

Genetic diversity study in germplasm lines of sesamum (*Sesamum indicum* L.)

**G. D. Arpitha, S. Manonmani, P. L. Viswanathan and
M. Raveendran**



ISSN: 0975-928X

Volume: 10

Number:2

EJPB (2019) 10(2):772-777

DOI:10.5958/0975-928X.2019.00102.9



Research Article

Genetic diversity study in germplasm lines of sesamum (*Sesamum indicum* L.)

G. D. Arpitha¹, S. Manonmani^{1*}, P. L. Viswanathan¹ and M. Raveendran²

¹Department of Oilseeds, Centre for Plant Breeding and Genetics, TNAU, Coimbatore -641 003,

²Department of Plant Biotechnology, CPMB&B, TNAU, Coimbatore - 641 003.

Tamil Nadu, India

*E-Mail: swamimano@yahoo.co.in

(Received: 27 Apr 2019; Revised: 05 Jun 2019; Accepted: 06 Jun 2019)

Abstract

Genetic diversity is an important factor for any crop which paves a way for its improvement and selection and divergent germplasm serve as source to obtain the highly diversified parents which possess desirable traits to improve the valuable traits which are useful to mankind. Totally 270 germplasm lines were selected to study the genetic diversity using Mahalanobis D^2 statistics. Six biometrical traits viz., days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of capsules per plant and seed yield per plant were used for clustering using Tocher's method and sixteen clusters were obtained. Out of sixteen clusters, cluster XIV and XV found to be highly divergent clusters as they showed highest inter-cluster distance and clusters II and V were the least divergent clusters which possess genotypes which are closely related. The highest cluster mean was observed in cluster XIV for the trait seed yield per plant and it is highest for the cluster XI for days to 50% flowering, cluster V for days to maturity, cluster II and XIII for plant height and cluster XV for primary branches per plant and capsules per plant. Based on the highest cluster mean of the particular trait, the genotypes can be selected from those clusters to produce the superior combinations to improve yield and oil content in sesamum.

Introduction

Sesamum (*Sesamum indicum* L.) is one of the oldest oilseed crop in the world and as per archeological records it has been used in India for more than 5000 years ago (Beatrice A Were *et al.*, 2005). As per FAO 2013, the total world output of sesame seed is 4.8 million tons, out of which 51.3% is contributed by Asia with the major share of India. In Productivity, Puducherry stands first (987 kg/ha), then West Bengal (933 kg/ha) and Tamil Nadu has got a productivity of 384 kg/ha (India Stat 2016-2017).

It is an important source of vegetable oil and possess highest oil content around 35-63% among all oilseed crops. Sesamum oil is very stable and has long shelf life due to the presence of antioxidants such as *Sesamin*, *Sesamol* and *Sesamol* and can be blended with less stable vegetable oils to improve their longevity and stability. Sesamum oil possess many medicinal properties like lowering the cholesterol level, hypertension and decreases the frequency of certain cancers in humans (Beatrice A Were *et al.*, 2005)

There are many factors which limit the Sesame production such as non availability of high yielding varieties or hybrids resistant to biotic and abiotic stresses, growing the crop on marginal land, lack of extension work. There comes the role of local and

exotic germplasm lines to evaluate and utilize them in breeding program to improve the total yield (Muhammad S. Hassan and F.Sh. Sedeck, 2015).

Genetic diversity is an important factor for any crop which paves a way for its improvement and selection (Revathi and John Joel 2012). Sesamum possess a richest diversity among the germplasm lines for various traits. To plan any effective breeding programme, the knowledge of nature and magnitude of genetic variability is important to increase yield performance of the genotypes (Kante Srikanth 2017). Biotic and abiotic stresses are the major challenges which limits the yield potential of Sesamum, hence identifying the diverse germplasm lines tolerant to drought and heat stress and resistant to phyllody and powdery mildew and for other yield attributing traits may help us to breed the high yielding varieties and hybrids. There are many tools available to assess the genetic divergence at inter-variatal and sub-species level among them, Mahalanobis D^2 statistics (1936) is widely used (Kante Srikanth 2017). This is one of the potent techniques to measure the genetic divergence in different breeding material. This genetic diversity results in high heterosis between the genotypes of diverse origin and produces more recombinants than between the closely related

species. The present study aims at studying the genetic diversity existing among the sesamum germplasm lines through morphological observations.

