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Determination of Genetic Diversity in Sesame (*Sesamum indicum* L.)

Chanchal Shakyawal [a*], Manju Singh [b++] and Rishabh Shukla [c]

[a] Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari - 396450, Gujarat, India.
[b] ASPEE Shakilam Biotechnology Institute, Navsari Agricultural University, Surat-395007, Gujarat, India.
[c] Department of Genetics and Plant Breeding, N.M. College of Agriculture, Navsari Agricultural University, Navsari - 396450, Gujarat, India.

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

Aim: To assess the degree of genetic divergence (D^2 statistics) among sesame genotypes with respect to various traits.
Study Design: The present experiment evaluated in the Randomized Block Design (RBD) with three replications.
Place and Duration of Study: Experiment was carried out during *Rabi*, 2023 at Niger Research Station, NAU, Vanarasi.
Methodology: To evaluate the genetic diversity among 30 sesame genotypes, Mahalanobis D^2 Statistics was utilized. The genotypes were classified into six distinct clusters using Tocher's method, revealing substantial diversity.

[++] Assistant Professor;
**Corresponding author: E-mail: chanchalkawai810@gmail.com;*

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Results: Cluster I contained the largest 17 genotypes followed by Cluster II with 9 genotypes. Clusters III, IV, V, and VI each included only a single genotype. The highest inter-cluster distance was observed between Cluster I and Cluster IV (25.29) followed by Cluster I and Cluster V (24.07). The lowest inter-cluster distance was 10.00 noted between Cluster IV and Cluster V, suggesting that the genotypes within these clusters are closely related. Cluster III was noted for its high mean values in days to 50% flowering (44.67) and days to maturity (94.33), Cluster IV excelled in capsule width (9.32), Cluster V showed superior traits in plant height (128.78), capsule length (3.23), 1000-seed weight (3.92), harvest index (40.06) and seed yield/plant (9.57), while Cluster VI had the highest values for capsules/plant (39.75) and oil content (46.43). The analysis revealed that the greatest contributions to total divergence were made by 1000 seed weight (51.95%), followed by seed yield per plant (16.32%) and oil content (15.17%). In contrast, plant height and capsule length contributed minimum, each with 0.00%.

Conclusion: These results indicate that Clusters III and IV, along with V and VI, exhibit the most significant divergence. This diversity highlights the potential for using these clusters as parent genotypes in breeding programs to achieve a wide range of variability and effective selection.

Keywords: Genetic diversity; mahalanobis D^2 statistics; cluster; sesame.

1. INTRODUCTION

Sesamum indicum (L.) known for its historical significance, it is one of the most important edible oilseed crops, grown extensively across both tropical and temperate regions worldwide. Often referred to as the "Queen of oilseeds," because of its oil rich in nutritional content [1]. Sesame seeds are a high-energy food, containing around 50-60% oil, 18-25% protein, and 13.5% carbohydrates. Sesame oil is cholesterol-free due to this it is frequently recommended for individuals with heart conditions. Additionally, sesame seeds are rich in compounds with antioxidant and anti-pathogenic properties, further enhancing their health benefits [2].

At the national level, the National Bureau of Plant Genetic Resources (NBPGR) is responsible for the secure and sustainable management of a wide array of crop plant germplasm. Currently, NBPGR conserves a total of 10,507 sesame accessions [3]. One key challenge in managing and utilizing these germplasm collections is developing strategies to reduce their size to a more manageable and accessible level. To conserve and use genetic diversity effectively, it is essential to comprehend its nature and structure. For hybridization, a broad range of genetic diversity among parent plants is necessary, making knowledge of the genetic diversity and relationships within sesame populations vital for plant breeding programs. By examining morphological and agronomic traits, researchers can uncover the genetic diversity present in crop species [4].

Sesame, often grown on marginal lands with suboptimal management practices, tends to yield poorly. This low productivity is partly due to the lack of cultivars that are well-suited to various agro-climatic conditions. Therefore, developing high-yielding, locally adapted cultivars is a critical priority. The aim of this research was to identify suitable diverse parent genotypes for hybridization [5]. Every crop needs genetic diversity because it creates opportunities for growth and selection. Understanding the nature and extent of genetic variability is crucial for designing any successful breeding programme that aims to improve genotype yield performance [6]. To achieve this, the Mahalanobis D^2 technique was employed, which is an effective method for assessing genetic divergence and the contributing traits among sesame genotypes.

