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Assessment of morpho-genetic diversity in germplasms of Sesamum (*Sesamum indicum* L.)

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Abstract
An experiment was conducted to investigate yield and quality traits in germplasms of sesamum, in order to generate information regarding the extent of genetic diversity present in those germplasms. The experiment was laid out during *kharif* 2015 in 10×10 simple lattice design with two replications. The genetic diversity analysis revealed the formation of 10 clusters indicated the existence of sufficient genetic diversity among the germplasms. The cluster I contained 63, cluster II contained 15 germplasms, cluster V contained 10 germplasms and cluster VII contained 6 germplasms. While cluster III, IV, VI, VIII, IX and X possessed only one germplasm. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that oil content followed by seed yield per plant, capsule per plant and seeds per capsule contributed maximum towards total genetic divergence. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster VI with the genotypes of cluster X and cluster VII, which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in sesame.

Keywords: Genetic divergence, D^2 statistic, clusters and sesamum

Introduction
Sesame (*Sesamum indicum* L., 2n = 26) is a historic oilseed crop used in India with groundnut, rapeseed, and mustard. It is a member of the order Tubiflorae and the family Pedaliaceae. It is predominantly a tropical and subtropical crop, although it has expanded to temperate locations across the world. Sesame is said to have originated in Africa, and it travelled quickly across West Asia to India, China, and Japan, which became secondary distribution hubs (Weiss, 1983) [13]. Sesame is a self-pollinated crop with a 4 to 5% cross pollination rate. However, depending on the pressure of pollinating agents, the percentage of out crossing varies from 0% to 50%, but wind has no effect on natural cross pollination. Sesame is one of the oldest oilseed crops from which oil was produced and utilised for religious purposes by the ancient Hindus (Weiss, 1983) [13]. Myanmar is currently the world's largest producer of sesame seed, followed by India, China, Turkey, and Pakistan in Asia; Egypt and Sudan in Africa; Greece in Europe; Venezuela, Argentina, and Columbia in South America; Nicaragua and El Salvador in Central America; and Mexico and the United States of America in North America. India is still the world leader with maximum (25.80%) production from the largest (29.30%) area and highest (40.00%) export of sesame in the world. In India, during 2013-14, sesame is cultivated in an area of 16.67 lakh ha with a production of 6.75 lakh tones annually and productivity of 405 kg/ha (Anonymous, 2017) [1]. It is widely farmed in the states of Uttar Pradesh, Rajasthan, Orissa, Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, West Bengal, Bihar, and Assam, and is the fourth most significant oilseed crop in Indian agriculture after groundnut, rapeseed, and mustard. In Gujarat, sesame was grown over an area of 2.36 lakh ha in 2013-14, yielding 1.24 lakh tonnes with a productivity of 525 kg/ha (Anonymous, 2017) [1]. During the kharif, semi-rabi, and summer seasons, this crop is often grown as a solo or mixed crop. Sesame productivity is quite low when compared to other oilseeds; thus, it is required to increase productivity and hence overall oilseeds output in order to satisfy the country's edible oil requirements. Genetic diversity is a critical aspect in determining the success of a hybridization programme, and its usefulness in crop development has long been recognised by breeders. The more different the parents are within the general boundaries of fitness, the greater the odds of heterotic F_1's and a broad range of diversity in each generation (Arunachalam, 1981; Falconer, 1989) [2, 4].

Yield and yield contributing traits are regulated by polygenes and heavily impacted by environment; hence, genetic diversity in available germplasms must be explored. As a result, assessing germplasm's suitability for local circumstances is critical. It is well acknowledged that information concerning germplasm diversity and genetic relatedness among top breeding material is a critical component in plant breeding (Mukhtar *et al.* 2002) [9]. Genetic variety is a critical component of any hybridization effort aimed at genetic yield enhancement, particularly in self-pollinated crops (Joshi and Dhawan, 1966) [6]. Different approaches have been tried to estimate genetic diversity, with the D^2 statistic developed by Mahalanobis (1936) [8] being the most effective tool for evaluating genetic divergence.

