Int.J.Curr.Microbiol.App.Sci (2020) *9*(12): 884-893

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 9 Number 12 (2020)**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2020.912.106

Genetic Diversity Studies in Sesamum

Rohini Y. Patil*, K. K. Barhate, B. A. Tagad and V. S. Girase

Botany Section, College of Agriculture, (M. S.), Dhule, India

**Corresponding author*

Keywords

Genetic diversity, Cluster distance, Sesame

Article Info

Accepted:
10 November 2020
Available Online:
10 December 2020

A B S T R A C T

Genetic Diversity Studies in Sesamum was carried for forty-two genotypes to study the nature and extent of genetic diversity for the characters *viz;* days to 50 % flowering, days to maturity, plant height at maturity (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight (g), oil content (%) and seed yield per plant (g). Analysis of variance revealed significant difference among the genotypes for all the characters. Based on D^2 value, the genotypes were grouped into nine clusters indicating wider genetic diversity in the germplasm collections of Sesamum from different geographical origin. Characters, plant height at maturity (48.03 %) contributed more in genetic divergence. Which was followed by number of capsules per plant (13.82 %), oil content (10.69 %), days to 50% flowering (9.06 %), seed yield per plant (5.87) and number of branches per plant (5.57 %) as main characters contributing to the genetic divergence in present material. The clustering pattern suggested that the genotypes of the same origin were distributed into different clusters indicating the absence of parallelism between clustering and geographical distribution. These genotypes were distinct and diverse and can be classified as promising genotypes. Inter-crossing among them would lead to upgrade base in the base population and opportunities for obtaining the high heterotic effect and also to recover desirable transgressive segregents and wide spectrum of variability in subsequent generations. Maximum inter-cluster distance was noticed between cluster VII and VIII (D^2=9.71).

Introduction

Sesame (*Sesamum indicum* L.) is probably the most ancient oilseed known and used by man its domestication is lost in the midst of antiquity The genus *Sesamum* belongs to the order tubiflorea, family pedaliaceae which consist of sixteen genera and sixty species, but only *Sesamum indicum* (2n=26) has been recognized as cultivated species *Sesamum indicum* L. which is known variously as sesamum, til, gingelly, sissim, gergelim etc. Sesamum is a self-pollinated crop.

Sesame seed is rich in oil, protein, carbohydrate, fibre and minerals. Sesamum is an important source of edible oil and is widely used in food products especially in bakery foods and animal feed. Sesamum seed contains 40-64 % oil and 25% protein with antioxidants lignins such as sesamolin and sesamin. Sesamum is better known as "Queen of Oilseeds".

Total area of sesamum in India is 19.51 lakh ha and production 8.50 lakh tons and productivity 436 (kg/ha). In Maharashtra, it is grown on area of 0.17 lakh ha with production of 0.038 lakh tons and productivity of 223 kg/ha.

The genetic diversity is a crucial factor in determining the success of hybridization programme and its important in crop improvement has long been recognized by breeder. The more diverse parents within overall limit of fitness, the greater are the chances of heterotic F_1's and broad spectrum of variability in segregating generation (Arunachalam, 1981; Falconer, 1989). Therefore, the first step in any crop breeding programme is to access genetic variability. Yield and yield contributing characters are controlled by polygene and highly influenced by environment; the exploration of genetic variability in available germplasm is prerequisite. Therefore, evaluation of germplasm to local conditions is very important.

Genetic diversity is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding. Genetic diversity is very important factor for any hybridization programme aiming at genetic improvement of yield especially in self-pollinated crops. Different methods have been used to assess genetic diversity, of which Mahalanobis's (1936) D^2statistic is the most efficient tool for estimating genetic divergence. Genetic diversity plays important role, because hybrids between closely related parents.

