Genetic diversity analysis in Sesame (*Sesamum indicum* L.)

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 RandomizedBlockDesign (RBD) with three replications.

Place and Duration of Study: Experimentwascarriedoutduring*Rabi*,2023at 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.

Results: Cluster I contained the largest 17 genotypes, followed by Cluster II with 9 genotypes. Clusters III, IV, V, and VI each included only asingle genotype. The highest inter-cluster distance was observed between Cluster I and Cluster IV (25.29), and between 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; MahalanobisD^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 (Hemanth *et al.*2023).

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 (Patel *et al.* 2023).

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. 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 (Rahna et al. 2023).

Sesame, often grown on marginal lands with suboptimal management practices, tends to yield poorly.

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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(Soundharya *et al*, 2017). 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 (Srikanth, 2017).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. MATERIAL AND METHODS

The experiment material consists of 30genetically diverse genotypes of sesame wascarriedoutduring*Rabi*,2023at Niger Research Station, NAU, Vanarasi. Experiment materialobtainedaccessions of sesame supplied by Project Coordinating UnitSesame & Niger, JNKKV, Jabalpur (MP) and Oilseeds Research Station, JAU, Amreli and further evaluated in RandomizedBlockDesign (RBD) with three replications. Recommendedpackageofpracticeswas followedtoraise goodandhealthycropstand.Plantheight,numberofcapsules/plant, capsule width (mm), capsule length (cm), 1000seedweight, harvest index, oil content andseedyield/plant for measure these traits fivecompetitiveplantswererandomlyselected.Daysto50% flowering, days to maturity were notedonplot 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

GeneticdiversitywasstudiedfollowingMahalanobis's(1936)D^2statisticsandclustering of genotypes was done on the basisofD^2 values according to Tocher's method asdescribed by Rao (1952).Statistical analysiswasdonebyINDOSTAT 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(Table1). similar result of formation of six clusters for sesame genotypes also observed by Tripathy *et al.* (2016), Begum *et al.* (2017), Soundharya *et al.* (2017) 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 withinthese clusters.

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

Cluster I and IV (25.29) shown maximum inter cluster distance followedby cluster I and V (24.07), cluster IV and VI(21.95), cluster V and VI (21.62), cluster IandIII(20.49)andcluster IIIandVI(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.Keepingthisinview,itisindicatedthathybridizationbetweenthegenotypeDC-27ofclusterIVwithgenotypeofclusterI;AT-395ofclusterVwithgenotypeofclusterI; DC-27 of cluster IV with AT-393 of cluster VI;A T-395 of cluster V with AT-393ofclusterVI; GT-10 of

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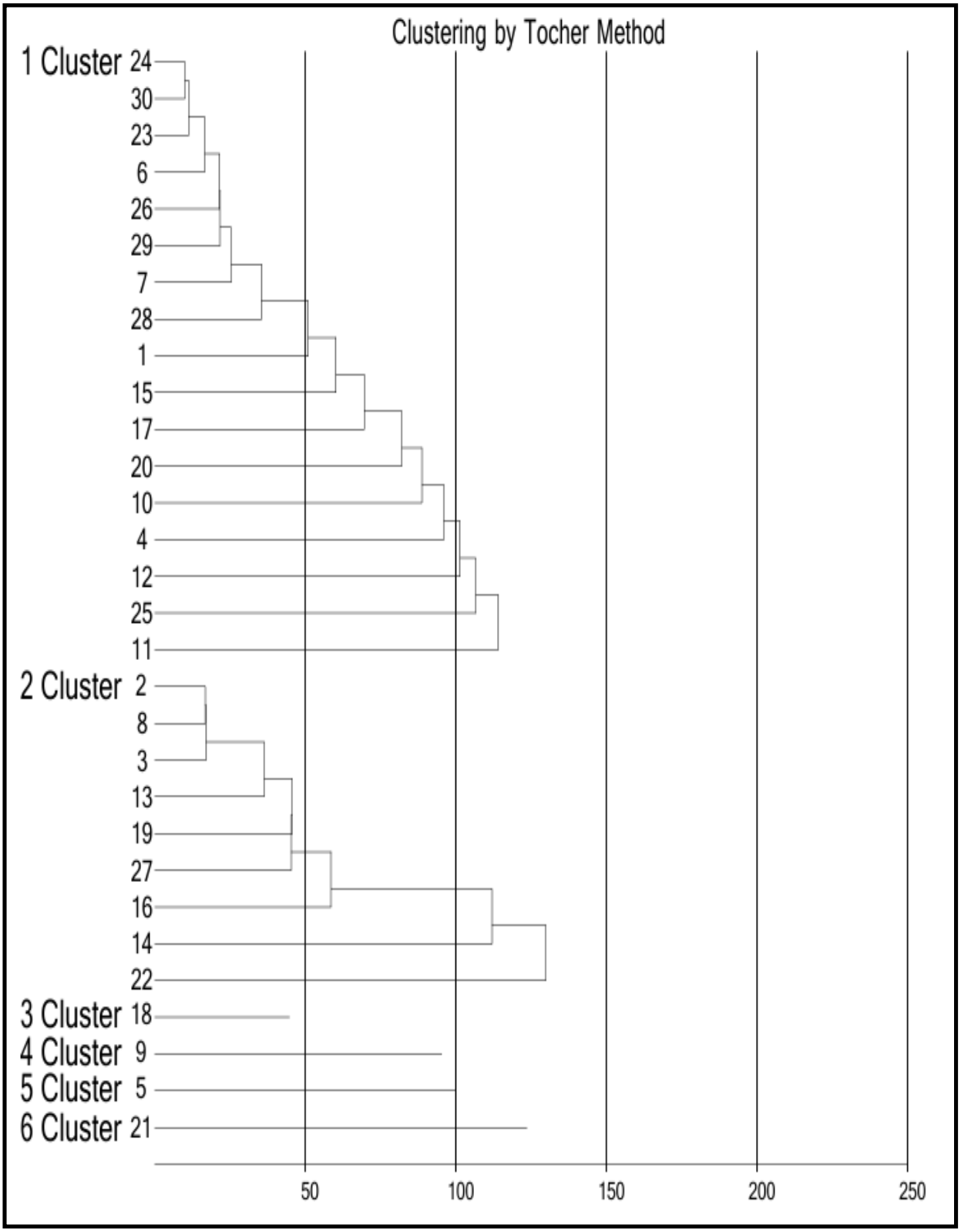
Clustering by Tocher Method
1 Cluster
24
30
23
6
26
29
7
28
1
15
17
20
10
4
12
25
11
2 Cluster
2
8
3
13
19
27
16
14
22
3 Cluster
18
4 Cluster
9
5 Cluster
5
6 Cluster
21
50
100
150
200
250