Materials and Methods

Two hundred and seventy sesamum germplasm collections maintained at the Department of Oilseeds, TNAU, Coimbatore were used in the study. They were planted during *kharif* 2017-2018 in a Randomized Complete Block Design (RCBD) with two replications with adopting a spacing of 30 x 10 cm. All the cultural operations were carried out at a definite interval and recommended package of practice was followed to maintain crop stand. A special care was taken to avoid yellowing and other diseases attack like phyllody and powdery mildew. Observations were taken from five randomly selected plants from each replication/entry for yield and yield attributing traits. Biometrical observations were taken on six quantitative traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of capsules per plant and seed yield per plant (g). All these observations were used to assess the genetic diversity existing among the 270 germplasm using Mahalanobis D^2 statistics (1936), wherein genotypes were grouped into different clusters based on Toucher's method.

Results and Discussion

Based on phenotypic data, the mean value of each genotype for each character was subjected to univariate ANOVA and wilk's statistic using Star software. The significance of all the genotypes for each trait suggested that these genotypes can be used for D^2 analysis to study the extent of genetic diversity. Based on D^2 statistics, 270 genotypes were grouped into sixteen clusters using Toucher's method (Radhakrishna Rao, 1952). The distribution of these genotypes into different clusters is represented in Table 1. Similar analysis was made in Sesamum by Adil Iqbal *et al.*, (2018), B. Soundharya (2016). As per analysis, cluster I found to be the largest comprising of 136 genotypes followed by cluster III with 63 genotypes, cluster IV with 35 genotypes, cluster VI with twelve, cluster VIII with 10, cluster XIV with four and remaining all other clusters *viz.*, II, V, VII, IX, X, XI, XII, XIII, XV and XVI had single genotype each.

The inter-cluster and intra-cluster D^2 values were presented in Table 2. The highest inter-cluster distance found between the genotypes of clusters XIV and XV (56.28), followed by between the clusters VIII and XIV (47.06), cluster V and XIV (46.02), cluster IX and XIV (45.81). Therefore one

should select the genotypes between the clusters XIV and XV as parents in hybridization programme as they possess highest inter-cluster distance and it is suited to exploit heterosis. As per the current study the germplasm *viz.*, SVPR 1, Si-395, Si-2143, NIC-1610 belonging to cluster XIV and genotypes such as NO 128 falling in cluster XV can be used as parents to obtain high heterotic combinations. The lowest inter-cluster distance was 4.02 between the clusters II and V followed by cluster V and IX (5.28). This indicates that the genotypes falling in these clusters have close relationship with each other. The intra-cluster distance ranged from 0 in clusters II, V, VII, IX, X, XI, XII, XIII XV and XVI to 16.55 in cluster VIII. Since the intra-cluster distance is 0 in clusters II, V, VII, IX, X, XI, XII, XIII, XV and XVI, indicating that each cluster contain only single genotype. As intra cluster distance in cluster VIII is 16.55, this indicated the genetic divergence is still exist to some extent among the genotypes belonging to that cluster and selection of genotypes in these clusters is possible based on the desirable trait which has got maximum mean.

Cluster mean values of six quantitative traits was estimated and furnished under Table 3. This indicates the difference existing among sixteen clusters for six different morphological traits. The maximum mean for days to 50% flowering (58.00) was observed in cluster XI followed by cluster XIII (57.00) and minimum cluster mean for days to 50% flowering was seen in cluster VII (42.00). Hence to obtain the early flowering genotypes, one can make a choice of parents from cluster VII as it possess lowest cluster mean value for days to 50% flowering (42.00). The highest cluster mean for days to maturity was observed in cluster V (105.50), followed by cluster VII (104.00) and lowest cluster mean for days to maturity was 93.00 in cluster X. Therefore to produce early maturing hybrids, parents from cluster X can be selected. For the trait plant height, cluster II and XIII had highest cluster mean of 146.00 followed by cluster IX (145.00) and cluster VII had lowest cluster mean of 80.00. As plant height is one of the yield contributing traits, the genotypes belonging to the clusters II and XIII may be chosen as parents as they got highest cluster mean value of 146.00 for plant height.