Materials and Methods

The experimental material comprising forty two genotypes of sesame were grown in Randomized Block Design with three replications at the research farm of Botany, College of Agriculture, Dhule, during *Kharif* season of 2019. Each entry was represented by single row of 4.5 meter length with spacing of 30 cm between the rows and 15 cm between the plants. Data were recorded on five randomly and competitive plants of each genotype from each replication for nine characters *viz*., days to 50% flowering, days to maturity, plant height at maturity (cm), number of branches per plant, number of capsules per plant, number of seeds per capsule, 1000 seed weight (g), oil content (%) and seed yield per plant (g). The mean of five plants was subjected to statistical analysis. The data for different characters were statistically analyzed for significance by using analysis of variance technique described by Panse and Sukhatme (1995). The analysis of divergence was carried out by D^2 statistic of Mahalnobis (1936) as described by Rao (1952). All D^2 values are arranged in matrix form, based on the degree of divergence (D^2 values) between any two genotypes. A logical grouping of genotypes was done following Tocher's method (Rao, 1952). The possible limits to parental divergence within which there were reasonably high chances for occurrence of heterosis were calculated following Arunachalam and Bandopadhyaya (1984). They advised to delineate the divergence among parents into four divergence classes (DC).

Results and Discussion

Plant breeding deals with the management of genetic variability. Hence, the presence of genetic variability in the available germplasm of a crop is of immense value to design a selection procedure and to identify the superior genotypes. It is, therefore, necessary to classify and utilize this variability systematically for genetic up-gradation of biological population (Table 1–9).

Table.1 Mean performance of forty-two genotypes for nine different characters in Sesamum

Sr.No.	Genotypes	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	No. of branches/ plant	No. of capsules/plant	No. of seeds/capsule	1000 seed weight (g)	Seed yield/plant (g)	Oil content (%)
1	DHS-1	47.33	103.33	84.33	2.23	36.23	43.46	3.06	5.93	49.16
2	DHS-2	45.33	103.66	94.86	2.43	52.36	47.86	3.20	7.40	47.76
3	DHS-3	43.66	102.66	102.46	3.10	35.23	52.43	3.06	6.49	48.66
4	DHS-4	46.00	102.33	118.30	3.16	47.63	47.23	3.43	8.48	44.33
5	DHS-5	46.66	103.00	151.66	3.20	57.43	52.70	2.96	9.92	46.80
6	DHS-6	47.00	104.00	167.16	2.56	32.53	50.23	3.16	6.61	44.13
7	DHS-7	44.33	104.00	90.20	1.96	34.96	47.93	2.83	5.79	45.40
8	DHS-8	44.33	103.33	123.86	3.06	47.36	45.73	2.93	6.55	50.16
9	DHS-9	45.66	103.00	107.53	2.63	44.16	50.36	3.13	8.05	51.86
10	DHS-10	47.33	102.66	84.46	2.00	23.63	44.30	3.20	6.05	44.30
11	DHS-11	42.33	101.66	69.66	2.73	47.70	43.26	2.96	7.71	52.36
12	DHS-12	45.33	103.33	74.16	2.00	33.43	48.73	2.63	5.54	46.00
13	DHS-13	47.33	101.66	84.00	2.50	41.70	46.93	2.66	6.87	46.33
14	DHS-14	47.33	101.66	89.66	2.26	34.63	49.23	3.10	6.32	33.46
15	DHS-15	41.66	103.00	85.33	2.16	36.46	47.30	2.83	6.28	49.70
16	DHS-16	45.00	102.00	164.93	2.70	46.76	51.03	3.06	8.25	46.60
17	DHS-17	40.66	101.00	83.50	2.00	36.96	48.60	2.73	8.20	47.63
18	DHS-18	42.00	102.33	101.33	2.83	55.86	50.40	3.10	9.59	49.00
19	DHS-19	41.00	103.33	149.80	2.83	48.96	52.03	2.80	8.30	45.36

