



# Morphological Characterization of Sesame (*Sesamum indicum* L.) Genotypes with DUS Descriptors

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## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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## ABSTRACT

The current study's objective is to characterize eight sesame genotypes (*Sesamum indicum* L.) using the DUS descriptors. At Adhiparasakthi Agri College, Research Farm, Kalavai, the experiment was carried out in Randomized Complete Block Design with three replications in April

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2023. Sesame varieties were assessed for 13 morphological features using DUS descriptors. Most of the analyzed traits showed a significant amount of variation. These differences in physical traits were useful for identifying particular sesame genotypes. The aforementioned study highlighted the distinctive qualities of sesame varieties and demonstrated that morphological variances exist in these genotypes due to variations in genetic makeup, suggesting that breeders may make greater use of these variations in the selection process based on their particular breeding programme. This is highly useful study for varietal identification and conservation.

**Keywords:** DUS characterization; sesame; genotypes; morphological variation.

## 1. INTRODUCTION

“The oldest oilseed that humans are aware of and have utilized is sesame (*Sesamum indicum* L.). In the tropics and warm subtropics, where it is often produced in tiny plots, it is grown as a rainfed crop. Sesamum is known as the "Queen of oilseeds" due to its high oil content (38–54%), protein content (18–25%), calcium, phosphorus, oxalic acid, and superior seed oil and meal characteristics” [1]. Due to the presence of lignans (Sesamin, Sesaminol, and Sesamolinal), which have outstanding antioxidant properties and resist oxidation, sesamum seed oil has a long shelf life.

“India ranks first in world with 1.95 million ha area and 0.87 million tonnes production. The average yield of sesame in India is 413 kg/ha, low as compared with other countries in the world is 535 kg/ha” (Singh et al. 2022). However, compared to other oilseed crops, the productivity of the sesame crop is typically quite low, primarily because there aren't many varieties with high yields. To maximize this crop's untapped potential for additional yield enhancement in the current situation, more active breeding efforts are needed [2]. Under changing climatic conditions, breeding of climate resilient varieties is becoming more important.

Understanding genetic diversity is essential for developing disease and pest resistance cultivars as well as selecting elite parents for high grain and oil yield. A new genotype must pass the DUS (distinctness, uniformity, and stability) tests in order to be registered as a commercial variety. To be registered as a commercial variety, a new genotype must be distinct (D) from all other released varieties, uniform (U), and stable (S). The characteristics of the plant and seed must be properly investigated and recorded in order to identify varieties/genotypes by morphological traits. Such characterization studies are lacking in sesamum.

Therefore, the present study was undertaken to characterize the genotypes of sesame using DUS descriptors.

## 2. MATERIALS AND METHODS

The Present investigation was carried out in the Department of Plant Breeding and Genetics, Research farm, Adhiparasakthi Agricultural College, Kalavai. Genotypes for this study were obtained from Regional research station, Virudhachalam. For this study, eight genotypes viz., VRI 2, VRI-3, VRI-4, VRI-5, TMV-4, TMV-7, SVPR-1 and Paiyur-1 were used to study the morphological variation by using DUS descriptor. Eight genotypes were evaluated in three replications using Randomized Block Design (RBD) with inter and intra-row space was 30×10 cm, respectively. The recommended agronomical and plant protection package of practices were followed for the raising successful crop. The observations were recorded on 5 randomly selected plants for each character in each replication at different crop growth stages. Data were collected on 13 qualitative traits including morphological characters. DUS characterization was done as per the guidelines developed by IPGRI Rome, Italy and NBPGR New Delhi, India. Observations were recorded on 13 morphological traits viz, Petal colour, Petal hairiness of flower, branching pattern, Stem hairiness, basal leaf margin, leaf lobe, No. of capsules per leaf axial, No. of flowers per leaf axil, corolla hairiness, number of locules per capsule, capsule shape, capsule hairiness, Capsule arrangement and Seed coat colour.

## 3. RESULTS AND DISCUSSION

DUS descriptors were used to analyze the morphological characteristics of the sesame cultivars. The eight genotypes could be distinguished from one another based on differences in morphology. The findings showed that almost all of the characters recorded had a significant amount of variation. The sesame

genotypes were divided into groups based on differences in physical traits, with the goal of identifying each genotype individually using descriptors. Based on morphological variation, the eight genotypes could be identified from each other. The result of characterization for each qualitative trait is presented in the Table 1. Results revealed wide range of variation among the eight genotypes for almost all the qualitative traits studied.