Cluster XV has got the maximum cluster mean of 9.00 for the character primary branches per plant followed by cluster II, XI and XVI (7.00) and minimum cluster mean for primary branches per plant was found in cluster VII and IX. The highest mean for the trait capsules per plant was observed in cluster XV (202.00) followed by cluster XVI



(178.50) and the lowest mean for capsules per plant was seen in cluster XII (21.00). 21.33 was the highest cluster mean in cluster XIV for the trait seed yield per plant followed by cluster XVI (10.12) and the lowest cluster mean for the same trait was found to be 1.01 in cluster XV. Hence, to improve the yield, genotypes belonging to cluster XIV might be selected. In total, to improve the particular trait, genotypes should be selected from those clusters which have got maximum mean value for that particular desirable trait.

The percent contribution of six characters towards diversity is given in Table 4. Out of six characters studied, seed yield per plant (26.97%) contributed maximum towards the genetic diversity followed by number of capsules per plant (25.64%), days to 50% flowering (25.20%), plant height (20.31%), days to maturity (1.38%) and number of primary branches per plant (0.51%). The genotypes falling in the clusters XIV and XVI which are widely diversified, have got high cluster mean for seed yield per plant, hence selection of these genotypes as parents in hybridization will help to develop hybrids with highest seed yield.

The above study concludes that, to produce hybrids with high heterotic combination, parents can be selected from the clusters XIV and XV as they possess highest inter-cluster distance. To improve the seed yield, genotypes from cluster XIV and XVI can be chosen as they got highest cluster mean for the trait seed yield. To breed the early flowering genotypes, lines from cluster VII may be used with lowest cluster mean value for days to 50% flowering. In order to produce early maturing types, genotypes from cluster X may be utilized.

To improve the yield, the genotypes from the clusters having highest cluster mean value for the yield attributing traits such as plant height, number of primary branches per plant, number of capsules per plant such as cluster II and XIII for plant height, cluster XV for primary branches and capsules per plant can be utilized. Hence to improve any desirable trait, genotypes should be made used from the clusters having highest cluster mean value for the desirable trait.

References

- Banerjee, P. P. and Kole, P. C. 2009. Analysis of genotypic diversity in sesame (*Sesamum indicum* L.) based on some physiological characters. Czech J. Genet. Plant Breed., **45**, 2009 (2): 72–78.
- Begum, T., A. Iqbal and Dasgupta, T. 2017. Genetic variability and divergence among genotypes of sesame (*Sesamum indicum* L.). Bangladesh J. Bot. **46**(3): 955-962.
- Begum, S., M. A. Islam, A. Husna, T.B. Hafiz and Ratna, M. 2011. Genetic divergence analysis in sesame (*Sesamum indicum* L.). SAARC J. Agri., **9**(2) ; 65-71.
- Hassan, M. S. and Sedeck, F.S. 2015. Combining ability and heterosis estimates in sesame. World Applied Sciences Journal **33** (5): 690-698.
- Iqbal, A., P. K. Pati, R. Akhtar, T. Begum and Dasgupta, T. 2018. Diversity in sesame accessions. International Journal of Agriculture, Environment and Biotechnology: **11**(5): 725-73.
- Jadhav, R. S. and Mohrir, M.N. 2013. Genetic divergence analysis in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding, **4**(1): 1090- 1092.
- Kadir, M. M., M. M. Ali, M. N. Islam, A. S. M. Golam Masum Akond and Islam, M. S. 2001. Genetic Divergence in sesame. Bangladesh J. Agril. Res. **26**(1) : 131-135.
- Parameshwarappa, S. G., M. G. Palakshappa, P. M. Salimath and Parameshwarappa, K. G. 2010. Analysis of genetic divergence in sesame, *Sesamum indicum* L. Karnataka J. Agric. Sci., **23**(2) : (227-230).
- Revathi, S., John Joel, A. and Manivannan, N. 2012. Genetic variability in sesame (*Sesamum indicum* L.). Electronic Journal of Plant Breeding, **3**(1):692-694.
- Singh, A., R. Bisen and Tiwari, A. 2017. Assessing inter: Relationship of sesame genotypes and their traits using cluster analysis and principal component analysis. International Journal of Chemical Studies 2018; **6**(1): 2151-2153.
- 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.
- Soundharya, B. 2016. Genetic diversity in sesame (*Sesamum indicum* L.). M.Sc. (Agri.) Thesis. Submitted to College of Agriculture Rajendranagar, Hyderabad.
- Srikanth, K. 2017. "Studies on genetic diversity, path analysis and correlation in sesame (*Sesamum indicum* L.)". M.Sc. (Agri.) Thesis. College of Agriculture, Latur.
- Were, B. A., A. O. Onkware, S. Gudu, M. Welander and A. S. Carlsson. 2006. Seed oil content and fatty acid composition in East African sesame (*Sesamum indicum* L.) accessions evaluated over 3 years. Field Crops Research **97** (2006) 254–260.



