Received:18 Jul 2022 | Revised: 08 Aug 2022 | Accepted: 28 Sep 2022

Electronic Journal of Plant Breeding

Research Article

Analysis of genetic diversity in sesame (*Sesamum indicum* L.) germplasm for yield and its attributing traits

B. P. Shwetha Yadav[1], V. Thiruvengadam[2]*, R. Sasikala[3] and L. Rajendran[3]

[1]Department of Genetics and Plant Breeding, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
[2]Department of Crop Improvement, AC & RI, Kudumiyanmalai, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
[3]Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore-641 003, Tamil Nadu, India.
***E-Mail:** thirugen@gmail.com

Abstract
The genetic diversity of 50 sesame genotypes was studied by Mahalanobis D^2 statistics. By using Tocher's method, genotypes were grouped into nine clusters based on 10 economically important traits *viz.,* days to flowering, days to 50% flowering, days to maturity, plant height, the number of primary branches, the number of secondary branches, the number of capsules per plant, the number of seeds per capsules, thousand seed weight and single plant yield. The largest intercluster distance among the nine clusters was found between clusters I and VIII, indicated that they were significantly more diverse and clusters IV and VI showed the lowest intercluster distance indicating that the genotypes under these clusters are closely related. The cluster with the highest cluster mean was found in cluster VIII for the number of capsules per plant, the number of primary and secondary branches, the number of seeds per capsule and single plant yield and cluster V for plant height and cluster VII for thousand seed weight. Taking into account the highest cluster mean for a trait, genotypes could be selected as parents in the hybridization program to create superior cross combinations.

Keywords : Genetic diversity, Cluster, Germplasm, Sesame, D^2 analysis

INTRODUCTION

Sesame (*Sesamum indicum L.*), is an annual diploid species with a chromosome number of 2n=26. Among the 36 species of genus *Sesamum* belonging to the Family Pedaliaceae, *Sesamum indicum* L. is the only cultivated species (Joshi, 1961). Sesame is one of the ancient oilseed crops and it is grown in various tropical and subtropical regions of the world. The archaeological remnants of charred sesame suggested that sesame was domesticated and used in India for more than 5000 years and has its roots in India (Were *et al*., 2006). Sesame is commonly known as the "Queen of oilseeds" because of its resistant to oxidative deterioration and rancidity as compared to other edible oils due to the presence of compounds like lignans mainly sesamin, sesamolin, sesamol and γ-tocopherol (Fukuda *et al*., 1986). Sesame is also well-known for its medicinal benefits, which include lowering blood pressure, cholesterol and the incidence of cancer in humans (Were *et al*., 2006).

The chemical composition of sesame consists of oil (50 – 60 %), protein (18 – 25 %), carbohydrates (13.5 %) and ash (5 %) (Anilakumar *et al*., 2010). In seeds of sesame, oil content ranges from 40 to 63 per cent and

contains significant amounts of oleic and linoleic acids (Abate and Mekbib, 2015). India occupies a 15.2 lakh ha area, despite having a large area, India owing to its poor national productivity (431 kg/ha) compared to the world average (512 kg/ha) (FAO Statistics, 2020). Despite being an important oilseed crop in India, productivity was lowered by several factors like non availability of varieties or hybrids for different agroclimatic conditions, low yield of existing varieties, low oil content of currently available varieties, lack of varieties resistance to different pests and diseases, susceptibility of the crop to uncertain rains and nonsynchronous maturity in available varieties. The effective use of the genetic diversity present in the sesame germplasm is one of the solutions to the problems mentioned above. The availability of genetic variation in any crop is the cornerstone of crop improvement. For the purpose of developing various breeding strategies for crop improvement, it is crucial to understand the kind and extent of genetic diversity in a crop. Assessment and identification of diverse parents having desired traits are easy with the help of Mahalanobis D^2 statistics (Mahalanobis, 1936). Once the parents had been determined, hybridization may be carried out to transfer the desired qualities to the cultivars already in existence and develop improved varieties. Keeping these points into consideration, the present study was carried out to assess the genetic diversity among 50 sesame genotypes for ten quantitative traits.

