Original Research Article

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

Abstract:

The aim of the present study is to characterize eight genotypes of sesame (*Sesamum indicum* L.) based on the DUS descriptors. The experiment was conducted in Randomized Complete Block Design with three replications at Adhiparasakthi Agri College, Research Farm, Kalavai during April 2023. On the basis of DUS descriptors, sesame varieties were characterized for 13 morphological traits. A significant amount of variation was observed for most of the traits studied. These distinctions in morphological characteristics were valuable in recognizable proof of individual sesame genotypes. Above study revealed the distinct characteristics of sesame varieties and indicated that morphological variations exist in these lines due to variation in genetic makeup and could be better utilized by breeders in the selection based on their specific requirement for breeding programme. This is highly useful study for varietal identification and conservation.

Keywords: DUS characterization, Sesame, Genotypes, Morphological variation.

Introduction

Sesamum (*Sesamum indicum* L.) is the oldest oilseed known and used by human being. It is grown as a rainfed crop in the tropics and warm subtropics, where it is usually grown in small plots. Sesamum is described as the "Queen of oilseeds" because it contains high oil (38-54%), protein (18-25%), calcium, phosphorous, oxalic acid and excellent qualities of seed oil and meal (Prasad, 2002). Sesamum seed oil has long shelf life due to the presence of lignans (Sesamin, Sesaminol, Sesamolinol), which have remarkable antioxidant function, resisting the oxidation.

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, the productivity of sesame crop is generally very low as compared to other oilseed crops which is mainly due to lack of high yielding cultivars. In present scenario, more aggressive breeding efforts are required to harness the untapped potential of this crop for further yield enhancement (Furat and Uzun 2010). Under changing climatic conditions, breeding of climate resilient varieties is becoming more important.

Knowledge about genetic diversity is necessary not only in selecting elite parents for high grain and oil yield but also for development of disease and pest resistant varieties. In order to introduce a new plant variety to the markets commercially, it is necessary to register newly bred variety, which relies upon the results of DUS (distinctness, uniformity, and stability) tests; that is, for a new genotype to be registered as a commercial variety, it needs to be distinct (D) from all other released varieties, uniform (U) and stable (S). For identification of varieties/genotypes through morphological characters the plant and seed characters need to be studied and thoroughly documented. Such characterization studies are lacking in sesamum. Therefore, the present study was undertaken to characterize the genotypes of sesame using DUS descriptors.

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.

Results and Discussion

Morphological traits of the sesame varieties were studied using DUS descriptors. Based on morphological variation, the eight genotypes could be identified from each other. Result revealed that a significant amount of variation was recorded on almost all the characters recorded**.** 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.

Petal colour is the important characters for 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 (2006), Bhagwat Singh *et al.* (2017) and Palakshappa *et al*. (2020). The genes determine the colour of the petal by developing or blocking of anthocyanin pigmentation.

Based on branching pattern the genotypes were grouped as top branching (VRI 2, VRI 3, TMV 4, TMV 7, Paiyur 1) and basal branching (SVPR 1, VRI 4 and VRI 5). Similar findings and grouping of genotypes based on flower and stem morphological characters were made by Parameshwarappa *et al.* (2008), Frary *et al*. (2015), Sarita *et al*. (2015), Azeez *et al.* (2017) and Ozcinar and Sogut (2017) in sesame.

Hairiness is a typical character of sesame and can be seen many parts of plant such as stem, leaf, corolla and capsules (Weiss, 1983). Strong hairiness character could be evaluated as advantages for insect pests and diseases of sesame. On the basis of Stem hairiness the genotypes were grouped as Sparse (VRI 2, VRI 3, TMV 4, TMV 4, TMV 7), Dense (VRI5), 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 Strong (VRI 3 and VRI 5), Weak (VRI 2, VRI 4, TMV 4, TMV 7, PAIYUR 1 AND SVPR 1). Suhasini (2006) and Palakshappa *et al.* (2020) 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, TMV 7, PAIYUR 1, SVPR 1, VRI 4 and VRI 5). Number of capsule per leaf axil in sesame is an important advantage in the efforts to increase seed yield per plant because genotypes with three capsules per leaf axil has potential to provide more capsules per plant in comparison to those of one capsule per leaf axil (Baydar, 2005).

Based on Capsule hairiness the genotypes were grouped as Sparse (VRI 2, VRI 3), Dense (VRI5 AND SVPR 1) and absent (VRI 4, TMV 4, TMV 7, and PAIYUR 1). Based on Shape of the capsule the genotypes were grouped as broad oblong (VRI 2, VRI 3, TMV 4, TMV 7 and SVPR 1), narrow oblong (VRI 4 and VRI 5), tapering (PAIYUR 1)**.** 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). All the genotypes had four No. of locules per capsule namely VRI 2, VRI 3, VRI 4, VRI 5, TMV 4, TMV 7, PAIYUR 1 and SVPR 1. 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, 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 .Recently, (Zhang *et al*.2013) using a high-density linkage map analyzed the genetic segregation and quantitative trait loci (QTL) for sesame seed coat color and showed that two major genes with additive dominant-epistatic effect along with polygenes were responsible for controlling the seed coat colour trait.

