88.45	3.18	23.51	48.37	6.31
CD (0.05)	7.86	1.13	13.03	0.19	1.60	1.43	1.05
CD (0.01)	10.48	1.51	17.37	0.26	2.13	1.91	1.40

Table.4 Cluster grouping of 20 Sesame genotypes

Cluster groups	No. of genotypes	Genotypes name
I	14	TMV7, TMV6, TMV5, TMV4, TMV3, VRI3, VRI5, VRI(SV1), VRI(SV2), CO1, SVPR1, DSS9, YLM17, DS5
II	3	YLM16, PYR1, Kayankulam1
III	2	YLM11, VRI4
IV	1	<i>Sesamum alatum</i>

Table.5 Distance (D^2) of intra and inter clusters

Cluster	I	II	III	IV
I	9.0257 (3.004)	99.8303 (9.991)	86.4647 (9.297)	47.2627 (6.875)
II		4.0240 (2.006)	16.8869 (4.109)	23.5695 (4.855)
III			12.3439 (3.513)	34.4124 (5.866)
IV				0.000 (0.000)

(The value in the parenthesis indicates D-value. The bold letters indicate intra cluster distance)

Table.6 Cluster means 7 characters for 20 genotypes

Clusters Vs Traits	I	II	III	IV
Plant height (cm)	108.41	97.98	108.79	115.37
Days to 50% flowering	32.87	35.26	36.13	46.13
No. of capsules per plant	80.02	45.68	72.59	366.50
1000 seed weight (gm)	3.23	3.31	3.21	2.03
Protein content (%)	23.03	23.46	22.17	20.80
Oil content (%)	48.14	46.80	48.69	20.80
Single plant yield (g/plant)	8.29	3.94	8.27	13.00

Fig.1 Conceptual Dendrogram of 20 sesame genotypes

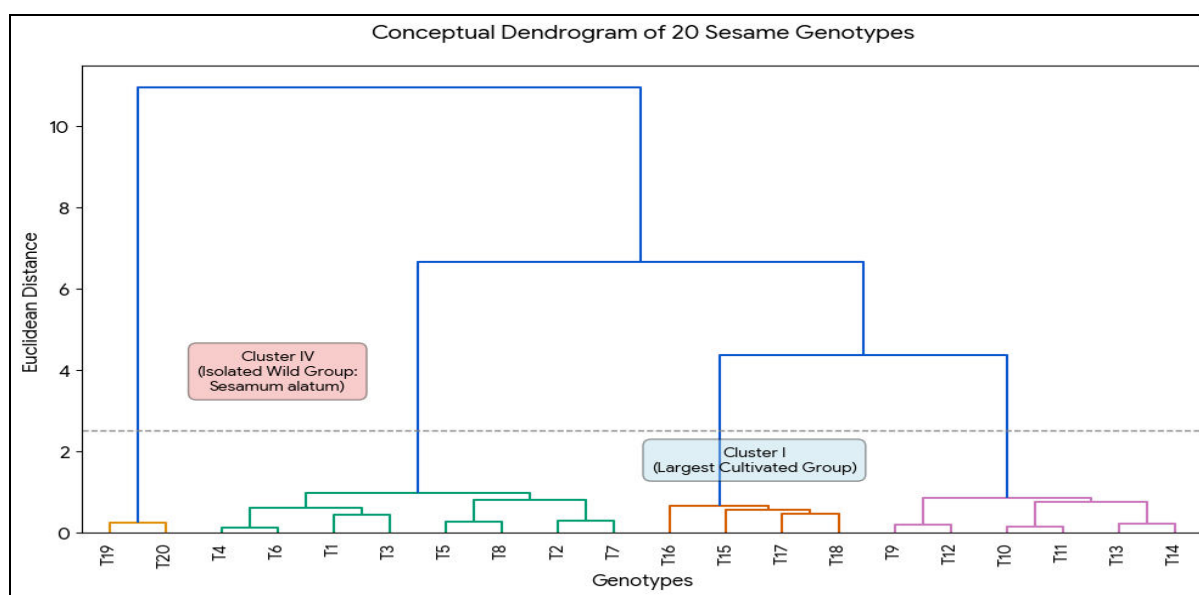
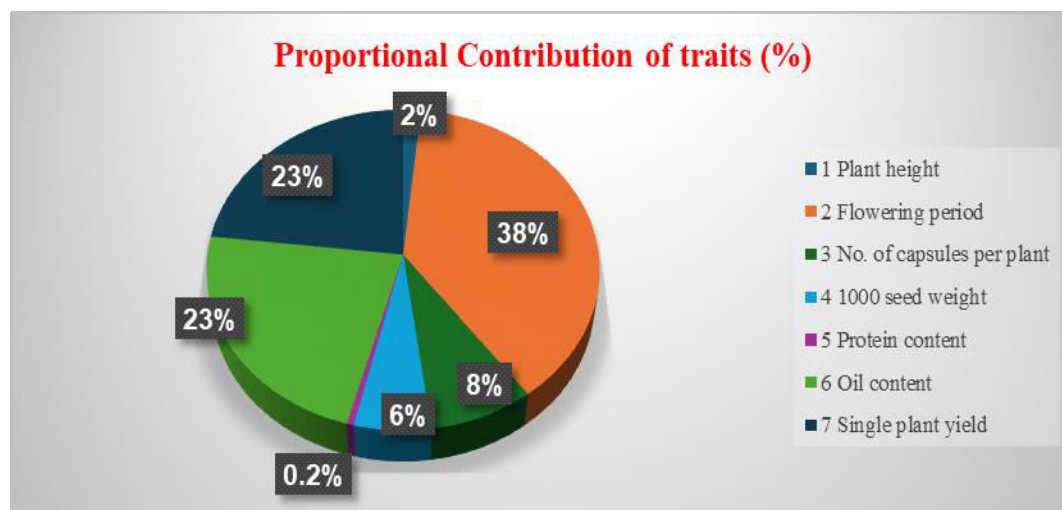