Fig. 1 dendrogram for 30 sesame genotypes of 10 characters

cluster III with genotype of cluster I; GT-10 of cluster III with AT- 393 of cluster VI areexpectedtoproducehighly heterotichybrids.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.

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

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

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**

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

Bold figures indicate intra cluster values

The dataindicated 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 andlowest means in cluster III (94.33) and IV, VI(87.67),respectively.ClusterVrecordedhighest meanfor plantheight(128.78cm),while lowest was in cluster III (91.13 cm). The number capsules/plant was highest in clusterVI (39.75)andlowestinclusterV(30.25).Cluster IV showed highest capsule width (9.32mm) while in cluster V it was low (6.64 mm).Cluster V and cluster VI had maximum (3.23 cm)andminimum(2.24)clustermeanscapsule length,respectively.Highest1000-seedweightwasrecordedincluster V (3.92 g) and lowest in cluster I(2.66g).

Cluster V expressedthe highestharvestindex(40.06%) andthelowest was recorded in cluster IV (26.91%). High oil content observed in cluster VI (46.43) and minimum in cluster V (37.04) and Highestseedyield/plantwasrecorded in cluster V (9.57 g) and lowest incluster 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

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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.

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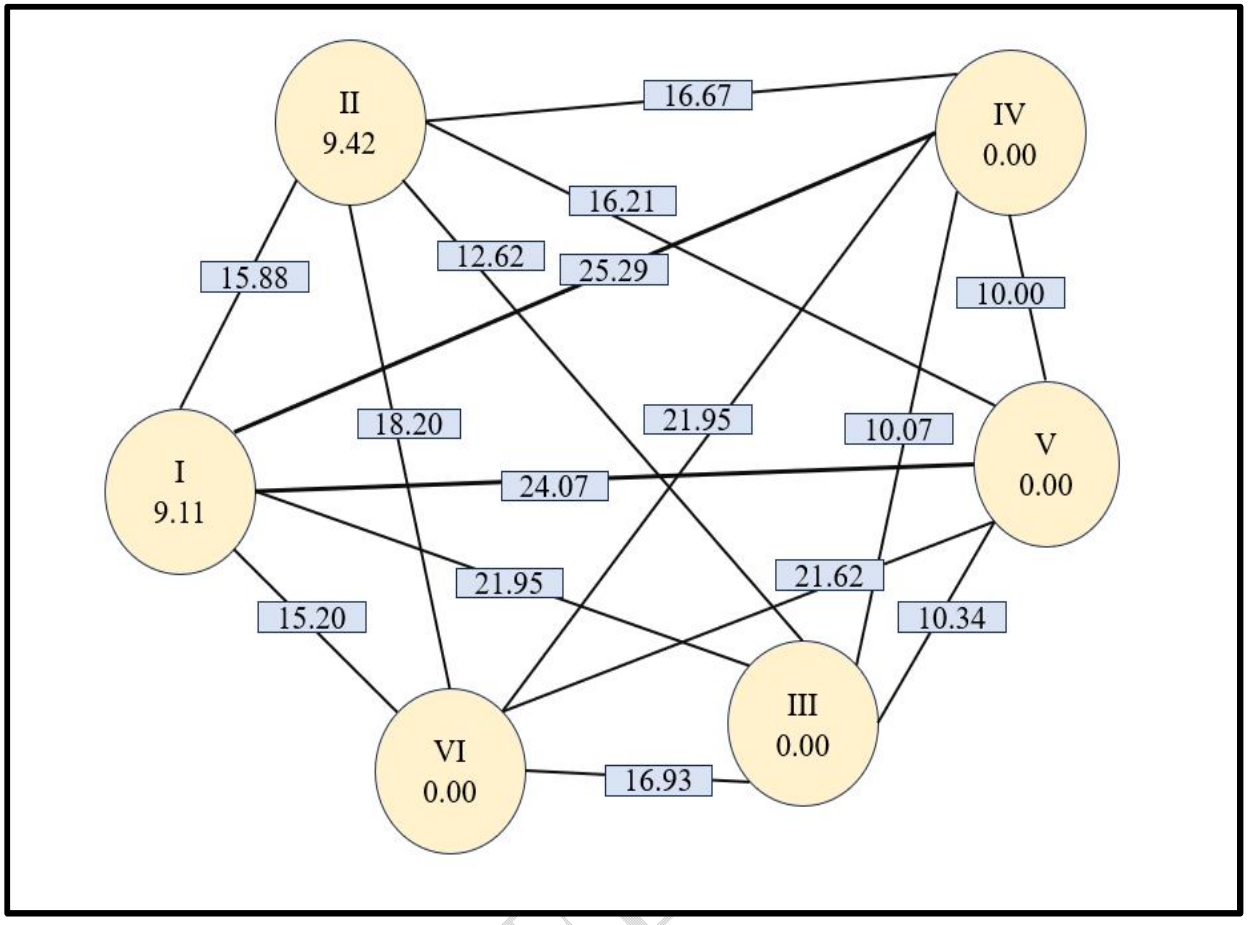

Fig. 2: Cluster diagram based on D2 statistics

Table.3Meanvaluesofclustersfor10characters in62sesamegenotypes(Tocher'smethod)

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

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

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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 %