Table.1 Contd…

20	**DHS-20**	**41.00**	**103.33**	**168.70**	**2.46**	**36.60**	**48.40**	**2.66**	**6.42**	**45.30**
21	DHS-21	44.33	105.33	103.93	2.60	42.43	45.00	3.20	7.08	49.56
22	DHS-22	47.66	108.00	94.93	2.03	38.60	53.00	2.70	7.43	51.46
23	DHS-23	47.00	108.66	118.00	3.16	55.40	54.06	2.80	9.09	48.96
24	DHS-24	47.66	102.33	90.20	2.73	48.00	51.23	2.90	8.24	45.90
25	DHS-25	47.00	105.00	63.60	2.36	37.20	48.66	2.90	6.49	45.20
26	DHS-26	47.33	106.33	107.76	2.03	47.46	45.43	3.13	7.64	51.73
27	DHS-27	46.66	107.33	110.33	3.16	46.46	51.03	3.23	8.64	52.43
28	DHS-28	46.66	104.00	127.40	2.93	53.43	49.50	2.96	8.82	46.66
29	DHS-29	42.33	102.33	75.33	3.03	43.20	49.66	2.73	6.96	46.00
30	DHS-30	41.33	106.00	77.90	2.63	47.40	51.20	2.96	8.50	44.86
31	DHS-31	46.33	108.33	105.96	2.40	36.93	43.06	3.00	6.07	46.10
32	DHS-32	47.00	105.33	95.50	2.63	47.50	49.16	2.90	7.92	45.86
33	DHS-33	43.00	103.00	117.43	3.33	47.46	56.60	3.00	9.57	50.20
34	DHS-34	41.33	109.66	94.90	2.36	40.96	49.40	3.16	7.70	46.60
35	DHS-35	48.00	105.00	101.70	2.80	50.63	54.76	3.16	9.67	46.33
36	DHS-36	42.66	104.00	165.40	3.36	52.13	50.46	3.06	8.93	45.66
37	DHS-37	41.00	101.66	91.06	3.40	50.66	46.10	2.96	8.63	49.40
38	DHS-38	44.66	105.33	95.90	2.43	40.96	54.20	2.90	7.28	51.06
39	DHS-39	48.00	102.66	97.93	2.23	38.53	50.50	2.93	6.86	47.23
40	DHS-40	43.00	104.00	94.33	2.26	39.26	50.10	3.10	7.02	47.00
41	JLT-408	43.00	105.00	121.43	2.96	56.23	51.33	3.13	8.16	48.56
42	JLT-7	44.00	106.00	127.26	3.10	60.10	50.66	3.10	8.11	49.40
	G Mean	**44.79**	**104.06**	**106.52**	**2.63**	**44.13**	**49.36**	**2.98**	**7.61**	**47.39**
	S.E (±)	**0.869**	**1.076**	**3.465**	**0.169**	**2.04**	**1.95**	**0.089**	**0.377**	**2.287**
	C.D at 5 %	**2.445**	**3.029**	**9.749**	**0.476**	**5.739**	**5.486**	**0.250**	**1.060**	**6.435**
	C .V. (%)	**3.36**	**1.79**	**5.63**	**11.12**	**8.00**	**9.84**	**5.16**	**8.57**	**8.36**

Table.2 Analysis of variance for different characters in sesamum

Sr. No.	Characters	Mean sum of square		
		Replication	Genotype	Error
1	Days to 50% flowering	5.746	17.202**	2.266
2	Days to maturity	6.698	13.093**	3.478
3	Plant height at maturity (cm)	4.055	2240.86**	36.025
4	Number of branches per plant	0.517	0.541**	0.086
5	Number of capsules per plant	15.827*	191.632**	12.485
6	Number of seeds per capsule	18.448	29.926*	11.407
7	1000 seed weight (g)	0.081	0.097**	0.023
8	Seed yield per plant (g)	0.447	4.090**	0.426
9	Oil content (%)	20.430	34.387*	15.699