Table 1. The distribution of 270 genotypes into sixteen clusters in Sesamum

Clusters	No of genotypes in each cluster	Germplasm lines
I	136	Si-889, NIC-2939, Si-1659, S0-111, Si-2186, Si-771, IS-148, G-53, IS-25, Si-702, Si-934-114, Si-1214, Si-3216, IS-249, NAE-79114/7, KMR-80, Si-97, NIC-8252, Si-1214, NIC 7940, Si-239, Si-1143-1, Turinoca, IS-112, IS-1841, Si-3279, ES-13, Si-2137, Si-70, Si-861/2, IC-2046-18, Si-760, Si-328, IC-20861, Si-2428, PSK-1992, Si-1841, Si-9185, Si-837, NIC-7939, PSR-2981, VS-9104, Si-861/2, B-203, Si-1883, Si-266, IC-1994-38, Si-1769, Si-3171, Multi capsuled, Krishna, Si-2192, NAE 79114/7, NIC-8328, GSK-24, Si-4721, KMR-342, Si-861, Si-925, SO-557, Si-1760/1, Si-861/2, Si-1847, IS-366, S0-453, PS-5, Si-3278/2, IC-194-29-A, RT-146, Si-1885, Si-1146, OMT 21 A, Si-440, Si-1727/1, Si-12, KMR-7, GUN-17, Si-987/1, Si-608, Si-769-2, Si-3012, Si-3224, Si-3257, Si-1041, 52-300, KMR-95, Si-3171/1, IC-205-206, IS-4996, SO-138-NL-1, ES-15, NAE-7911, ORM-7, NS-9101, KMR-7, Si-925, Si-2334, Si-2210, SP-7613, NIC-7928, VRI-1, IS-1516, Si-3136, DS-1, Si-1771, ES-71, Si-1236, TC-25, KMR-73, Si-3165, AST-5, IS-29-1, Si-242, Si-3216, DCP-2060, JLS-80, JLS-57, Si-3178, NIC-8509, Si-7613, Si-3112, Si-80-1, TMV 5, TKG-84, S0-245, Si-930, Si-1065, Si-3280, GUN-18, Si-301, G-49, Si-345, SO-0-11, NIC-8509, Madhavi NC-2, IC-110062
II	1	G-53
III	63	GUN-3-NL-1, PSR-2000, IC-131651, AKT-64, Si-1143-1, Si-1760-1, IS-112, Thilathara, IC-2050-7, Si-1720/1, TMR-4, Si-440, IS-621, Si-3279, 725, ES-71, Si-2143, ACU-2, 78-1-1, KMR-43, Si-983/1, AKT 69, Si-1260, KMR87, Si-2147, Si-1804, Si-17574, Paiyur-1, GT-4, Si-5959, Si-3279, ES-21, NIC-8317, Si-1236, Si-1260, Si-2186, Si-918, DPI-15-25, Si-345, KMS-4343, Si-3100, Si-1657, EO-63, TSS-11, Si-1760-1, Si-775, TMV-5, Si-328, Si-930, Si-1485, NIC-8283, Si-1041, NIC-8261, Si-2289-2,175, T-13, OTS-2, DCP-1810, IS-562-B, Si-2334, Si-2595/2, NIC-9940, IS-842, Si-97
IV	35	IS-237, PKD-512, Si-801, KMR-95, KMR-108, Si-837, SHIKAR, DCT-15, Si-3106, Si-395, Si-1818, DSR-3003, G-46, EO-63, Si-3280, Si-533, TKG 67, Si-490, OMT-21-A, Si-2428, Si-1684, Si-7212, Si-1861/2, Si-259, EO-94, Annamalai NC-1, Si-837, Si-769-2, PS-5, Si-1847, IS-366, GUN-18, ESN-32, Si-256, G-53,
V	1	Kandappan kurichy
VI		NIC-9984, Si-3472, Si-702, Si-3099, Si-328, Si-1712, VRI-2, JLSC-96, GENE-9301, Si-3178/1, BS-27, G-10
VII	1	Si-2143
VIII	10	NIC-16106, Si-1760, Si-1967, Si-490, Si-3296, Kayakulam 2, TMV 5, Si-1978, ES-3707, Si-2334,
IX	1	NIC-16358
X	1	RSS-379-2
XI	1	Si-769-2
XII	1	Si-987/1
XIII	1	IS-842
XIV	4	SVPR 1, Si-395, Si-2143, NIC-1610
XV	1	NO 128
XVI	1	Si-266