MATERIALS AND METHODS

A total of 50 sesame germplasm accessions were collected from the Department of Plant Genetic Resources, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu and used for diversity analysis. The experiment was carried out during *Rabi/Summer* 2021-22 on the research field of the Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. The experimental layout followed was Randomized Block Design (RBD) with two replications wherein each genotype was sown with a spacing of inter-row 30 cm and intra row 30 cm. The crop was raised with all the recommended package of practices and necessary preventive measures were taken against pests (leaf webber and leafhopper) and diseases (phyllody, wilt and powdery mildew). Biometrical observations were taken with five randomly selected plants in each germplasm line for 10 quantitative traits namely days to flowering (days), days to 50% flowering (days), plant height (cm), the number of primary branches, the number of secondary branches, days to maturity (days), the number of capsules per plant, the number of seeds per capsules, thousand seed weight (g) and single plant yield (g). The data was subjected to genetic diversity analysis by using Mahalanobis D^2 statistics (Mahalanobis,1936) and the grouping of genotypes into various clusters was carried out utilising Tocher's method. (Rao, 1952) using INDOSTAT software.

RESULTS AND DISCUSSION

Based on the ten phenotypic characters, the replicated data of each biometrical trait for the 50 sesame genotype was subjected to analysis of variance (ANOVA), which showed that genotypes differed significantly from one another for all traits indicating the existence of diversity among the genotypes studied.

Clustering analysis based on Tocher's method grouped the 50 sesame germplasm into nine clusters. The genotype distribution into different clusters was presented in **Table 1**. A similar kind of analysis was done in *Sesamum* by Sirisha *et al*. (2020), Arpitha *et al.* (2019) and Tanwar and Bisen (2018). As per the diversity analysis, with 20 genotypes, cluster II was the largest, followed by cluster I with 16 genotypes and cluster VI with seven genotypes, cluster VIII with two and remaining all clusters *viz*., III, IV, V, VII and IX comprising of one genotype each.

The intra-cluster and inter-cluster D^2 and D values were represented in **Table 2**. The maximum inter-cluster distance was found between clusters I and VIII (48.57),

Table 1. The distribution of 50 sesame germplasm lines into nine clusters

Clusters	Number of germplasm	Name of germplasm
I	16	SI-889, IS-25, ORM-17, SI-112, KMR-108, TKG-97, ES-3707, SI-490, ES-13, 175, AST-5, TVS-1604, NIC-8509, SI-2334, PS-5, SI-1885
II	20	SI-987/1, DCT-15, TVS-1606, NIC-9984, IS-366, SI-3099, SI-983/1, G-53, SI-3171, MADHAVI-NC-2, ESN-32, JLS-57, SI-3178, VRI 2, SI-961/2, IS-366, SO-453, EO-63, SI-1146, GENE-9301.
III	1	GSK-24
IV	1	SI-17574
V	1	DPI-15-25
VI	7	SI-702, SI-801, SI-328, ACU-2, GUN-18, SI-1260, SI-4721
VII	1	IC-131651
VIII	2	OMT-21, KMS-4343
IX	1	SI-97

Table 2. Average intra and inter-cluster $D^2$and D values for different clusters

	I	II	III	IV	V	VI	VII	VIII	IX
I	122.10 (11.05)	327.97 (18.11)	193.48 (13.91)	739.29 (27.19)	210.25 (14.05)	904.20 (30.07)	262.44 (16.2)	2359.04 (48.57)	407.23 (20.18)
II		134.56 (11.6)	249.64 (15.08)	252.17 (15.88)	269.61 (16.42)	364.04 (19.08)	298.25 (17.27)	1283.78 (35.83)	307.65 (17.54)
III			0	458.38 (21.41)	311.17 (17.64)	549.43 (23.44)	448.59 (21.18)	1756.44 (41.91)	412.09 (20.30)
IV				0	750.76 (27.40)	115.13 (10.73)	570.25 (23.88)	556.01 (23.58)	305.55 (17.48)
V					0	915.66 (30.26)	294.12 (17.15)	2322.27 (48.19)	620.01 (24.90)
VI						170.04 (13.04)	769.50 (27.74)	526.24 (22.94)	445.21 (21.10)
VII							0	1943.98 (44.09)	211.41 (14.54)
VIII								100.80 (10.04)	1274.49 (35.70)
IX									0