*, ** Indicates significance at 5% and 1% level, respectively

Table.3 Grouping of forty-two Sesamum genotypes into different clusters

Sr. No.	Cluster	No. of genotypes	Name of genotypes
1	I	10	JLT-408, JLT-7, DHS-28, DHS-23, DHS-33, DHS-27, DHS-4, DHS-35, DHS-9, DHS-18.
2	II	16	DHS-24, DHS-32, DHS-2, DHS-38, DHS-21, DHS-40, DHS-39, DHS-22, DHS-26, DHS-13, DHS-31, DHS-7, DHS-1, DHS-3, DHS-15, DHS-14.
3	III	1	DHS-12
4	IV	1	DHS-17
5	V	5	DHS-11, DHS-29, DHS-30, DHS-37, DHS-25.
6	VI	1	DHS-34
7	VII	6	DHS-16, DHS-36, DHS-19, DHS-5, DHS-20, DHS-6.
8	VIII	1	DHS-10
9	IX	1	DHS-8

Table.4 Average intra and inter-cluster distance (D^2 values) for nine characters in sesamum

Clusters	I	II	III	IV	V	VI	VII	VIII	IX
I	2.83	4.58	6.84	5.58	5.53	4.72	5.84	7.25	3.45
II		2.94	3.67	3.55	4.11	3.66	7.60	4.22	3.89
III			0.00	3.10	4.15	4.68	9.70	3.11	5.76
IV				0.00	3.19	3.64	8.74	4.28	5.14
V					3.15	3.92	9.47	5.37	5.51
VI						0.00	8.17	5.06	4.91
VII							3.75	9.71	4.96
VIII								0.00	6.26
IX									0.00

(Underlined figures indicate intra-cluster D^2 values)

Table.5 Cluster means of forty-two genotypes for nine characters in Sesamum

Sr. No.	Characters	Clusters									Average
		I	II	III	IV	V	VI	VII	VIII	IX	
1	Days to 50% flowering	45.20	45.81	45.33	40.67	42.80	41.33	43.89	47.33	44.33	44.07
2	Days to maturity	104.67	104.23	103.33	101.00	103.33	109.67	103.28	102.67	103.33	103.94
3	Plant height at maturity (cm)	115.07	94.23	74.17	83.50	75.51	94.90	161.28	84.47	123.87	100.77
4	No. of branches per plant	3.01	2.38	2.00	2.00	2.83	2.37	2.86	2.00	3.07	2.50
5	No. of capsules per plant	51.74	40.69	33.43	36.97	45.23	40.97	46.07	23.63	47.37	40.67
6	No. of seeds per capsule	51.60	48.55	48.73	48.60	47.78	49.40	50.81	44.33	45.73	48.39
7	1000 seed weight (g)	3.11	2.97	2.63	2.73	2.91	3.17	2.96	3.20	2.93	2.95
8	Oil content (%)	48.78	47.28	46.00	47.63	47.57	46.60	45.64	44.30	50.17	47.10
9	Seed yield per plant (g)	8.82	6.92	5.54	8.20	7.66	7.70	8.08	6.06	6.56	7.28

Table.6 Relative per cent contribution of different characters towards total genetic divergence in sesamum

Sr. No.	Characters	Times ranked 1st	Per cent contribution
1	Days to 50% flowering	78	9.06
2	Days to maturity	26	3.02
3	Plant height at maturity (cm)	448	52.03
4	Number of branches per plant	48	5.57
5	Number of capsules per plant	119	13.82
6	Number of seeds per capsule	17	1.97
7	1000 seed weight (g)	17	1.97
8	Seed yield per plant (g)	16	1.86
9	Oil content (%)	92	10.69
	TOTAL	**861**	**100**

Table.7 Divergence classes

	DC 4	DC 3	DC 2		DC 1
↓	↓	↓		↓	↓
X	m-s	m		m+s	Y
(2.83)	(3.48)	(4.57)		(5.66)	(9.70)

Table.8 Distribution of different clusters combinations into four divergence classes based on D^2 values between them. (Cluster combinations)