Materials and Methods
The material for the current study consisted of 100 germplasms out of these, 96 germplasam lines of sesamum (*sesamum indicum* L.) these germplasms of sesamum was procured from project coordinating unit, AICRP (Sesamum & Niger) Jabalpur and four checks were obtained from oil seed scheme, ZARS, GKVK, Bengaluru. The experiment was carried out in of K-2-5, ZARS, GKVK, University of Agriculture sciences, Bengaluru during *kharif* 2015 to study the genetic variability. The field lay out was done in 10×10 simple lattice design with two replications. Geographically it lies at 12^0 15' N and longitude of $77^0$35' E and at an altitude of 930 M mean sea level (MSL).The crop was raised under recommended package of practices of UAS Bengaluru along with prophylactic protection measures. Observations were taken on days to 50% flowering, days to maturity, plant height (cm), branches per plant, leaves per plant, capsules per plant, capsule length, capsule width, seeds per capsule, seed yield per plant (gm), 1000-seed weight (g) and oil content. The data of mean values for all the character were analysed for their variance following simple lattice design outlined by Cochran and Cox (1957). Analysis was done using INDOSTAT 9.1 computer programming software. The data were analysed as per the multivariate analysis of genetic divergence using Mahalanobis (1936) [8] D^2 statistic. The genotypes were grouped into different clusters following the Tocher's method (Rao, 1952) [10].

Results and Discussion
The amount of diversity available in the crop decides the success of any crop improvement programme with manifold objectives. Assemblage and assessment of divergence in germplasm is essential to know the spectrum of diversity. Mahalanobis's generalized distance occupies unique place in plant breeding. The choice of parent is of the paramount importance in any plant breeding programme. It is suggesting that crosses should be effective among germplasm of said cluster for improving more than one economic trait to develop potential segregants and future selection needs to be made to develop high yielding cultivars of sesame. In present investigation, 100 germplasms of sesame were considered for the assessment of nature of genetic diversity by multivariate analysis. The genetic diversity prevalent in germplasms was assessed by adopting Mahalonobis's (1936) [8] concept of generalized distance (D^2), considering twelve important characters. The 100 germplasms were randomly distributed into 10 clusters based on tocher's method. The cluster I contained 63 germplasms followed by cluster II contained 15 germplasms, cluster V contained 10 germplasms and cluster VII contained 6 germplasms. While cluster III, IV, VI, VIII, IX and X are solitary (Table 1).

Table 1: Distribution of 100 germplasm lines of Sesamum into different clusters

Cluster Number	Number of Genotypes	Germplasm Number/ Name
I	63	(62, 86, 60, 6, 10, 31, 74, 91, 33, 70, 26, 92, 97, 4, 35, 84, 18, 17, 16, 75, 7, 44, 71, 5, 100, 9, 67, 94, 22, 72, 65, 85, 1, 2, 21, 95, 23, 63, 19, 24, 47, 61, 20, 98, 48, 96, 52, 43, 30, 27, 73, 66, 78, 28, 37, 14, 25, 99, 46, 12, 87, 90, 79) IC-14146-C, IS-346, NIC-16221, VOSI-5846, EC-334952, IS-118, NIC-8017, GRT-8630-C, SI-982, RJS-798-1-84, SI-3265-5, ES-141-1-84-C, IS-425-C, EC-100043, PCU-35, NIC-17362-A, IS-200, IS-136, IS-101, IC-81563, VOSI-8458, NIC-8322, IC-54035, SP-41, SI-2670, EC-14121, IS-335, IS-201-5, IS-146, IS-101-3, IC-204533, S-0062-A, KIS-357-A, KIS-297-2, IS-92-2, ES-310420, IS-113, NIC-8225, IS-750-1-84, SI-1032, IS-207, MT-67-18, IS-184-1, BELAL LOCAL, SI-3270, OMT-4, EC-303426, PCU-43, SI-983, SI-44, S-0527, LOLGIDA LOCAL, S-0268-C, SI-205-1, PCU-37, IS-172, SI-931, GT-10, SI-3265, NIC-8202, NIC-17274-C, ES-742-B, EC-303423-C.
II	15	(76, 81, 59, 64, 69, 83, 82, 89, 54, 57, 58, 77, 56, 29, 88) S-0223, JUBOND SESAME, NIC-13586, ES-58, KMR-69, GSM-21, SI-1865-1-B, 847-1-C, SI-3262, S-0175, IC-204500, IS-62-1, NAC/25/11/42/5/1, NAVILE, S-01159-C.
III	1	(53) S-0241
IV	1	(8) EC-31045
V	10	(32, 40, 42, 45, 39, 3, 34, 36, 41, 93) IS-107, PCU-40, PCU-36, PCU-41, GRT-8336, RJS-29, PCU-34, PCU-39, RJS-44, PCU-42.
VI	1	(80) S-0403
VII	6	(38, 55, 50, 13, 15, 11) PCU-38, NIC-16073, GT-1, IS-445, NIC-8025, IC-132408.
VIII	1	(68) ES-78
IX	1	(49) SI-3281
X	1	(51) RJS-6