Fig.2 Proportional Contribution of traits (%) towards divergence



Crossing genotypes from these two highly divergent clusters can maximize heterosis and expand transgressive segregation in subsequent generations. The minimum inter-cluster distance between Cluster II and Cluster III (16.887) indicates a closer genetic affinity, pointing toward a potentially shared evolutionary pathway or parallel breeding pressures for those lines. (Yahaya & Falusi, 2025).

Cluster means: The cluster mean analysis reveals distinct trait combinations across the four groups: Cluster IV is the highest-yielding and tallest population, producing the maximum number of capsules per plant (366.50) and single-plant yield (13.00 g), though it is late-maturing and lowest in seed weight, protein, and oil content. Conversely, Cluster II represents a high-quality but low-yielding group, recording the lowest capsule count and yield but the highest protein content (23.46%) and seed weight (3.31 g). Clusters I and III represent balanced, high-oil genotypes characterized by a similar moderate yield (~8.28 g) and peak oil content (up to 48.69 % in Cluster III), with Cluster I achieve the earliest maturity at 32.87 days to 50% flowering.

Hybridization between genotypes belonging to cluster with superior mean performance is expected to produce superior segregants in subsequent generations (Gelashe & Ndeve, 2026). Clusters I and II offer a balanced alternative, maintaining steady, moderate yields alongside the highest oil content, with Cluster I offer the added benefit of the earliest flowering time. To break the negative link between high yield and low quality, breeders should cross parents from Cluster IV with Cluster II to combine high capsule counts with bolder seeds, or cross Cluster IV with Cluster III to pair high yields with peak oil content (Vanishree & Parmeshwarappa, 2021). Mean of clusters is represented in table 6.

Proportional contribution: The high contribution of the flowering period (38%), combined with oil content (23%) and single plant yield (23%), indicates that these three traits drive most of the genetic diversity among the evaluated genotypes. This massive, combined influence (~84%) suggests that selection and breeding strategies should prioritize variations in maturity and yield-linked quality components. Flowering time and oil content show such strong proportional weight, breeders can effectively use these specific criteria to select highly divergent parental lines, maximizing the chances of capturing strong heterosis and desirable recombinants in

subsequent generations (Nanthakumar *et al.*, 2020). Represented in figure 1.

In conclusion, Differences among the treatment means were not due to experimental error but rather to the actual influence of treatments. YLM 16 genotypes having high *per se* performance for single plant yield (g/plant). Genotypes with appreciable oil as well as protein content (DS 5) are identified as dual purpose types that break the negative oil-protein correlation. Therefore, the genotypes YLM 16 (Cluster II) and DS 5 (Cluster I) are recommended as parental materials for future sesame breeding programme to exploit maximum heterosis (hybrid vigour) and produce superior segregants in later generations.

Author Contributions

S. Keerthana: Investigation, formal analysis, writing—original draft. R. Dhanush: Validation, methodology, writing—reviewing. M. Dharanichselvan:—Formal analysis, writing—review and editing. M. Gokul: Investigation, writing—reviewing. J. Hanesh: Resources, investigation writing—reviewing. M. Harinadhan: Validation, formal analysis, writing—reviewing. S. Harish: Conceptualization, methodology, data curation, supervision, writing—reviewing the final version of the manuscript. V. Kalideeshwaran: Investigation, formal analysis, writing—original draft. K. Manikandan: Validation, methodology, writing—reviewing. K. Muthu Pandi:—Formal analysis, writing—review and editing. V. K. Ohm Harini Vasam: Investigation, writing—reviewing.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