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)

8	SVPR 1	WHITE WITH PINK SHADING (2)	DENSE (5)	BASAL BRANCHING (1)

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)

Morphological characterization

Figure 1 :Capsule Arrangement

Opposite Alternate Cluster

Figure 2 :Capsule number per leaf axil

One capsule per leaf axil More than one capsule per leaf axil

Figure 3 : flower petal color

White Light purple Dark purple

Figura 4 : No of flowers per leaf axil

Figure 5 Stem hairiness

Figure 6 : Seed coat colour

Results and Discussion

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 8 genotypes could be identified from each other. Result revealed that a significant amount of variation was recorded on almost all the characters recorded.

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 (2006)’ Bhagwat Singh *et al.* (2017) and Palakshappa *et al*. (2020). 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.* (2008), Frary *et al*. (2015), Sarita *et al*. (2015), Azeez *et al.* (2017) and Ozcinar and Sogut (2017) 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 (2006) and Palakshappa *et al.* (2020) 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 (Jagadeesh Babu *et al*., 2008).

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.

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.

References

Azeez MA, Olowookere MB, Animasaun DA, Bello BO. Utility of some floral characters in the assessment of genetic diversity in sesame (*Sesamum indicum* L.). Acta Agriculturae Slovenica, 2017; 109(1):61-70.

Baydar H (2005) Breeding for the improvement of the ideal plant type of sesame. Plant Breed. 124:263-267.

Bhagwat S, Rajani B, Akanksha T. DUS Testing of Sesame (*Sesamum indicum* L.) varieties using Morphological Descriptors. Bull. Env. Pharmacol. Life Sci. 2017;6(1):5-12.

Falusi O (2007). Segregation of genes controlling seed colour in sesame (*Sesamum indicum L*.) From Nigeria. Afr. J. Biotechnol. 6(24): 2780-2783.

Frary A, Tekin P, Celik I, Furat S, Uzun B, Doganlar S. Morphological and Molecular Diversity in Turkish Sesame Germplasm and Core Set Selection. Crop Sci. 2015; 55:702711

Furat S, Uzun B (2010) The use of agro-morphological characters for the assessment of genetic diversity in sesame (*Sesamum indicum* L). Plant Omics J 3:85-91

Jagadeesh Babu, C. S., Byre Gowda, M., Girish, G. and Gowda, T. K. S. 2008. Screening of Dolichos germplasm for pod borers and bruchids. Environment and Ecology. 26 (4c): 2288-2290 ,

Ozcinar AB, Sogut T. Analysis of sesame (*Sesamum indicum* L.) accessions collected from different parts of turkey based on qualitative and quantitative traits. J Crop Breed. Genet. 2017; 3(1):45-51.

Parameshwarappa, S.G. Palakshappa, M.G. Salimath, P.M. and Parameshwarappa, K.G. 2009. Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.). Karnataka J. of Agri. Sci., 22(2): 252- 254

Palakshappa MG, Harshiya Banu, Parmeshwarappa SG, Rajani B, Nagappa H, Pooja H. DUS Testing of Sesame (*Sesamum indicum* L.) Accessions Using Morphological Descriptors and Evaluation for Foliar Diseases of Sesame. Int. J Curr. Microbiol. App. Sci. 2020;9 (1):18371852.

Prasad, R. 2002. Text Book of field Crops Production, Indian Council of Agricultural Research, New Delhi, p 821.

Sarita, K. Pandey, Arna Das and Tapash Dasgupta. 2013. Genetics of seed coat color in sesame *(Sesamum indicum* L.). African Journal of Biotechnology. 12 (42): 6061-6067.

Sarita K, Arna D, Pooja Rai, Tapash Dasgupta. Morphological and genetic diversity assessment of sesame (*Sesamum indicum* L.) accessions differing in origin. Physiol. Mol. Biol. Plants., 2015; 21(4):519-529.

Subashini, G. 2003. Genetic analysis for yield and yield components in sesame (*Sesamum indicum* L.). M. Sc. (Ag) Thesis, AC&RI, Madurai.

Suhasini KS. Characterization of sesame genotypes through morphological, chemical and RAPD markers. M.Sc. thesis submitted to the University of Agricultural Sciences, Dharwad; c2006.

Weiss EA (1983). Sesame, oilseed crops. Longman Inc., New York

Zhang, H., Miao, H., Wei, L. Li, C., Zhao, R. and Wang, C. 2013. Genetic analysis and QTL mapping of Seed coat colour in Sesame (Sesamum indicum L.) PLoS ONE. 8: e 63 898 doi 101371