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Research Article

Analysis of genetic diversity in sesame (*Sesamum indicum* L.) advanced breeding lines and varieties collected from major breeding centers in India

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Abstract
Genetic diversity study was carried out among 41 sesame genotypes using seed yield and its component characters. Based on the present investigation the 41sesame genotypes were grouped into seven clusters suggesting that considerable amount of genetic diversity present across genotypes. The maximum diversity was contributed by capsules per plant followed by number of branches per plant, plant height and days to maturity. Cluster II was the largest one comprising of 17 genotypes followed by cluster I with 12 genotypes, cluster IV with five genotypes, cluster III with four genotypes, cluster V,VI, and VII, were represented by each single genotype indicating high degree of heterogeneity among the genotypes.The maximum inter cluster distance was observed between IV and VI clusters followed by clusters IV and V and clusters VI and VII while it was low between clusters V and VI, followed by clusters I and V, clusters II and VII. Maximum intra cluster distance was observed in cluster VI, followed by cluster IV, cluster III, cluster II and cluster I. The inter cluster distance in most of the cases were higher than the intra-cluster distance indicating wider genetic diversity among the genotypes of different groups. Four characters *viz.*, capsules per plant, followed by number of branches, plant height and days to maturity contributed more than 90% towards genetic divergence. Hence, these four characters are very important for selection indices.

Key words
Genotypes, Genetic diversity, Mahalanobis's D^2– technique, Inter Cluster distance, Intra cluster distance.

Introduction

Sesame (*Sesamum indicum* L.) is one of the most important ancient cultivated oilseeds crop belongs to family Pedaliaceae. The crop is grown in the tropical and subtropical countries of the world (Ashri, 1994).Sesame seeds are highly nutritive contain protein and 50 -60 per cent highly stable oil. It can be used in number of food products,manufacturing of paints, soaps, perfumes, insecticides pharmaceuticals and cosmetic products *etc*., (Bedigian and Harlan, 1986).Myanmar, India and China are the top three sesame producing countries in the world. But, the productivity of sesame in India is very low (432 kg/ha) as compared to China (1382 kg/ha) and Myanmar (565 kg/ha) (FAO, 2017). The key constraints in production are lack of high yielding non shattering determinate varieties in India. In India, the yield plateau and poor productivity can be overcome by commercial exploitation of heterosis and reshuffling of genes to get better recombinants or transgressive segregants by hybridization using suitable parents. Genetic divergence among the parents is an important factor while selecting the parents for hybridization. Rao (1960) and Ramanujam *et al.* (1974) also observed that a cross involving genetically diverse parents is more likely to produce high heterotic effect as compared with lines which are more closely related with each other. While performing selections, more importance should be given to the characters which contribute more towards diversity. Hence the present study was undertaken to study the genetic diversity among the 41 sesame advanced breeding lines and varieties and identify the lines for further hybridization.

Materials and Methods

The experiment was laid out in Randomized Block Design with two replications. Each genotype was grown in a row of 2m length with a row spacing of 30 cm and plant to plant spacing of 10-15 cm.The recommended doses of nutrients (40:20:20 kg of N: P: K per ha) were supplied in the form of urea, single super phosphate and muriate of potash. Fifty per cent of nitrogen (20kg/ha) and entire quantity of phosphorus and potash were applied in the rows 5 cm away from the seed during sowing. Remaining 50 per cent of nitrogen was applied 30 days after sowing as top dressing. Thinning was done 15 days after sowing leaving a single healthy seedling at a distance of about 10 cm per hill. The crop was kept weed-free and three hand weedings were carried out during the crop growth period. Proper soil moisture was maintained throughout the crop growth period through supplementary irrigations. Necessary plant protection measures

were taken to control pests and diseases.The data on 10 characters *viz.*, plant height (cm), number of branches per plant, first capsule height (cm), capsule length (cm), capsules per plant, diameter of stem (cm), number of seeds per capsule, days to maturity, 1000-seed weight (g) and seed yield per plant (g) were recorded.