- Arya, D. K., Vishwakarma, H., Ali, S., Kumari, K., Sharma, K., Kumari, H., Modgill, N., Sharma, G., Pradheep, K., Singh, K., Rangan, P., Mahalingam, A., Bhardwaj, R., Singh, M., Singh, B., Rao, M., Kalia, S., Singh, G. P., & Yadav, R. (2026). Systematic phenotypic approach to explore wild sesame germplasm for enhancing yield attributing traits in cultivated sesame. *Plant Genetic Resources*, 24(3), 172–182.
- Baydar, H. (2005). Sesame (*Sesamum indicum* L.). In R. J. Singh (Ed.), *Genetic resources, chromosome engineering, and crop improvement: Oilseed crops* (Vol. 4, pp. 225–256). CRC Press.
- Bisen, R., Singh, B., & Tiwari, A. (2017). DUS testing of sesame (*Sesamum indicum* L.) varieties using morphological descriptors. *Bulletin of Environment, Pharmacology and Life Sciences*, 6(Special Issue 1), 5–12.
- Gelashe, F. B., Ndeve, A. D., Menamo, T. M., Gandhi, H., & Chiulele, R. M. (2026). Genetic diversity and collection structure studies of sesame (*Sesamum indicum* L.) accessions across Ethiopian research centers. *Genes*, 17(3), Article 300.
- Madhu, B., Padmaja, D., Srikanth, T., & Balram, N. (2025). DUS-based morphological evaluation of sesame (*Sesamum indicum* L.) genotypes. *Journal of Advances in Biology & Biotechnology*, 28(5), 690–702.
- Nanthakumar, G., Singh, K. N., & Vaidyanathan, P. (2020). Relationships between cultivated *Sesamum* spp. and the wild relatives based on morphological characters, isozymes and RAPD markers. *Journal of Genetics and Breeding*, 54(1), 5–12.
- Pavani, K., Lal Ahamed, M., Ramana, J. V., & Sirisha, A. B. M. (2020). Morphological characterization of sesame (*Sesamum indicum* L.) genotypes using DUS descriptors. *Journal of Plant Development Sciences*, 12(6), 349–354.
- Petkar, D. S., Gite, B. D., Shinde, S. M., Sayyad, R. A., Tekade, K. S., & Dhande, U. A. (2026). Genetic diversity studies in sesame (*Sesamum indicum* L.). *International Journal of Agriculture and Food Science*, 8(2), 352–356..
- Phatate, G., Barela, A., Srivastava, S., Parveen, S., Pathak, S. K., & Yadav, P. K. (2025). Morphological characterization and hierarchical cluster analysis of sesame (*Sesamum indicum* L.) genotypes using DUS descriptors. *Plant Archives*, 25(2), 602–608.
- Sala, M., Divyadarshini, V. B., Sridevi, R., Raja Raja Cholan, J., Mohamed Yaseen, S. K., & Harish, N. (2023). Morphological characterization of sesame (*Sesamum indicum* L.) genotypes with DUS descriptors. *International Journal of Plant & Soil Science*, 35(18), 1044–1051.
- Seay, D., Szczepanek, A., De La Fuente, G. N., Votava, E., & Abdel-Haleem, H. (2024). Genetic diversity and population structure of a large USDA sesame collection. *Plants*, 13(13), 1765.
- Teklu, D. H., Abbas, A. A., You, J., & Wang, L. (2025). Genes and QTLs discovery for sesame (*Sesamum indicum* L.) breeding traits: A review. *Oil Crop Science*, 10(3), 240–258.
- Valarmathi, G., Kumar, M., & Saravanan, N. A. (2004). *Genetic variability and correlation studies for seed related traits in sesame (Sesamum indicum L.)*. *Sesame and Safflower Newsletter*, 19, 7–9.
- Vanishree, S. G., Parmeshwarappa, S. G., Harshiya Banu, M., Palakshappa, M. G., & Holeyannavar, P. (2022). Morphological characterization of sesame (*Sesamum indicum* L.) germplasm accessions with DUS descriptors. *The Pharma Innovation Journal*, 11(12), 938–945.
- Yahaya, S. A., Falusi, O. A., Daudu, O. A. Y., Muhammad, L. M., & Abdulkarim, B. M. (2014). Evaluation of seed-oil and yield parameters of some Nigerian sesame (*Sesamum indicum* L.) accessions. *International Journal of Agriculture and Crop Sciences*, 7(10), 661–664.

How to cite this article:

Keerthana S., Dhanush R., Dharanichselvan M., Gokul M., Hanes J., Harinadhan M., Harish S., Kalideeshwaran V., Manikandan K., Muthu Pandi K. and Ohm Harini Vasam V. K. 2026. Assessment of Distinctness, Uniformity and Stability (DUS) traits for Genetic Diversity in Sesame (*Sesamum indicum* L.). *Int.J.Curr.Microbiol.App.Sci*. 15(8): 89-96. doi: <https://doi.org/10.20546/ijemas.2026.1508.010>