followed by clusters V and VIII (48.19), clusters VII and VIII (44.09), clusters III and VIII (41.91) and clusters II and VIII (35.83). Therefore, to exploit higher heterosis and to create superior cross combinations, sesame breeders may choose the genotypes between clusters I and VIII to serve as parents during the hybridization program because of the presence of large diversity. The present study showed that the genotypes namely SI-889, IS-25, ORM-17, SI-112, KMR-108, TKG-97, ES-3707, SI-490, ES-13, 175, AST-5, TVS-1604, NIC-8509, SI-2334, PS-5 and SI-1885 of cluster I and genotypes OMT-21 and KMS-4343 of cluster VIII can be used in hybridization for the exploitation of heterosis. Similar results were obtained by Tanwar and Bisen (2018) and Tripathi *et al.* (2013). The minimum inter-cluster distance was found between clusters IV and VI (10.73) followed by clusters I and III (13.91) indicating that genotypes included in these clusters are closely related. The maximum intra-cluster distance found in cluster VI (13.04) demonstrated that the genotypes within each of this cluster still showed some genetic diversity. The characters with maximum mean value may be used to execute selection within these clusters.

The cluster mean value of ten biometrical traits was listed in **Table 3**. This demonstrated that there was enough variation among ten quantitative traits. The maximum mean value for days to flowering and days to 50% flowering (43.50, 45.50) was found in cluster V followed by cluster II (38.85, 42.15) and the minimum cluster mean value for days to flowering and days to 50% flowering was observed in cluster III (34.50, 36.00). Hence, for the breeding of early flowering genotypes, the genotypes lying in cluster III could be used as a parent

Table 3. Cluster mean of ten biometrical traits in 50 sesame germplasm lines

	Days to flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of capsules per plant	Number of seeds per capsule	Single plant yield (g)	Thousand seed weight (g)
Cluster I	36.50	39.34	87.44	112.32	3.59	2.15	57.14	61.63	5.4	1.26
Cluster II	38.85	42.15	90.93	141.36	3.96	3.14	85.77	58.60	9.14	1.24
Cluster III	34.50	36.00	87.00	101.59	4.20	1.20	58.00	63.60	8.38	1.27
Cluster IV	38.50	43.00	86.50	134.31	5.20	5.40	110.20	61.60	12.82	1.25
Cluster V	43.50	45.50	96.50	164.19	3.70	3.20	56.80	54.80	5.67	1.25
Cluster VI	37.79	40.64	90.07	121.20	4.11	3.60	114.19	60.54	13.18	1.24
Cluster VII	36.50	41.50	83.50	128.82	4.40	3.20	87.30	49.60	6.05	1.33
Cluster VIII	38.00	40.50	91.50	146.68	5.61	5.91	171.13	64.61	18.37	1.29
Cluster IX	35.50	39.00	83.50	91.70	4.30	4.10	110.60	65.20	8.35	1.25

Table 4. The relative contribution of ten biometrical traits towards total genetic diversity in sesame

S. No.	Characters	Number of the first ranks	Per cent contribution
1	Days to flowering	27	2.20
2	Days to 50% flowering	0	0.00
3	Days to maturity	12	0.98
4	Plant height	98	8.00
5	Number of primary branches	33	2.69
6	Number of secondary branches	20	1.63
7	Number of capsules per plant	355	28.98
8	Number of seeds per capsule	54	4.41
9	Thousand seed weight	9	0.73
10	Single plant yield	617	50.37
	Total	**1225**	**100**

for the development of short duration varieties. Cluster V (96.50) showed the highest mean for days to maturity, followed by cluster VIII (91.50) and the lowest cluster mean for days to maturity was 83.50 in cluster VII and cluster IX. Therefore, parents from clusters VII and IX could be used to create hybrids for early maturity. Cluster V (164.19 cm) showed the highest cluster mean for plant height, followed by cluster VIII (146.68 cm) and the lowest cluster mean for plant height was 91.70 cm in cluster IX. As plant height is one of the significant yield-contributing factors, the genotypes belonging to clusters V and VIII could be used in the breeding programme. As the number of primary and secondary branches play an important role to realize the expected yield, the genotypes belonging to cluster VIII having the highest mean (5.61, 5.91) can be used as parents for hybridization.

The highest cluster mean value for the number of capsules per plant was observed in cluster VIII (171.13), followed by cluster VI (114.19) and the lowest cluster mean for the number of capsules per plant was 56.80 in cluster V. The highest cluster mean for the number of seeds per capsule was observed in cluster IX (65.20), followed by cluster VIII (64.61) and the lowest cluster mean for the number of seeds per capsule was 49.60 in cluster VII. For the improvement of yield, the cluster which is having highest mean for the number of capsules per plant and the number of seeds per capsule i.e. cluster VIII could be utilized. The highest mean for single plant yield was observed in cluster VIII (18.37 g), followed by cluster VI (13.18 g) and the lowest mean observed in cluster I (5.40 g). The highest mean for thousand seed weight was found in cluster VII (1.33 g) and the lowest in clusters II and VI. Hence, for the improvement of yield, genotypes representing cluster VIII for single plant yield and cluster VII for thousand seed weight can be used as donor sources for exploitation of heterosis.