Collected data was subjected to statistical analysis for genetic diversity analysis using Mahalanobis's D^2 statistics (Mahalanobis, 1936). The genotypes were grouped into clusters as per Tocher's method following the formula cited by Rao (1952) and Singh and Chaudhary (1977). All the statistical analysis was carried out using INDOSTAT Computer software.

Results and Discussions

For a successful breeding programme, genetic diversity of parents is of utmost importance, since the crosses made between the parents with maximum geneticdivergence are more likely to yield desirable recombinants in the progenies. Hence, it is desirable to select suitable genetically divergent parents based on information about the genetic variability and genetic diversity present in the working collection of germplasm.

The multivariate analysis using Mahalanobis's D^2 statistic provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together. It also provides a quantitative measure of association between geographic and genetic diversity based on generalized distance (Mahalanobis, 1936). Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between the populations.

The percent contribution towards genetic divergence by all the 10 contributing characters is presented in Table 1. The maximum contribution towards genetic divergence was by the character, number of capsules per plant (76.10%), followed by no.of branches per plant (7.68%), plant height (5.37%), days to maturity (3.41%), capsule length (3.17%), no.of seeds per capsule (1.59%), diameter of stem (1.46%), 1000 seed weight (0.85%), first capsule height (0.24%) and seed yield per plant (0.12%).These results are in accordance with the reports of Dhamu *et al.* (1984) and Gawali *et al.* (2007) for number of capsules per plant; Manivannan and Nadarajan (1996) for plant height, no.of branches, Ayyaswamy *et al.* (1987) for 1000-seed weight, seed yield and days to maturity; and Srivani (2001) for number of seeds per capsule.

Forty one genotypes were grouped into 7 clusters based on D^2 values using Tocher's method (Rao 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 2 and Fig 1. Out of 7 clusters, cluster II was the largest comprising of 17 genotypes followed by Cluster I with 12 genotypes, cluster IV with 5 genotypes, cluster III with 4 genotypes and cluster V,VI,VII were represented each by a single genotype indicating high degree of heterogeneity among these genotypes.The pattern of distribution of genotypes from different breeding centers into various clusters was random indicating that there has been free flow of germplasm among the breeding centers. The choice of suitable diverse parents selected on the basis of genetic diversity analysis would be more rewarding than the choice made on the basis of origin of materials. These findings are in agreement with the reports of Murthy and Arunachalam (1966), Sheriff and Shivashankar (1992) and Patil and Sheriff (1994).

The average intra and inter cluster D^2 values are presented in Table 3. Intra-cluster D^2 values ranged from zero (cluster V, VI, and VII,) to 79.21 (cluster IV). Maximum intra cluster distance was observed in cluster IV (79.21), followed by cluster III (59.90), indicating that high divergence existed among the genotypes. Promising genotypes included in cluster IV that had maximum intra cluster distance are Rajeswari, Swetha, YLM-17, IsAgi-95-10 and Nirmala, which are highly divergent among themselves. This could be made use in the yield improvement through recombination breeding.

The inter-cluster D^2 values ranged from 34.81 (cluster V and VI) to 1760.64(cluster IV and VI). The maximum inter cluster distance (1760.64) was observed between IV and VI clusters followed by clusters IV and V (1394.27) and cluster VI and VII (1114.22) suggesting that the crosses involving lines from these clusters would give desirable recombination. While, the minimum inter cluster distance of 34.81 was recorded between cluster V and VI, followed by cluster I and V (77.26), cluster II and VII (108.36) indicating that genotypes of these clusters had maximum number of gene complexes.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. The greater the distance between two clusters, the wider the genetic diversity between the genotypes. Keeping this in view, it is indicated that useful

segregants may be created by crossing Rajeswari, Swetha, YLM-17, IsAgi-95-10 and Nirmala of cluster IV with AT-213 and JLS-408-2 of clustersVI and V respectively, AT-213 (cluster VI) with Hima (cluster VII). The genotypes of these clusters may be used as parents in the crossing programme to generate high hetrotic hybrids.