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) whilePlant 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 diversityin 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.

REFERENCES

Begum, T.; Iqbal, A. and Dasgupta, T. (2017). Genetic variability and divergence among genotypes of sesame (*Sesamum indicum* L.). *Bangladesh J. Bot*., **46**(3): 955-962.

Hemanth, S. and Patil, L. C. (2023). Selection index and genetic variability for morpho-phenological traits in sesame (*Sesamum indicum* L.). *J. Pharma. Innov*., **12**(6): 1880-1883.

Mahalanobis, P.C., 1936. On the Generalizeddistanceinstatistics.ProceedingsofNational Academy of Science India. 2:49-55.

Patel MK, Singh D, Sharma V, Tiwari D, Ola MP, Kumar S et al. Stability Analysis in Sesame (Sesamum indicum L.) under different Doses of Fertilizers. Biol. Forum Int. J. 2023; 15(2):365-70.

Rahna, K.; Kalaiyarasi, R.; Umadevi, M.; Senthil, A. and Sudha, M. (2023). Genetic variability and diversity analysis in sesame (*Sesamum indicum* L.) germplasm. *Electron. J. Plant Breed.*, **14**(3): 1055-1062.

Rao,C.R.,1952.Advancedstatisticalmethodsinbiometricalresearch.JohnWiley and Sons INC., New York. 357-363.

Soundharya, B. H.; TS, V. R. and Edukondalu, B. (2017). Genetic divergence studies in sesame (*Sesamum indicum* L.) genotypes. *Int. J. Curr. Microbiol. Appl. Sci*, **6**(9): 2615-2619.

Srikanth, K. 2017. “Studies on genetic diversity, path analysis and correlation in sesame (Sesamum indicum L.)”. M.Sc. (Agri.) Thesis. College of Agriculture, Latur.

Tripathy, S. K.; Mishra, D. R.; Senapati, N.; Nayak, P. K.; Dash, G. B.; Mohanty, S. K. and Mohanty, M. R. (2016). Assessment of morpho-genetic diversity

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in sesame (*Sesamum indicum* L.). *Int. J. Curr. Agric. Sci.*, **6**(4): 24-28.

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