	Y (9.70)
DC 1	(I,III), (I,VII), (I,VIII), (II,VII), (III,VII), (III,IX), (IV,VII), (V,VII),(VI,VII),(VII,VIII), (VIII,IX)
	m+s (5.66)
DC 2	(I,II), (I,IV), (I,V), (III,VI),(IV,IX), (V,VIII), (VI,IX), (VI,VIII), (VI,IX), (VII,IX)
	m (4.57)
DC 3	(I,IX), (II,III), (II,IV), (II,V), (II,VI), (II,VIII), (II,IX), (III,V), (IV,VI), (IV,VIII), (V,VI), VII,VII)
	m-s (3.48)
DC 4	(I,I), (II,II),(III,IV), (III,VII), (IV,V), (V,V)
	X (2.83)

Table.9 Characters improvement on the basis of source clusters

Sr. No.	Characters	Source Clusters
1	Days to 50 % flowering (Early)	IV,VI,V
2	Days to maturity (Early)	IV,VIII,VII,III,V
3	Plant height at maturity (cm) (Tall and Dwarf)	VII,IX,I
4	Number of branches per plant (Maximum)	IX,I,VII,V
5	Number of capsules per plant (Maximum)	I,IX,VII,V
6	Number of seeds per capsule (Maximum)	I,VII,VI,III,II
7	1000 seed weight (Maximum)	VIII,VI,I,II
8	Oil content (Maximum)	IX,I,IV,V,II
9	Seed yield per plant (Maximum)	I,IV,VII,V

Genetic divergence which is due to genetic factors is the basis for heritable improvement. The plant breeders have always therefore been fascinated by great amount of diversity in crop plants. The precise information about the genetic divergence therefore, is crucial for effective breeding programme.

The genetically diverse parents are known to produce high heterotic effects and consequently gives desirable recombinants in the breeding material or wide spectrum of transgressive segregants in segregating generations. Hence, the systemic management

of plant genetic resources is very important to augment productivity of sesamum.

The Mahalanobis D^2 statistics are computed for all possible pair of forty-two genotypes in order to assess the genetic diversity present among the genotypes under study. Wilk's criterion showed the significant differences between the genotypes for the pooled effect of nine characters (Wilk's criteria $X^2 = 13241.45$ at 390 df.) hence further analysis was carried out to calculate the D^2 values. The calculated D^2 values ranged from 2.015 (DHS-32) to 289.463 (DHS-7) based upon the observation of nine characters.

In the present study, the genotypes belonging to the same geographical region or same location fall into different clusters and accordingly these clusters were separated by high genetic distances.

Hays and Johansson (1939) and East and Hays (1942) obtained maximum heterosis from crosses between diverse parent than those between closely related ones. Bhatt (1970) advocated the use of multivariate analysis for the selection of parents. He also stated that statistical distance of all possible cluster combination may be considered arbitrarily as a guideline and suggested that it would be logical to effect crosses between genotypes belonging to cluster separated by high estimated statistical distance.

Grouping of cluster pairs into the divergence class (DC) are presented in Table 8. In the light of discussion, initial choice of parents should be made from the cluster combinations falling in the divergence classes DC2 and DC3. While crossing among the genotypes of a cluster, the per se performance of the genotypes for different traits such as earliness (days to 50% flowering and days to maturity), plant height at maturity, number of branches per plant, number of capsules per plant, number of seeds per capsule, seed yield per plant, 1000 seed weight and oil content etc. should be taken into account. So, that desirable transgressivie segregants would be obtained after hybridization.

The cluster means presented in Table 6 considering, the cluster means or the various clusters which can provide the desired parents for hybridization programmes for improvement in the characters shown against them are listed (Table 7 and 9).

Keeping in view all the above aspects, the following genotypes in the present studies, deserve to be considered as potent parents for future crossing programme for improvement of seed yield and yield contributing characters.

1	DHS-5	6	DHS-17
2	DHS-11	7	DHS-33
3	DHS-18	8	DHS-35
4	DHS-22	9	DHS-38
5	DHS-28	10	DHS-36

Considering the inter-cluster distance, cluster means, per se performance of genotypes and divergence class, the above genotypes may be utilized in future breeding programme for creating maximum spectrum of variability for different yield contributing characters which will facilitate to develop superior genotypes with respect to more than one characters and also possible to improve more than one character simultaneously.