2. MATERIALS AND METHODS

The experiment material consists of 30 genetically diverse genotypes of sesame was carried out during *Rabi*, 2023 at Niger Research Station, NAU, Vanarasi. Experiment material obtained accessions of sesame supplied by Project Coordinating Unit Sesame & Niger, JNKKV, Jabalpur (MP) and Oilseeds Research Station, JAU, Amreli and further evaluated in Randomized Block Design (RBD) with three replications. Recommended package of practices was followed to raise good and healthy crop stand. Plant height, number of capsules/plant, capsule width (mm), capsule length (cm), 1000 seed weight, harvest index, oil content and seed yield/plant for measure these traits five competitive plants were randomly selected. Days to 50% flowering, days to maturity were noted on plot basis. The average measurements from five plants were analyzed statistically, and Wilk's criterion was applied to assess the significance of differences in mean values across all ten traits.

2.1 Statistical Analysis

Genetic diversity was studied following Mahalanobis's [7] D^2 statistics and clustering of genotypes was done on the basis of D^2 values according to Tocher's method as described by Rao [8]. Statistical analysis was done by INDOSTAT program.

3. RESULTS AND DISCUSSION

According to the D^2 analysis, 30 genotypes were grouped into six distinct clusters. Cluster I was the largest, containing 17 genotypes, while Cluster II had nine genotypes. Clusters III, IV, V, and VI each included only a single genotype. This distribution indicates a high level of genetic diversity among the sesame genotypes (Table 1). similar result of formation of six clusters for sesame genotypes also observed by Tripathy et al. [9], Begum et al. [10], Soundharya et al. [5] and Tesfaye et al. (2021).

Table 2 presents the average D^2 values for intra-cluster and inter-cluster comparisons. The intra-cluster D^2 values varied from zero for clusters III, IV, V, and VI to 9.42 for cluster II. The highest intra-cluster distances were observed in clusters I (9.42) and II (9.11), suggesting that genetic diversity remains among genotypes within these clusters.

Table. 1 Distribution of thirty genotypes into six different clusters based on Mahalanobis's D^2 statistics (Tocher`s method)

Clusters	No. of genotypes	Genotypes
I	17	DS-51, IC-91248, NIC-8476, TBS-6, IC-199433, AT-410, TKG-1501, AT-253, SVT-333, IC-23309, IC-132281, AT-388, DS-1810, JLS-2420, JLS-120, JLS-2696, IC-204681
II	9	JLS-2611, GT-3, JCS-3202, RT-85, DC-6739, TKG-506, AT-334, DSM-1711, AT-412
III	1	GT-10
IV	1	DC-27
V	1	AT-395
VI	1	AT-393

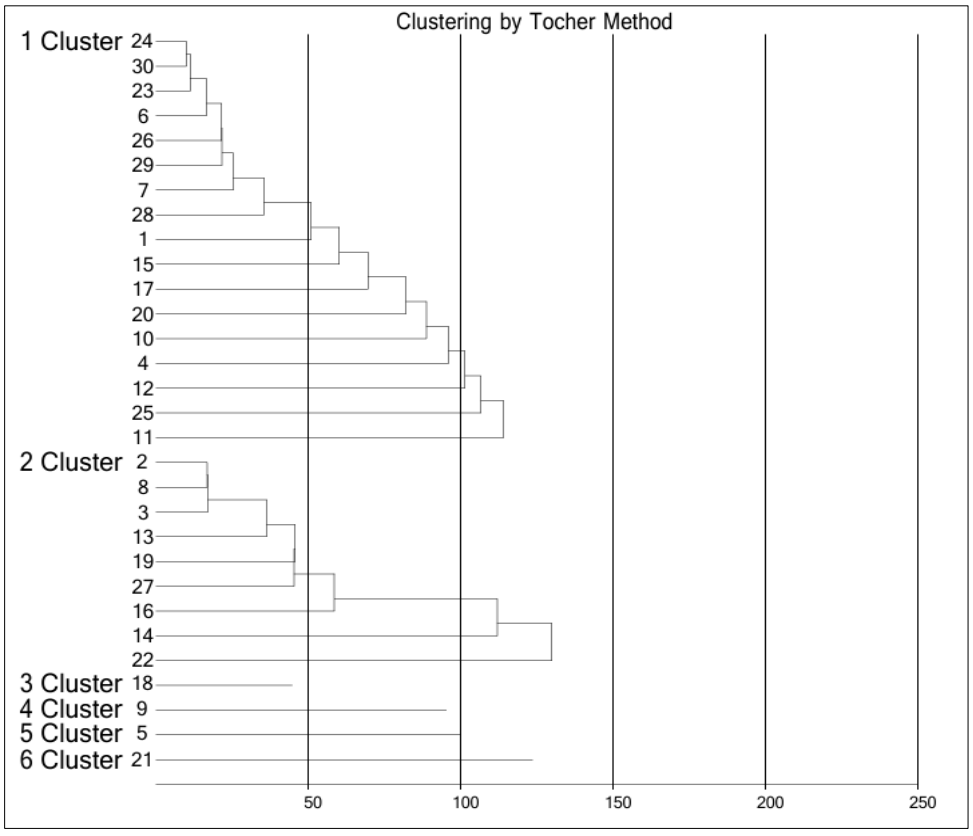

Fig. 1. Dendrogram for 30 sesame genotypes of 10 characters

Table 2. Estimation of average intra and inter cluster distances for ten characters in thirty genotypes

