Assessment of Genetic Diversity in Sesame (*Sesamum indicum* L.) Based on Agro-Morphological Traits

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ABSTRACT

Genetic divergence among parents is of paramount importance in selecting them for hybridization programme for crop improvement. Genetic divergence was assessed among 30 sesame genotypes which were evaluated in RBD with an objective to classify and understand the nature and magnitude of genetic diversity with regard to grain yield, yield components and quality traits using Mahalanobis D^2 statistics. The genotypes differed significantly regarding the characters studied and displayed marked divergence and were grouped into four clusters following Tocher's method. Cluster I had twenty-seven genotypes while the Cluster II, cluster III and cluster IV were monogenotypic comprised only one genotype each. The oil content exhibited maximum contribution towards divergence. The maximum inter cluster distance was recorded between cluster III and IV (2717.76) followed by cluster I and IV (1760.59), cluster II and III (991.96), cluster I and II (695.67), cluster I and III (637.32) and cluster II and IV (584.59) indicating the chances of getting high yielding recombinants would be better if the crosses are made among the

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genotypes of these groups under timely sown condition. The genotypes in cluster III and cluster IV, due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. The analysis of divergence indicated significant differences among parental lines for all the agro-morphological characters. Based on results obtained in the present investigation, it is concluded that the allelic diversity can be used for future breeding program. The traits under study are largely associated with each other and should be taken into consideration either simultaneously or alone for selecting a high yielding sesame genotype.

1. INTRODUCTION

Sesame (*Sesamum indicum* L.) is a crop, which is cultivated in diverse agroecological situations. It is called as the "Queen of oil seeds" because of its excellent qualities of the seed, oil and meal. Sesame is highly nutritive (oil 50%, protein 25%) and its oil contains an antioxidant called sesamol which imparts a high degree of resistance against oxidative rancidity. It is also an industrial food crop because of its high nutritional value [1].

India ranks first in the world in sesame cultivation (27.7% area) but its productivity is quite low (368 kg/ha) as compared to the world's average (489 kg/ ha) (www.fao.org). Sesame oil has highest antioxidant content and contains several fatty acids such as oleic acid (43 %), linoleic acid (35%), palmitic acid (11%) and stearic acid (7%) and stablility against oxidative raincidity owing to the occurrence of the natural antioxidants namely, lignans (sesamin, sesamolin and sesamol), and γ-tocopherol, which offers long shelf life to the sesame oil [2] and [3]. Sesame has a relatively superior oil quantity as well as quality in comparison to many major oil crops.

Even after being such an important oilseed crop in India, its large scale cultivation continues to be hindered by several factors like low oil content of currently available varieties, low seed production of existing varieties, non-availability of varieties suited to different agro-climatic conditions, susceptibility of the crop to untimely rains, lack of phyllody tolerance and non-synchronous maturity. One of the solutions to these problems is the proper utilization of genetic diversity available in sesame germplasm.

The success of any crop improvement programme essentially depends on the nature and magnitude of genetic variability present in the crop [4]. The knowledge of nature and magnitude of genetic variability is of immense value for planning efficient breeding programme, to improve the yield potential of the genotypes. Improvement in yield, is normally attained through exploitation of the genetically diverse parents in breeding programmes. Genetic divergence among parents is essential since the crossing programme involving genetically diverse parents is likely to produce high heterotic effects and also more variability could be expected in the segregating generations. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents. D² analysis is a use full tool for quantifying the degree of divergence between biological population at genotypic level and in assessing relative contribution of different components to the total divergence both in intra and inter-cluster level. It is also helpful in assessment of relative contribution of different components to the total divergence at both intra and inter-cluster level [5]. Genetic diversity between populations/genotypes indicates the differences in gene frequencies. For identifying such diverse parents for crossing, multivariate analysis using [6] D² statistic has been used in several crops. This is a valuable tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants. The present study was, thus, carried out to ascertain the nature and magnitude of genetic divergence among thirty sesame genotypes.

2. MATERIALS AND METHODS

The experiment comprised of thirty genetically diverse genotypes of sesame was carried out during *kharif,* 2018 at Instructional Farm, Tirhut College of Agriculture, Dholi, Muzaffarpur, Bihar, India. Agro climatically Instructional Farm is situated between 25.980 N latitude and 85.670 E longitudes at 51.8m above mean sea level. Experiment material obtained from All India Coordinated Research Project on Sesame & Niger (ICAR), JNKVV Campus, Jabalpur, Madhya Pradesh. The design adopted was Randomised Block Design (RBD) with three

replications. Each genotype in each replication was sown in three row plots of 4.0m length, adopting a spacing of 30 cm between rows and 20 cm between the hills. Recommended package of practices were applied to raise a good and healthy crop.