The study revealed that D^2 values ranged from 36.60 TO 293.43 indicating the prevalence of greater magnitude of variability in the material studied. The inter cluster D^2 values exhibited a wide range from 52.12 (cluster - IV and cluster - VII) to 293.43 (cluster -VI and cluster -X) suggesting the presence of considerable amount of diversity among the clusters. It was further confirmed by range of intra cluster D^2 values which was from (cluster -II) to 65.28 (cluster -V). Similar results were reported by Ramesh (1993). In view of their evolution under near identical ecological niches or as a result of natural selection pressure, there was gradual increase of D^2 values over the range of germplasms. In contrast to

above findings, trehan *et al.* (1974) [12], Kulkarni (1985) Kulkarn [7] and Solanki and gupta (2004) [11] have reported the limited diversity in sesame. So the clusters showing high intercluster distance, meant wider genetic base could be used in hybridization programme and segregants could be obtained (Table 2).
Cluster means were computed for all the 12 characters studied on pooled basis and presented in table 3.

Table 2: Intra-cluster (diagonal) and inter-cluster D^2 and D values for 10 clusters formed by germplasm lines of Sesamum

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	38.19 (6.18)	82.99 (9.11)	59.13 (7.69)	67.24 (8.20)	95.844 (9.79)	61.46 (7.84)	98.01 (9.90)	132.71 (11.52)	149.08 (12.21)	159.76 (12.64)
II		36.60 (6.05)	155.00 (12.45)	74.99 (8.66)	154.50 (12.43)	164.35 (12.82)	117.50 (10.84)	72.42 (8.51)	168.74 (12.99)	79.38 (8.91)
III			0	135.25 (11.63)	135.95 (11.66)	64 (8)	137.35 (11.72)	182.79 (13.52)	196.84 (14.03)	240.56 (15.51)
IV				0	86.30 (9.29)	69.72 (8.35)	52.12 (7.22)	182.25 (13.50)	76.56 (8.75)	173.18 (13.16)
V					65.28 (8.08)	93.12 (9.65)	131.33 (11.46)	218.44 (14.78)	84.64 (9.20)	232.75 (15.24)
VI						0	110.67 (10.52)	260.17 (16.13)	156.50 (12.51)	293.43 (17.13)
VII							57.45 (7.58)	202.20 (14.22)	115.99 (10.77)	170.04 (13.04)
VIII								0	246.49 (15.70)	69.72 (8.35)
IX									0	253.12 (15.91)
X										0

Table 3: Mean values of 10 clusters of germplasm lines of Sesamum for quantitative traits

Clusters	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11	X12
I	46.21	89.89	90.82	3.45	92.28	30.48	2.33	0.84	47.91	5.52	2.68	46.39
II	46.00	91.77	94.23	3.38	88.80	30.26	2.27	0.78	48.86	6.11	2.72	38.17
III	47.00	95.50	120.50**	4.40**	90.25	23.90*	2.21	0.82	53.40	4.70	2.66	50.90
IV	44.00	91.50	86.10	3.90	83.00	46.00	1.95*	0.80	47.20*	9.69	2.92	44.65
V	48.85**	92.50	91.04	3.86	115.00	60.30	2.47	0.99	49.26	6.04	2.78	47.07
VI	44.00	89.00	80.50*	3.00	82.90	40.10	2.33	0.69 *	58.50*	7.83	3.00**	51.92**
VII	42.25*	90.58	107.05	3.75	122.39	41.03	2.48**	0.89	49.32	10.60**	2.71	45.32
VIII	45.00	93.00	105.40	2.80*	74.63*	25.50	2.42	0.84	57.30	3.55*	1.70*	36.21
IX	46.50	102.00**	113.64	3.80	97.27	67.00**	2.38	1.48 **	51.00	8.54	3.01	45.04
X	42.50	87.00*	100.40	3.78	177.60**	29.25	2.28	0.77	52.60	5.30	2.41	33.35*