Clusters	I	II	III	IV	V	VI
I	**9.11**					
II	15.88	**9.42**				
III	20.49	12.62	**0.00**			
IV	25.29	16.67	10.07	**0.00**		
V	24.07	16.21	10.34	10.00	**0.00**	
VI	15.20	18.20	16.93	21.95	21.62	**0.00**

Bold figures indicate intra cluster values

Therefore, selection within these clusters could be based on the highest mean values for desirable traits.

Cluster I and IV (25.29) shown maximum inter cluster distance followed by cluster I and V (24.07), cluster IV and VI (21.95), cluster V and VI (21.62), cluster I and III (20.49) and cluster III and VI (16.93).

The genetic diversity between genotypes from two clusters increases with the distance between those clusters. Breeding programs focused on creating high-performing hybrids would benefit significantly from using highly divergent and superior genotypes. The smallest inter-cluster divergence was observed between clusters IV and V (10.00), followed closely by clusters III and IV (10.07), suggesting that the genotypes within these clusters are more closely related.

The highest amount of heterosis are expected in cross combinations where the parent genotypes originate from the most divergent clusters. However, plant breeders also aim to achieve other desirable traits beyond just high heterosis. As the distance between two clusters increases, so does the genetic diversity between the genotypes from those clusters. Keeping this in view, it is indicated that hybridization between the genotype DC-27 of cluster IV with genotype of cluster I; AT-395 of cluster V with genotype of cluster I; DC-27 of cluster IV with AT-393 of cluster VI; AT-395 of cluster V with AT-393 of cluster VI; GT-10 of cluster III with genotype of cluster I; GT-10 of cluster III with AT- 393 of cluster VI are expected to produce highly heterotic hybrids. Genotypes from these clusters can be utilized as parents in crossing programs to produce breeding material with enhanced genetic diversity. Table 3 provides the cluster means for each of the ten characters. The data indicate significant differences across all the characters analyzed.

The data indicated that the cluster mean for days to 50% flowering was highest in cluster III (44.67) and the lowest in cluster IV (38.00). Days to maturity were exhibited highest and lowest means in cluster III (94.33) and IV, VI (87.67), respectively. Cluster V recorded highest mean for plant height (128.78 cm), while lowest was in cluster III (91.13 cm). The number capsules/plant was highest in cluster VI (39.75) and lowest in cluster V (30.25). Cluster IV showed highest capsule width (9.32 mm) while in cluster V it was low (6.64 mm). Cluster V and cluster VI had maximum (3.23 cm) and minimum (2.24) cluster means capsule length, respectively. Highest 1000-seed weight was recorded in cluster V (3.92 g) and lowest in cluster I (2.66 g).

Table 3. Mean values of clusters for 10 characters in 62 sesame genotypes (Tocher's method)

Clusters	DFF	DM	PH	CPP	CW	CL	TSW (g)	HI (%)	OC (%)	SYP (g)
I	40.25	89.46	99.83	**30.25**	8.20	2.44	**2.66**	29.61	43.04	**3.63**
II	39.19	89.59	100.71	33.00	8.54	2.57	3.61	33.31	42.03	4.07
III	**44.67**	**94.33**	**91.13**	34.17	9.28	2.72	3.75	39.76	40.70	8.67
IV	**38.00**	87.67	99.47	35.00	**9.32**	3.08	3.88	**26.91**	38.33	9.17
V	43.67	92.67	**128.78**	34.04	**6.64**	**3.23**	**3.92**	**40.06**	**37.04**	**9.57**
VI	43.00	**87.67**	96.41	**39.75**	9.07	**2.24**	2.92	38.60	**46.43**	8.90