Five competitive plants were randomly selected for recording viz., plant height (cm), days to first flowering, days to 50% flowering, days to maturity, number of productive branches per plant, height of 1st capsule (cm), number of productive capsules per plant, number of seeds per capsule, biological yield per plant (g), harvest index (%), 1000 seed weight (g), stearic acid (%), linolenic acid (%), linoleic acid (%), oleic acid (%), palmitic acid (%), oil content (%), oil yield per plant (g) and seed yield per plant (g) on plot basis. For the oil content (%) thirty gram seed sample taken from clean seeds with 10-12 percent moisture of each genotype. The oil was extracted from whole seeds of each sample by Nuclear Magnetic Resources (N.M.R) at IIOR Rajendranagar, Hyderabad, India and expressed in percent. Fatty acid profile was observed with the help of standard equipment Gas liquid chromotograph at IIOR Rajendranagar, Hyderabad, India. The data recorded on different characters were statistically analyzed using software WINDOSTAT version 7.0 developed by Indostat Services Ltd., Hyderabad, India. The data were subjected to [6] D^2 analysis. Genetic diversity was estimated as per [6] D^2 statistics and clustering of genotypes was done according to Tocher's method as described by [7]. The percent contribution of characters towards genetic divergence was calculated according to [8].

3. RESULTS AND DISCUSSION

Based on D^2 statistics analysis the pattern of distribution of all the genotypes were grouped into four different clusters. The clustering pattern of genotypes is presented in Table 1. Clustering pattern indicated that 27 out of 30 genotypes belongs to the same cluster (cluster I); and remaning clusters (II, III and IV) were solitary clusters having single genotype in each (monogenotypic). Clustering pattern of sesame genotypes based on Tocher's method revealed a dendrogram Fig. 1. Clustering of genotypes was not associated with the geographical distribution and mainly grouped due to their morphological differences. Thus, showing evidence that geographical isolation is not the only factor causing genetic diversity in sesame. Clustering

pattern was random and independent. The clustering pattern suggested that geographic diversity may not necessarily be related with genetic diversity rather than geographic diversity and these results are in concordance with [9] and [10].

Among four clusters in sesame, maximum intra-cluster distance (240.64) was observed in cluster I while the lowest intra-cluster distance (0.00) was recorded with each cluster II, cluster III and cluster IV, whereas the highest inter cluster distance was recorded between cluster III and IV (2717.76) followed by cluster I and IV (1760.59), cluster II and III (991.96), cluster I and II (695.67), cluster I and III (637.32) and cluster II and IV (584.59). The highest intra-cluster distance observed in cluster I which indicates that the germplasm of cluster I was more diverged than any other cluster. There was comparative divergence of one cluster from another and higher divergence seen between clusters III and IV (2717.76) followed by clusters I and IV(1760.59), selection of lines to use them as parents for hybridization programme from these clusters will result in unique genotypes and generation of promising crossed material as proposed by [1,4,11-18].

There is another way by which superior lines are selected that is based on performance of lines with respect to cluster mean values Table 4. Nineteen quantitative character mean value had considerable differences with respect to all character studied. Cluster-I had high mean value for harvest index and oil content. The genotype GSM-21 in cluster-II has high mean value for trait number of productive branches per plant, height of first capsule and oleic acid. NIC-13586 genotype in cluster-III possesses highest mean value for trait plant height, days to first flowering, days to 50% flowering, days to maturity, number of productive capsules per plant, number of seeds per capsule, biological yield per plant, 1000 seed weight, palmitic acid, oil yield and seed yield per plant. The genotype ES-78 in Cluster-IV had high mean value of stearic acid, linolenic acid and linoleic acid. While, cluster-I had low mean value for traits such as plant height, height of first capsule, number of productive capsules per plant, and 1000 seed weight. The genotype GSM-21 in cluster-II had low mean value for harvest index stearic acid, linoleic acid, palmitic acid and oil content. The genotype NIC-13586 in cluster-III possesses lowest mean value for number of productive branches per plant and linolenic acid. The

genotype ES-78 in Cluster-IV possesses lowest mean value for days to first flowering, days to 50% flowering, days to maturity, number of seeds per capsule, biological yield per plant, oleic acid, oil yield and seed yield per plant. The genotype in comparable with check has good or better performance will be considered. The cluster with good mean value for traits are used in hybridization and superior genotypes can be produced.