### 3.1 Morphological Characterization

Petal colour is the important characters for morphological characterization. Based on petal colour, the genotypes were grouped as white (TMV 4 & Paiyur 1), white with pink shading (VRI 2, VRI 4 VRI 5 & SVPR1), white with deep pink shading (VRI 3, TMV7). Based on Petal hairiness of flower, the genotypes were grouped as sparse (VRI 2, VRI 3 TMV 4, TMV 7 and Paiyur 1) and dense (VRI 4, VRI 5 and SVPR 1). This observation in sesame is in accordance with Suhasini [3]. Bhagwat Singh et al. [4] and Palakshappa et al. [5]. The genes determine the colour of the petal by developing or blocking of anthocyanin pigmentation.

In the present study basal and top branching patterns were observed and it was indicated that the inheritance of branching habit was determined by one single dominant gene. Based on branching pattern the genotypes were grouped as top branching (VRI 2, VRI 3, TMV 4, TMV 7, Paiyur 1) and basal branching (SVPR1, VRI 4 and VRI 5 ). Similar findings and grouping of genotypes based on flower and stem morphological characters were made by

Parameshwarappa et al. [6], Frary et al. [7], Sarita et al. [8], Azeez et al. [9] and Ozcinar and Sogut [10] in sesame.

On the basis of Stem hairiness the genotypes were grouped as Sparse (VRI 2, VRI 3, TMV 4, TMV 4, TMV 7), Dense (VRI 5 ), absent (PAIYUR 1 and SVPR1). Based on leaf lobes the genotypes were grouped as deeply lobed (VRI 2, VRI 3, TMV 4, TMV 7 and PAIYUR 1) and absent (VRI 4, VRI 5 and SVPR1).

On the basis of leaf Margin the genotypes were grouped as Entire (VRI 2, VRI 3, VRI 4, TMV 4, TMV 7, PAIYUR 1 and SVPR 1), Serrate (VRI 5). Suhasini [3] and Palakshappa et al. [5] observed the similar results in sesame.

Based on No. of capsules per leaf axial the genotypes were grouped as one (VRI 2, VRI 3, VRI 4, TMV 4, TMV 7), two (VRI 5), three (SVPR1). No. of locules per capsule the genotypes were grouped as four (VRI 2, VRI 3, TMV 4, VRI 4, VRI 5, TMV 7, PAIYUR 1 ).

Based on Shape of the capsule the genotypes were grouped as broad oblong (VRI 2, VRI 3, TMV 4, TMV 7, SVPR1), narrow oblong (VRI 4, VRI 5), tapering (Paiyur 1). "Hairiness is the significant character for improving more seed yield and natural defense mechanism for biotic and abiotic factors. So this character may be recognized as ideal plant type. Based on Capsule hairiness the genotypes were grouped as sparse (VRI 2, VRI 3), dense (VRI 5, SVPR1), absent (VRI 4, TMV4, TMV 7, Paiyur 1). Hairiness and pubescence is reported in effective for conferring resistance to insect pests in Dolichos bean" [11-14].

**Table 1. Morphological characteristics of sesame genotypes**

S.No.	Genotypes	1. Petal colour of flower	2. Petal hairiness of flower	3. Branching pattern
1	VRI 2	White with pink shading (2)	Sparse (3)	Top branching (2)
2	VRI 3	White with deep pink shading (3)	Sparse (3)	Top branching (2)
3	VRI 4	White with pink shading (2)	Dense (5)	Basal branching (1)
4	VRI 5	White with pink shading (2)	Dense (5)	Basal branching (1)
5	TMV 4	White (1)	Sparse (3)	Top branching (2)
6	TMV 7	White with deep pink shading (3)	Sparse (3)	Top branching (2)
7	PAIYUR 1	White (1)	Sparse (3)	Top branching (2)