Bold figures indicate minimum and maximum mean values for 10 traits

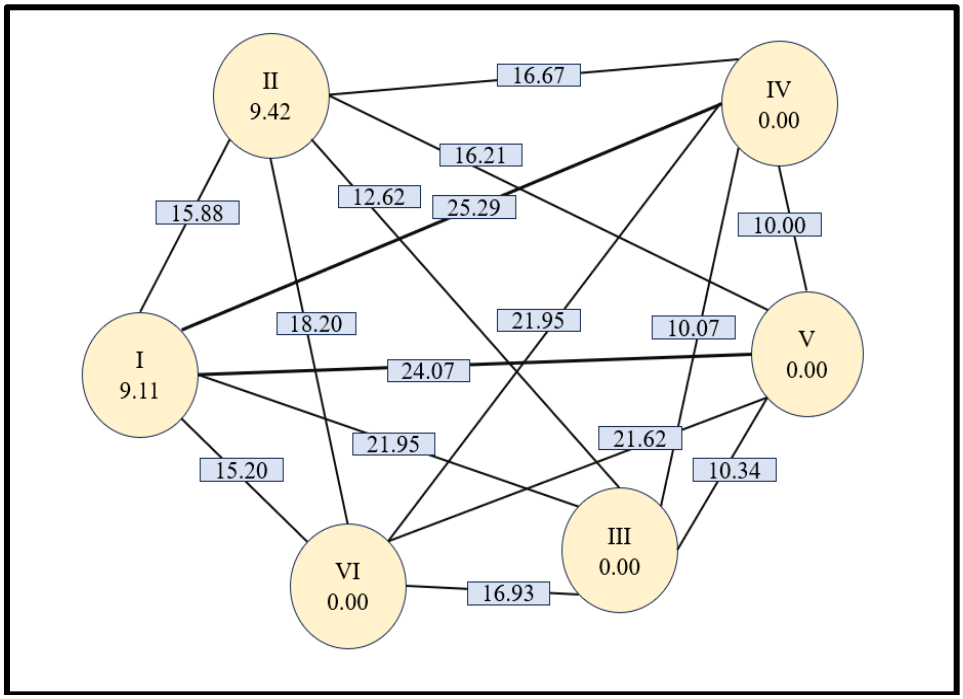

Fig. 2. Cluster diagram based on D2 statistics

Table 4. Relative contribution of different characters to genetic diversity in thirty genotypes

Source	Times ranked 1st	Contribution %
Days to 50% flowering	31	7.13 %
Days to maturity	1	0.23 %
Plant height (cm)	0	0.00 %
Capsules/plant	9	2.07 %
Capsule width (mm)	24	5.52 %
Capsule length (cm)	0	0.00 %
1000 seed weight (g)	226	51.95 %
Harvest Index (%)	7	1.61 %
Oil content (%)	66	15.17 %
Seed yield/plant (g)	71	16.32 %

Cluster V expressed the highest harvest index (40.06%) and the lowest was recorded in cluster IV (26.91%). High oil content observed in cluster VI (46.43) and minimum in cluster V (37.04) and Highest seed yield/plant was recorded in cluster V (9.57 g) and lowest in cluster I (3.63 g). The results suggest that selecting genotypes with high mean values for specific traits within their clusters can be advantageous for hybridization programs aimed at improving those traits. For instance, Cluster V excels in plant height, capsule length, 1000-seed weight, harvest index, and seed yield per plant, while Cluster VI is notable for capsules per plant and oil content. Cluster III has the highest mean values for days to 50% flowering and days to maturity, and Cluster IV stands out for capsule width. The genotypes identified as promising from these clusters, showing high average values for several traits, may be directly employed for adaptation or used as breeding stock for future hybridizations.

The choice will be influenced by the objectives of the breeding programme, particularly in terms of achieving the development of superior transgressive segregants."

To effectively select parents for hybridization from different clusters, it is essential to focus on traits that contribute the most to genetic divergence. Table 4 presents the frequency and percentage contribution of each yield component to genetic divergence. The results show that the 1000 seed weight, which contributed 51.95% and ranked first 226 times, had the greatest impact on genetic divergence. This was followed by Seed yield/plant (16.32%, 71 times), Oil content (15.17%, 66 times), and Days to 50% flowering (7.13%, 31 times). Other significant contributors include Capsule width (5.52%, 24

times), Capsules/plant (2.07%, 9 times), Harvest Index (1.61%, 7 times), Days to maturity (0.23%, 1 times) while Plant height and capsule length (0.00%, 0 times) showed the least variation and contributed minimally to genetic divergence.

4. CONCLUSION

The current study offers insights into the characters and their potential applications in hybridization programs, highlighting that genetic diversity plays a crucial role in generating variability. Cluster analysis grouped thirty genotypes into six clusters which indicates existence of more genetic diversity in the genotypes evaluated.Based on cluster analysis, the highest inter cluster distance was observed between I and IV followed by cluster I and V then cluster IV and VI, therefore crossing between the above-mentioned clusters are likely to produce high heterotic progeny as compared to other clusters. These findings revealed that clusters III and IV as well as V and VI had the most divergence, demonstrating their ability to use genotypes as parents, resulting in a wide range of variability for efficient selection.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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