Table 1. List of 30 sesame genotypes studied

Sl. no.	Genotypes	Sl. no.	Genotypes
1.	NIC-8202	16.	IC-14146-C
2.	IS-172	17.	ES-78
3.	IS-101	18.	IC-81563
4.	IS-750-1-84	19.	S-0223
5.	SI-199-2-84	20.	IS-62-1
6.	PCU-41	21.	EC-303423-C
7.	PCU-42	22.	S-0403
8.	PCU-43	23.	SI-1865-1-B
9.	RJS-44	24.	GSM-21
10.	IS-207	25.	IS-346
11.	S-0241	26.	S-01159-C
12.	NAC/125/11/42/5/1	27.	IS-201-S
13.	IC-204500	28.	OMT-4
14.	NIC-13586	29.	PRAGATI
15.	MT-67-18	30.	KRISHNA
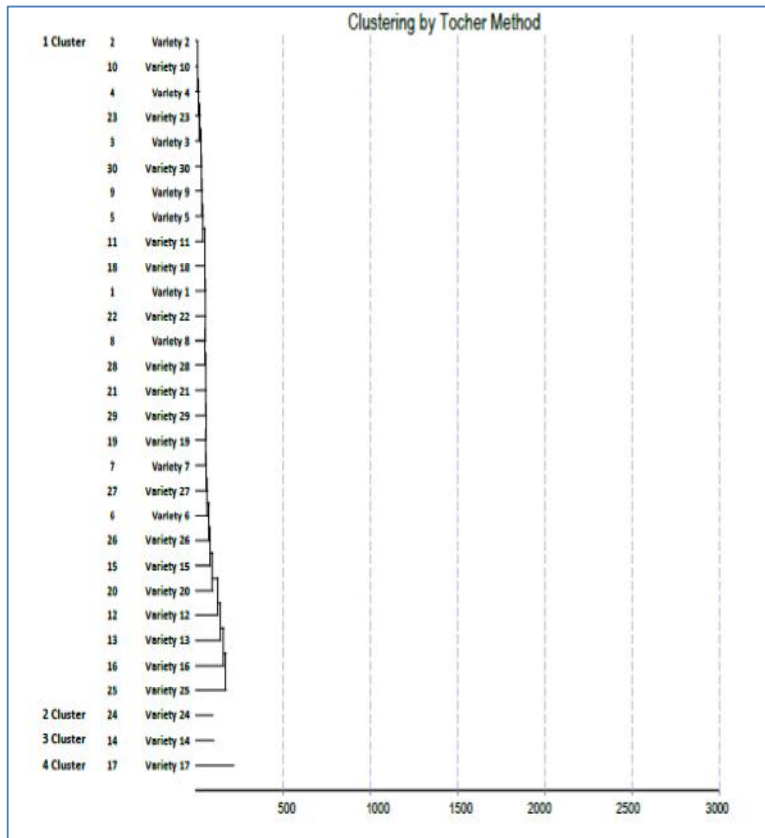
Fig. 1. Clustering pattern of 30 sesame genotypes on the basis of D^2 statistics by Tocher's method

Table 2. Distribution of 30 genotypes of sesame in different clusters based on D^2 statistics

Cluster	Number of genotypes	Genotypes included
I	27	IS-172, IS-207, IS-750-1-84, SI-1865-1-B, IS-101, KRISHNA, RJS-44, SI-199-2-84, S-0241, IC-81563, NIC-8202, S-0403, PCU-43, OMT-4, EC-303423-C, PRAGATI, S-0223, PCU-42, IS-201-S, PCU-41, S-01159-C, MT-67-18, IS-62-1, NAC/125/11/42/5/1, IC-204500, IC-14146-C, IS-346
II	1	GSM-21
III	1	NIC-13586
IV	1	ES-78

Table 3. Intra and Inter cluster distance (D^2) among four clusters in sesame

Sources	Cluster Ist	Cluster IInd	Cluster IIIrd	Cluster IVth
Cluster Ist	**240.64**	(695.67)	(637.32)	(1760.59)
Cluster IInd		**0.00**	(991.96)	(584.59)
Cluster IIIrd			**0.00**	(2717.76)
Cluster IVth				**0.00**

Intra-cluster (D^2): in bold
Inter-cluster (D^2): in parentheses

The percentage of contribution towards genetic divergence by all the characters is presented in Table 5. The trait Oil Content (%) contributed maximum to genetic divergence by taking times first rank followed by linolenic acid, stearic acid, biological yield per plant, number of productive capsules per plant, linoleic acid, harvest index, palmitic acid, seed yield per plant, oleic acid, number of productive branches per plant. Lowest contribution was given by the plant height and days to 50 % flowering by taking one time rank first. The remaining traits in manifestation of genetic divergence was zero towards divergence.