Similar studies was carried out by Bandila *et al.*, (2011), Ahadu (2012), Narayanan and Murugan (2013), Chandra (2014), Hira *et al.*, (2014), Hemalata and Saundarya (2015), Iqbal *et al.*, (2016), Yirga Belay Kindeya (2017), Saundharya *et al.*, (2017).

References

Ahadu, M. 2012. Phenotypic variability, divergence analysis and heritability of characters in sesame (*Sesamum indicum* L.) genotypes. *Journal of Nature and Science Research*, 10(10):117-121.

Arunachalam, V. 1981. Genetic distances in plant breeding. *Indian Journal of Genetics*, 41: 226-236.

Arunachalam, V. and A. Bandopadhay. 1984. Limits to genetic divergence for occurrence of heterosis experimental evidence from crop plants. *Indian Journal of Genetics*, 44 (3): 548-554.

Bandila, S. Chanta, A. Natrajan, S. and Subramanian. 2011. Determination of genetic variation in Indian sesame genotypes for morphological traits. *Journal of Research in Agriculture Science*. 7(2): 88-89.

Bhatt, G. M. 1970. Multivariate analysis approach to selection of parents for hybridization, assuming of yield improvement in self-pollinated crops. *Australian Journal of Agriculture Research*, 21: 1-17.

Chandra, M. 2014. Variability and genetic divergence in sesame (*Sesamum indicum* L.). *International Journal of applied biology and pharmaceutical technology*, 5 (3):0976-4550.

East, E. M. and Hayes, H. K. 1942. Heterozygosis in evolution and plant Breeding U.S.D.A. *Bureau of plant Industry Bulletin* 243: 1-58

Falconer, D. S. 1989. An introduction to Quantitative Genetics. Longman, New York.

Hays, H. K. and Johnson, I. J. 1939. The breeding of self-improved lines of corn. *Journal of American Society of Agronomy*, 31: 710-724.

Hemalatha, V., and Soundharya, B. (2015), Genetic diversity studies in sesame (*Sesamum indicum* L.) genotypes. Thesis submitted to Prof. Jayashankar Telangana State Agricultural University. Hyderabad.

Hika, G.; Gelata, N. and Jaleta, Z. 2014. Correlation and Divergence analysis for phenotypic traits in sesame (*Sasamum indicum* L.) Genotypes. *Science Technology Arts Research Journal*, 3(4): 01-09.

Iqbal, A., Akhtar, R., Begun, T. and Dasgupta T. 2016. Genetic estimates and diversity study in Sesame (*Sesamum indicum* L.). *Journal of Agriculture and Variability Science,* 9:2319-2372.

Kindeya, Y. B. 2017. Correlation and cluster analysis of white seeded sesame (*Sesamum indicum* L.) genotypes oil yield in northern Ethiopia. *African Journal of Agricultural Research*, 12(12): 970-978.

Mahalanobis, P.C., 1936. On the generalized distance in statistics. *Proceedings of the National Academy of Science*, 2:55-79.

Narayanan, R. and Murugan, S. 2013. Studies on genetic diversity and heritability in sesamum. *International Journal of current Agriculture Research,* 2 (11):52-55.

Panse, V. G. and Sukhatmate, P. V. 1995. Statistical method for Agricultural worker. ICAR, New Delhi 4thEdn. pp. 145-150.

Rao, C. R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Willey and Sons, New York.

Soundharya, B., Hemlatha, V., Shobha Rani T and Edukondalu, B. 2017. Genetic divergence studies in Sesame (*Sesamum indicum* L.) genotypes. *International Journal of Current Microbiology and Applied Sciences,* 6(9), 2615-2619.

How to cite this article:

Rohini Y. Patil, K. K. Barhate, B. A. Tagad and Girase, V. S. 2020. Genetic Diversity Studies in Sesamum. *Int.J.Curr.Microbiol.App.Sci.* 9(12): 884-893.
doi: https://doi.org/10.20546/ijcmas.2020.912.106