The cluster means for each of 10 characters are presented in Table 4. From the data, it can be inferred that considerable differences existed for all 10 characters under study. Cluster VII had high mean value for plant height (130.42 cm), number of branches per plant (7.80), no. of seeds per capsule (71.85), first capsule height (21.50 cm) and 1000 seed weight (3.35 g), and low for days to maturity (86.00 days), Cluster IV had high mean value for capsules per plant (106.37) and seed yield per plant (20.07), Cluster V had high mean value for capsule length (3.64 cm) and Cluster I had high mean value for diameter of stem (1.48 cm). The result indicated that selection of genotypes having high, low values for particular trait could be made and used in the hybridization programme for improvement of that character.

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Table 1. Relative contribution (%) of each character to the genetic diversity in sesame

S. No.	Characters	Times ranked first	Contribution (%)
1	Plant height (cm)	44	5.37
2	Number of branches per plant	63	7.68
3	First capsule height (cm)	2	0.24
4	Capsule length (cm)	26	3.17
5	Capsules per plant	624	76.10
6	Diameter of stem (cm)	12	1.46
7	Number of seeds per capsule	13	1.59
8	Days to maturity	28	3.41
9	1000-seed weight (gm)	7	0.85
10	Seed yield per plant (g)	1	0.12

Table 2. Clustering pattern of sesamegenotypes

Cluster No	Number of genotypes	Name of the genotypes
I	12	TKG-22, TKG-87, VS-07-023, LT-8, CST-2001-1, CST-2008-2, JLS-9707-2, Nana Bhamodra-5, JL-Sel-05-3, Paten-64, Prachi, Nesadi Selection
II	17	DS-1, JLS-403-33, TMV-3, JLT-408, SVPR-1, Hawari, G.Til-10, G.Til-2, DSS-9, G.Til-1, DS-5, RT-358, RT-125, VRI-2, RT-356, JCS-1020, DS-10
III	4	MT-10-81, RT-346, Madhavi, DS-30
IV	5	Rajeswari, Swetha, YLM-17, IsAgi-95-10, Nirmala
V	1	JLS-408-2
VI	1	AT-213
VII	1	Hima

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Table 3. Mean intra (bold) and inter cluster distance among seven clusters of sesame genotypes

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII
Cluster I	**6.09**	19.09	11.41	30.41	8.79	12.95	22.65
	(37.08)	(364.42)	(130.18)	(924.76)	(77.26)	(167.702)	(513.02)
Cluster II		**6.43**	11.47	13.75	25.95	30.5	10.41
		(41.34)	(131.56)	(189.06)	(673.40)	(930.2)	(108.36)
Cluster III			**7.74**	21.73	17.31	21.9	14.07
			(59.90)	(472.19)	(299.63)	(479.61)	(197.96)
Cluster IV				**8.9**	37.34	41.96	12.55
				(79.21)	(1394.27)	(1760.64)	(157.50)
Cluster V					**0.00**	5.9	28.88
					(0.00)	(34.81)	(834.05)
Cluster VI						**0.00**	33.38
						(0.00)	(1114.22)
Cluster VII							**0.00**
							(0.00)

Note: Values in parenthesis indicates D^2 values

Table 4. Mean values of clusters obtained by Tocher's method in sesame

Cluster Number	Plant height (cm)	Number of branches per plant	First capsule height (cm)	Capsule length (cm)	Capsules per plant	Diameter of stem (cm)	Number of seeds per capsule	Days to maturity	1000-seed weight (gm)	Seed yield per plant (g)
Cluster I	71.47	4.26	15.74	3.34	60.80	**1.48**	64.58	93.49	2.98	12.93
Cluster II	89.42	4.55	20.09	3.02	89.03	1.44	62.65	90.74	3.11	15.87
Cluster III	84.94	5.25	18.63	3.35	73.70	1.37	60.40	91.41	3.19	14.36
Cluster IV	109.00	5.75	21.05	2.95	**106.37**	1.46	65.54	90.90	3.14	**20.07**
Cluster V	73.09	4.25	17.25	**3.64**	49.15	1.31	62.45	100.50	2.90	12.45
Cluster VI	67.09	4.15	13.50	3.07	42.05	1.29	68.00	87.00	3.10	11.30
Cluster VII	**130.42**	**7.80**	**21.50**	2.90	92.10	1.45	**71.85**	**86.00**	**3.35**	15.05