Per cent contribution of ten quantitative traits towards genetic divergence was shown in **Table 4.** In the present study, single plant yield (50.37 %) contributed more towards the genetic divergence with 617 of ranking first followed by the number of capsules per plant (28.98 %) by 355 times and plant height (8.00 %) by 98 times. Moderate to low contribution was exhibited by the number of seeds per capsule, the number of primary branches, days to flowering, the number of secondary branches, days to maturity, thousand seed weight and days to 50% flowering.

The current study has provided information about 10 quantitative characters contributing toward genetic divergence among 50 sesame genotypes and their possible use in hybridization programs for the exploitation of heterosis. Among the nine clusters, the genotype of clusters I and VIII can be used as parents in crossing as it exhibits the highest inter-cluster distance. For breeding early maturing varieties, genotypes from clusters VII and IX may be used. For breeding early flowering genotypes, cluster III can be selected as it exhibits the least cluster mean for this trait. To improve the seed yield, breeders can select genotypes lying in cluster VIII. To improve the yield, genotypes having the highest mean from different clusters for yield contributing traits such as the number of capsules per plant, the number of primary and secondary branches, seeds per capsule and single plant yield from cluster VIII and plant height from cluster V, cluster VII for thousand seed weight can be utilized. Hence, for the improvement of any traits, genotypes should be selected from clusters possessing the highest intercluster distances with the highest cluster mean for desirable traits.

REFERENCES

Abate, M. and Mekbib, F. 2015. Study on genetic divergence in low-altitude sesame (*Sesamum indicum* L.) germplasm of Ethiopia based on agro morphological traits. J. *Adv. Studies in Agri. Biol. Environ. Sci.*, **2**(3): 78-90.

Anilakumar, K. R., Pal, A., Khanum, F. and Bawa, A. S. 2010. Nutritional, medicinal and industrial uses of sesame (*Sesamum indicum* L.) seeds – an overview. *Agric. Conspec. Scientificu,* **75** (4)**:**159-168.

Arpitha, G. D., Manonmani, S., Viswanathan, P. L. and Raveendran, M. 2019. Genetic diversity study in germplasm lines of sesamum (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, **10**(2): 772-777. [Cross Ref]

Food and Agricultural Organisation. QCL Crops and livestock products 2020. Available from: https://www.fao.org/faostat/en/#data/QCL

Fukuda, Y., Nagata, M., Osawa, T. and Namiki, M. 1986. Contribution of lignan analogues to antioxidative activity of refined unroasted sesame seed oil. J. *Am. Oil Chem. Soc.,* **63**:1027–1031. [Cross Ref]

Joshi, Amarchaud B., Narayanan, E. S. and Vasudeva, R. S. "Sesamum." *Sesamum.* 1961.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. Procurement National Institute Science, India, **2**: 49- 55.

Rao, C.R. 1952. Advanced statistical methods in Biometric Research, John Wiley & Sons, Inc., New York. Pp. 357-363.

Sirisha, A. B. M., Banu, S. H. and Saritha, R. 2020. Genetic divergence studies using Mahalanobis D square analysis in sesame (*Sesamum indicum* L.) Germplasm. *Int. J. Curr. Microbiol. App. Sci*, **9**(8): 2224-2229. [Cross Ref]

Tanwar, A. and Bisen, R. 2018. Genetic diversity analysis in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *Electronic Journal of Plant Breeding*, **9**(1): 9-17. [Cross Ref]

Tripathi, A.N.J.A.Y., Bisen, R.A.J.A.N.I., Ahirwal, R.P., Paroha, S., Sahu, R. and Ranganatha, A.R.G., 2013. Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *The bioscan*, **8**(4):1387-1391.

Were, B. A., Onkware, A. O., Gudu, S., Welander, M. and Carlsson, A. S. 2006. Seed oil content and fatty acid composition in East African sesame (*Sesamum indicum* L.) accessions evaluated over 3 years. *Field Crops Research,* **97**:254–260. [Cross Ref]