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 [19]. It has also been observed that the most productive hybrids may come from high yielding parents with a high genetic diversity [17].
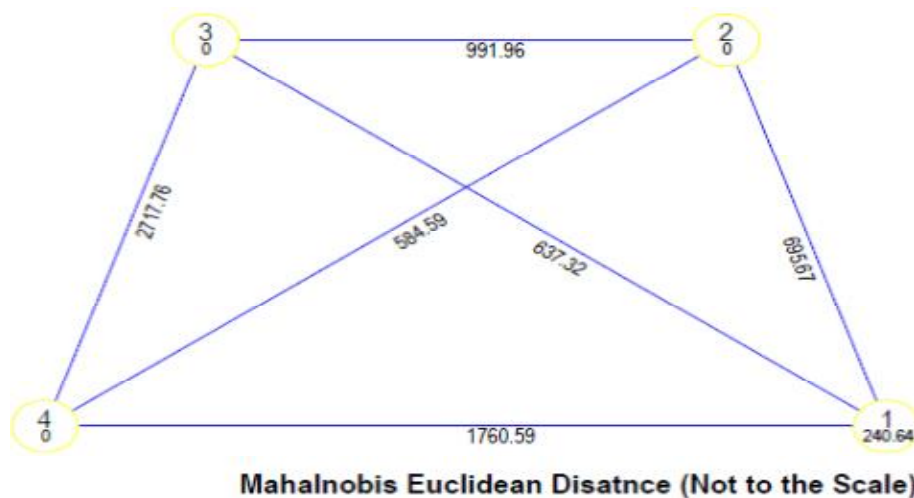
Fig. 2. Intra and inter cluster distance (D^2) among four clusters in sesame by Tocher's method

Table 4. Cluster mean for nineteen characters among the genotypes in sesame

	PH (cm)	DFF	D50% F	DM	NPB/P	HFC (cm)	NPC/P	NS/C	BY/P(g)	HI (%)	TSW (g)	SR Acid (%)	LEN Acid (%)	LEI Acid (%)	OL Acid (%)	PM Acid (%)	OC (%)	OY (%)	SY/P (g)
Cluster I[st]	166.91	45.59	51.74	97.02	6.65	108.00	118.51	64.98	124.64	11.79	3.55	4.61	0.38	43.90	41.78	9.33	36.77	4.74	12.92
Cluster IInd	215.83	45.00	51.33	95.00	9.00	154.00	122.67	64.67	250.40	5.25	3.87	4.50	0.62	41.81	43.87	9.19	27.53	3.63	13.17
Cluster IIIrd	225.17	55.67	60.33	100.33	5.67	142.80	171.00	95.33	369.83	5.69	4.47	4.89	0.37	44.24	40.09	10.40	34.84	7.31	20.98
Cluster IVth	169.67	41.67	49.33	93.67	6.00	112.23	136.00	55.67	110.35	6.86	3.73	5.36	0.85	44.76	39.53	9.50	29.67	2.26	7.63

PH: Plant Height (cm)
DFF: Days to First Flowering
D50%F: Days to 50% Flowering
DM: Days to Maturity
NPB/P: Number of Productive Branches/Plant
HFC: Height of First Capsule (cm)
NPC/P: Number of Productive Capsules /Plant
NS/C: Number of Seeds /Capsule
BY/P: Biological Yield/Plant
HI: Harvest Index (%)
TSW: Thousand Seed Weight (g)
SR ACID: Stearic Acid (%)
LEN ACID: Linolenic Acid (%)
LEI ACID: Linoleic Acid (%)
OL ACID: Oleic Acid (%)
PM ACID: Palmitic Acid (%)
OC: Oil Content (%)
OY: Oil yield/ plant (%)
SY/P: Seed Yield/ Plant (g)

Table 5. Independent character contribution towards total divergence in nineteen characters of sesame

Sl. no.	Source	Time ranked first	Percent of contribution
1	Plant height (cm)	1	0.23
2	Days to first flowering	0	0.00
3	Days to 50% flowering	1	0.23
4	Days to maturity	0	0.00
5	Number of productive branches per plant	2	0.46
6	Height of 1st capsule (cm)	1	0.23
7	Number of productive capsules per plant	23	5.29
8	Number of seeds per capsule	0	0.00
9	Biological yield per plant (g)	37	8.51
10	Harvest index (%)	7	1.61
11	1000 seed weight (g)	0	0.00
12	Stearic acid (%)	54	12.41
13	Linolenic acid (%)	71	16.32
14	Linoleic acid (%)	11	2.53
15	Oleic acid (%)	3	0.69
16	Palmitic acid (%)	6	1.38
17	Oil content (%)	213	48.97
18	Oil yield per plant (%)	0	1.15
19	Seed yield per plant (g)	5	0.00

4. CONCLUSION

The present study revealed that the selection of parents for genetic improvement should be based on their inter cluster distance and better mean performance for yield, yield components and quality traits and contribution of different characters towards total genetic divergence. Among the four clusters, cluster I consists of maximum number of genotypes forming the largest cluster and rest of the clusters were found to be mono-genotypic. The genotype in cluster III and cluster IV due to maximum inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized in future for heterosis breeding programme for getting high yielding recombinants.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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