Germplasm lines grouped within cluster VII were relatively early to flower (42.25 days) whereas; germplasm line grouped under cluster V was relatively late in flowering (48.85 days). Cluster III with one germplasm line exhibited the highest mean for plant height with 120.50 cm, whereas the cluster VI with one germplasm line had the lowest average of plant height 80.50 cm. Cluster III and Cluster IV consist of one germplasm line each, exhibited highest and lowest mean performance for capsule per plant of 67 and 23.9. Cluster VI and IV Cluster consist of one germplasm line each, exhibited highest and lowest mean performance for seed per capsule of 58.5 and 47.2. Cluster VII with six germplasm line exhibited the highest mean for seed yield per plant with 10.6, whereas the cluster VIII with one germplasm line had the lowest average of 3.55 for seed yield per plant. Cluster IX and Cluster VIII consist of one germplasm line each, exhibited highest and lowest mean performance for 1000 seed weight of 3.01 and 1.70. Cluster VI and Cluster X consist of one germplasm line each, exhibited highest and lowest mean performance for oil content of 51.92 and 33.35.Based on inter cluster distance farthest cluster and nearest cluster were made. The germplasms showing farthest inter cluster distance are need to be consider as parents in hybridization as they are showing higher diversity. Suppose if we chose the germplasm

from cluster I as one parent the opposite parent should be selected from cluster 10 as they are showing high inter cluster distance like this the germplasms from other cluster also selected from table 4.

Table 4: The nearest and the distant clusters from each cluster based on D^2 values

Cluster Number	Number of Germplasm	Nearest clusters	Farthest cluster
I	63	3	10
II	15	8	9
III	1	1	10
IV	1	7	8
V	10	9	10
VI	1	1	10
VII	6	4	8
VIII	1	10	6
IX	1	4	10
X	1	8	9

It is observed that 100 germplasms were distributed random among the clusters formed, based on their genetic distance. It was observed that oil content was the largest contributor towards divergence followed by seed yield per plant, capsule

per plant, plant height, days to maturity, 1000 seed weight, seeds per capsule, branches per plant, days to maturity, 1000 seed weight, seeds per capsule, branches per plant, days to 50 per cent flowering, capsule length and seeds per capsule. Similar kind of results was reported by Gangadhar Rao (2006) [5].Contribution of each character for genetic divergence was estimated from the number of times each character appeared in first rank. The germplasms of outstanding mean performance from the selected divergent clusters I, II, III, IV, V, V, VII, VIII, IX and X which may serve as potencial parents for hybridization programme are presented in table 5.

Table 5: percent contribution of each character towards genetic divergence

Character	(%) Contribution	Ranking
Days to 50% flowering	3.54	VII
Days to Maturity	4.42	VI
Plant height	0.89	XI
Branches per plant	0.69	XII
Leaves per plant	4.85	V
Capsules per plant	16.28	III
Capsule length (cm)	1.74	X
Capsule width (cm)	2.71	VIII
Seeds per Capsule	6.10	IV
Seed yield per plant (g)	18.61	II
1000 seed weight (g)	2.08	IX
Oil Content (%)	38.10	I
Total	100	

Germplasm from distant cluster are to be considered for inclusion in hybridization programme, while doing so, the germplasm developed with better values of characters are ought to be considered.

Conclusion
It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981) [2]. Therefore, based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster VI (S-0403) with the genotypes of cluster X (RJS-6) and cluster VIII (ES-78), which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in sesame.

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