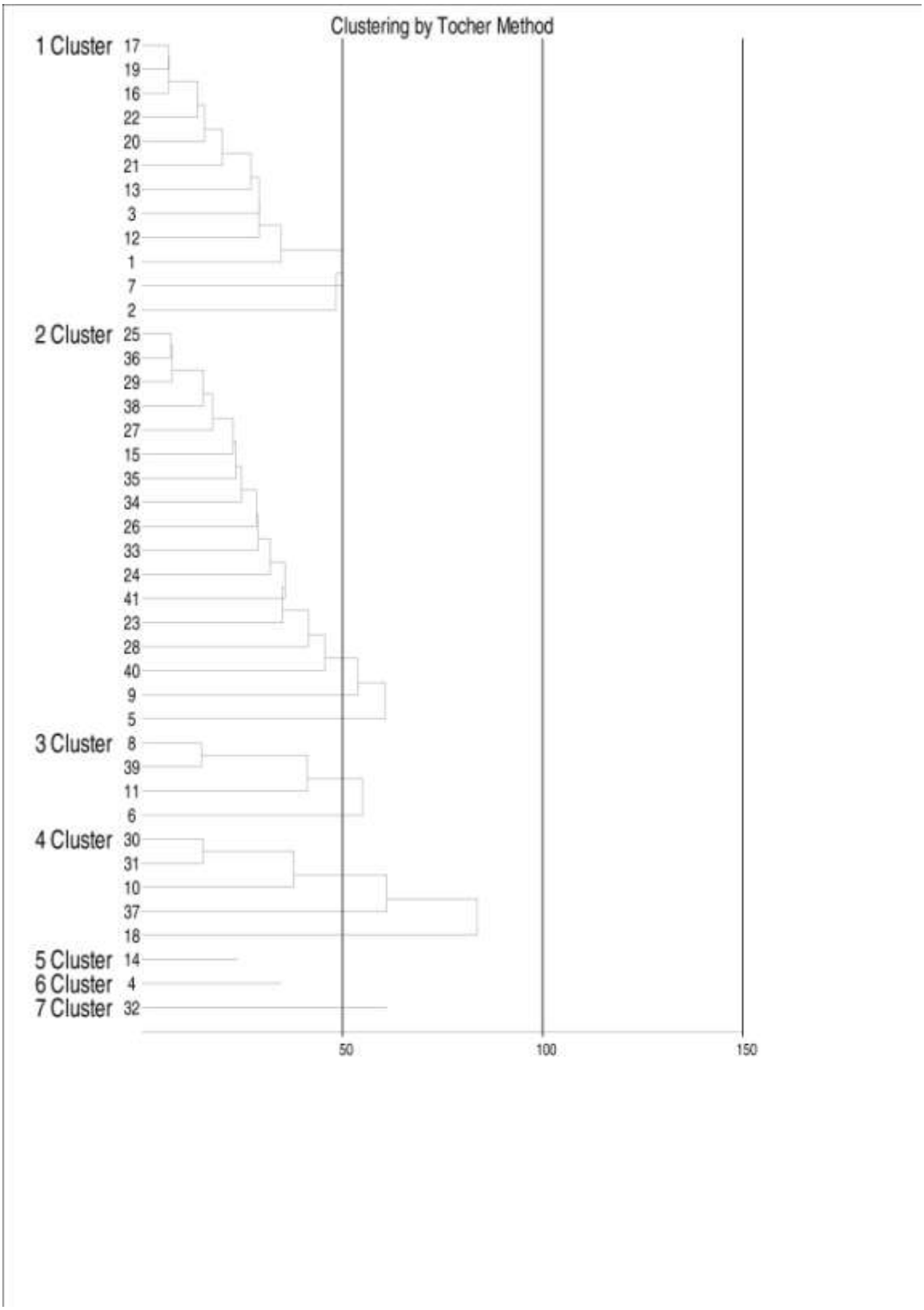

Fig. 1. Clustering pattern of 41sesame genotypes by Tocher's method