**Table 2. Morphological characteristics of sesame genotypes**

S. No.	Genotypes	4. Stem hairiness	5. Leaf lobes	6. Leaf margin
1	VRI 2	Sparse (3)	Deeply lobed (2)	Entire (1)
2	VRI 3	Sparse (3)	Deeply lobed (2)	Entire (1)
3	VRI 4	Sparse (3)	Absent (0)	Entire (1)
4	VRI 5	Dense (5)	Absent (0)	Serrate (2)
5	TMV 4	Sparse (3)	Deeply lobed (2)	Entire (1)
6	TMV 7	Sparse (3)	Deeply lobed (2)	Entire (1)
7	PAIYUR 1	Absent (1)	Deeply lobed (2)	Entire (1)
8	SVPR 1	Absent (1)	Absent (0)	Entire (1)

**Table 3. Morphological characteristics of sesame genotypes**

S. No.	Genotypes	7. No. of capsules per leaf axial	8. Capsule hairiness	9. No. of flowers per leaf axil
1	VRI 2	One (1)	Sparse (3)	One (1)
2	VRI 3	One (1)	Sparse (3)	Two (2)
3	VRI 4	One (1)	Absent (0)	Two (2)
4	VRI 5	Two (2)	Dense (5)	Two (2)
5	TMV 4	One (1)	Absent (0)	Two (2)
6	TMV 7	One (1)	Absent (0)	Two (2)
7	PAIYUR 1	One (1)	Absent (0)	Two (2)
8	SVPR 1	Three (3)	Dense (5)	Two (2)

**Table 4. Morphological characteristics of sesame genotypes**

SN.	Genotypes	10. No. of locules per capsule	11. Shape of the capsule	12. Capsule arrangement
1	VRI 2	Four (3)	Broad oblong (3)	Alternate (1)
2	VRI 3	Four (3)	Broad oblong (3)	Alternate (1)
3	VRI 4	Four (3)	Narrow oblong (2)	Alternate (1)
4	VRI 5	Four (3)	Narrow oblong (2)	Opposite (2)
5	TMV 4	Four (3)	Broad oblong (3)	Alternate (1)
6	TMV 7	Four (3)	Broad oblong (3)	Alternate (1)
7	PAIYUR 1	Four (3)	Tapered (1)	Alternate (1)
8	SVPR 1	Four (3)	Broad oblong (3)	Opposite (2)

**Table 5. Morphological characteristics of sesame genotypes**

SN.	Genotypes	13. Seed coat colour
1	VRI 2	Dark brown (4)
2	VRI 3	White (1)
3	VRI 4	Dark brown (4)
4	VRI 5	White (1)
5	TMV 4	Dark brown (4)
6	TMV 7	Dark brown (4)
7	PAIYUR 1	Black (5)
8	SVPR 1	White (1)



Opposite



Alternate



Cluster

**Fig. 1. Capsule arrangement**



One capsule per leaf axil



More than one capsule per leaf axil

**Fig. 2. Capsule number per leaf axil**



White



Light purple



Dark purple

**Fig. 3. Flower petal color**





**Fig. 4. No of flowers per leaf axil**



**Fig. 5. Stem hairiness**



**Fig. 6. Seed coat colour**

Based on seed coat colour the genotypes were grouped as dark brown (VRI2, VRI 4, TMV4, TMV7 ), black ( Paiyur 1), white (SVPR1, VRI 3, VRI 5 ). A wide range of variation, i.e. white, grey, and light brown, dark brown and black was observed for seed coat colour against the reported white, brown and black. All earlier

researchers in sesame, outlined seed coat colour to be under digenic control with several confusing segregants. Based on variation in physical characteristics, it was attempted to group the sesame genotypes and identify each and every one of them through descriptors. Based on morphological variation, the eight

genotypes could be identified from each other. The result of characterization for each qualitative trait is presented in the Table 1. Results revealed wide range of variation among the eight genotypes for almost all the qualitative traits studied [15-17].

#### 4. CONCLUSION

Morphological features of genotypes have been a major component of varietal identification. It is not possible to identify varieties using any single parameter. A detailed morphological description of plants and seeds should therefore be prepared. Utilization of these features in sequential fashion is useful and convenient to distinguish different genotypes. The information about inheritance of three capsules per leaf axil could be beneficial for genetic improvement of sesame targeting higher seed yield.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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