Table 2 . Average inter and intra-cluster D^2 values of Sesamum germplasm lines falling in different clusters

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI
I	10.39	12.90	14.88	16.04	12.75	17.05	13.08	21.49	13.49	12.82	22.49	16.08	20.77	39.94	32.59	30.05
II		0.00	16.21	18.28	4.02	22.66	18.92	21.81	5.51	7.48	25.42	20.11	20.50	45.04	33.67	34.28
III			11.27	17.67	16.14	19.09	20.40	20.28	19.14	17.07	17.57	15.25	15.98	40.15	32.98	30.30
IV				13.18	18.08	18.24	21.66	18.80	18.56	20.38	16.64	24.50	16.89	36.58	27.33	21.31
V					0.00	23.21	17.96	20.59	5.28	9.29	25.40	19.97	21.32	46.02	32.17	33.58
VI						12.69	19.47	27.39	23.70	22.66	19.38	20.25	20.27	28.78	38.28	28.32
VII							0.00	26.68	18.14	17.10	29.58	14.83	29.57	43.14	36.07	34.56
VIII								16.55	22.41	24.19	20.95	27.78	21.72	47.06	20.69	23.57
IX									0.00	8.38	27.65	22.76	22.96	45.81	32.90	33.78
X										0.00	27.96	18.12	22.35	45.38	36.17	36.49
XI											0.00	26.44	10.36	31.71	30.65	19.82
XII												0.00	25.63	42.95	40.73	38.75
XIII													0.00	33.75	33.80	25.72
XIV														13.33	56.28	38.00
XV															0.00	20.91
XVI																0.00



Table 3. Cluster mean values of six quantitative traits in Sesamum germplasm lines

Cluster	Days to 50% flowering	Days to maturity	Plant height	No of primary branches per plant	No of capsules per plant	Seed yield per plant
I	46.28	100.78	110.91	5.33	62.45	3.92
II	47.00	102.00	146.00	7.00	60.00	1.74
III	56.73	99.90	114.65	5.63	65.44	4.65
IV	46.37	100.99	121.11	6.33	102.66	6.56
V	47.50	105.50	141.50	4.50	66.50	1.15
VI	46.67	101.83	101.58	6.58	56.50	9.48
VII	42.00	104.00	80.00	4.00	47	2.46
VIII	52.45	99.45	117.10	5.80	129.90	2.80
IX	42.50	102.00	145.00	4.00	67.00	1.43
X	46.00	93.00	133.00	4.50	44.50	1.66
XI	58.00	102.50	121.00	7.00	108.50	10.11
XII	56.50	101.00	84.50	5.00	21.00	3.16
XIII	57.00	95.50	146.00	4.50	87.50	9.01
XIV	44.75	103.00	113.25	5.25	53.88	21.33
XV	46.50	97.00	101.50	9.00	202.00	1.01
XVI	44.50	99.00	102.00	7.00	178.50	10.12

Table 4 . The percent contribution of six characters towards diversity in Sesamum

Sl.No	Character	Percent contribution
1	Days to 50% flowering	25.20
2	Days to maturity	1.38
3	Plant height	20.31
4	No of primary branches per plant	0.51
5	No of capsules per plant	25.54
6	Seed yield per plant	26.97

