Plant Archives Vol. 25, Supplement 2, 2025 pp. 2198-2204 e-ISSN:2581-6063 (online), ISSN:0972-5210

Plant Archives

Journal homepage: http://www.plantarchives.org
DOI Url : https://doi.org/10.51470/PLANTARCHIVES.2025.v25.supplement-2.279

MORPHOLOGICAL CHARACTERIZATION OF SESAME (*SESAMUM INDICUM* L.) GENOTYPES

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(Date of Receiving : 03-04-2025; Date of Acceptance : 11-06-2025)

ABSTRACT

Sesamum indicum, the cultivated type, is originated in India (Ogasawara *et al.*,, 1988). Characterization and quantification of genetic diversity has long been a major goal in evolutionary biology. The analysis of genetic variation within and among elite breeding materials is of fundamental interest to plant breeders. It contributes to monitoring of germplasm and can also be used to predict potential genetic gains. The knowledge of genetic variability in germplasm will help in the selection and breeding of high yielding, good quality cultivars that will increase production. India is wealthy of sesame germplasm and some local cultivars provide raw material for improved varieties (Ali *et al.*,, 2009). To determine the level of diversity in relation to geographical origins and morphological characteristics, a total of 60 accessions collected from different parts of the India were analyzed using statistical techniques for thirteen quantitative and four qualitative parameters using D^2 analysis. Number of seeds per capsule contributed highest towards the divergence. The distribution pattern of genotypes in different clusters indicates that genetic divergence was not related to geographical differentiation.
Keywords: D^2 analysis; Euclidean distance; genetic diversity; morphological traits; *Sesamum indicum* L.

Introduction

Sesame (*Sesamum indicum* L., Pedaliaceae) is the most commonly cultivated edible oil crop species out of over 30 species in the genus *Sesamum* (Nayar and Mehra 1970; Kobayashi *et al.,* 1990. India, China, Burma and Sudan are the major sesame producing countries that contribute to about 60% of the total world production. Sesame is one of the nine major oilseed crops of India. It is an important kharif crop mainly cultivated in states of Gujarat, Rajasthan, Andhra Pradesh, Tamil Nadu, Madhya Pradesh, Maharashtra, Karnataka, Uttar Pradesh, West Bengal, Orissa and Assam. Genetic diversity in crop species can be determined by using the agro-morphological as well as biochemical and molecular markers (Liu 1997; Geleta *et al.,* 2007, 2008). Studies on sesame genetic diversity and divergence have been mainly based on agro-morphological traits. Several of these agro-morphological trait based studies have found a high genetic diversity in sesame populations (Bisht *et al.,* 1998; Arriel *et al.,* 2007). Amelioration of productivity necessitates us to detection or cataloguing of sesame genotypes along with the assessment of genetic variability in sesame germplasm. (Manisha *et al.,* 2020)

Materials and Methods

Plant Material

Germplasm of *Sesamum indicum* L. collected and stored by National Bureau of Plant Genetic Resources (N.B.P.G.R) Rajendranagar, Hyderabad from eight different states of India, were selected for the present study. Details of the germplasm accessions are furnished in Table 1. The experiment was carried out during late *Kharif* 2008-09. The experimental materials were sown in simple Randomised Block Design with 60 ×10 cm spacing in three replications at College Farm, College of Agriculture, PJTSAU, Rajendranagar, Hyderabad. Recommended agronomic practices and prophylactic measures were adopted for raising a good crop for field observation.

Table 1: Details of the experimental material included for the study

S.No	Accession No.	State	S.No	Accession No.	State
1	IC751	Maharastra(13)	31	IC14329	Madhyapradesh(24)
2	IC16225		32	IC21705	
3	IC16236		33	IC23233	
4	IC16238		34	IC23271	
5	IC16243		35	IC23321	
6	IC16248		36	IC23325	
7	IC16249		37	IC23327	
8	IC16250		38	IC23332	
9	IC41906		39	IC23335	
10	IC41910		40	IC23341	
11	IC41911		41	IC23346	
12	IC41912		42	IC41932	
13	IC41978		43	IC41948	
14	IC14080	Rajasthan(8)	44	IC41953	
15	IC14106		45	IC41962	
16	IC14135		46	IC41964	
17	IC14155		47	IC41966	
18	IC14174		48	IC42200	
19	IC26303		49	IC52585	
20	IC42965		50	IC52586	
21	IC42987		51	IC52592	
22	IC14163	Gujarat(8)	52	IC52593	
23	IC43169		53	IC52599	
24	IC43171		54	IC52600	
25	IC43177		55	IC96098	Uttar Pradesh(3)
26	IC43179		56	IC96109	
27	IC43181		57	IC96113	
28	IC43185		58	IC16832	Punjab(2)
29	IC43217		59	IC31379	
30	IC20156	Nagaland(1)	60	IC96079	Himachal Pradesh(1)

Statistical Analysis

The data recorded were subjected to the following statistical analysis:

Anova

Difference between genotypes for various characters was tested for significance by using analysis of variance technique as suggested by Panse and Sukhatme (1957).

Variance

The genotypic and phenotypic variances were calculated as per the formula suggested by Burton and Devane (1953).

Genetic diversity

The genetic diversity in 60 genotypes for characters was estimated using Mahalanobis's (1936) D^2 statistic technique.

Contribution of individual characters towards divergence

In all the combinations, each character was ranked on the basis of its contribution towards divergence between two entries ($d_{i} = y_{it} - y_{jt}$). Rank- I was given to the highest mean difference and rank-P to the lowest differences. 'P' is the total number of characters considered.

Heirarchial method of clustering of genotypes into various clusters

Clustering of genotypes into different clusters was done by using Euclidean method.

Intra and inter cluster distances

Based on D^2 values, average intra and inter cluster distances were calculated as per Euclidean method.

Results

Sixty sesame germplasm accessions were characterized for the morphological characters using descriptor guidelines developed by IPGRI. The

descriptors were unambiguous and easily identifiable. Characterization was done for each genotype to establish their diagnostic features.

The experimental material exhibited large variability for all of the morphological characters.

Mean performance

Mean performance for the thirteen quantitative characters are presented in Table 2.

Table 2 : Mean performance for the thirteen quantitative characters

Trait / Accession	Plant height (cm)	Branches /plant	No of leaves/ plant	leaf length (cm)	leaf width (cm)	No of nodes/ mainstem	Internode length (cm)	No.of flowers / plant	No. of flowers / Axil	No.of capsules / plant	No. of seeds / capsule	seed weight (gm)	Seed yield /Plant (gm)
Mean	**25.6297**	**4.0628**	**72.3097**	**3.2953**	**1.0820**	**3.6783**	**3.7453**	**43.8588**	**1.0333**	**43.4770**	**50.8995**	**2.7243**	**5.6336**
C.V.	15.0773	43.5200	21.7463	20.9874	28.6289	45.4369	18.7708	19.9311	0.0000	17.2046	11.3103	5.7380	25.2867
F ratio	1.7242	1.7007	3.2847	1.6387	1.1001	1.8242	1.1609	4.1567	0.0000	6.2651	11.9878	2.6299	4.9843
F Prob.	0.0063	0.0075	0.0000	0.0119	0.3266	0.0029	0.2450	0.0000	1.0000	0.0000	0.0000	0.0000	0.0000
S.E.	2.2310	1.0208	9.0787	0.3993	0.1788	0.9649	0.4059	5.0469	0.0000	4.3186	3.3237	0.0903	0.8225
C.D. 5%	6.2481	2.8589	25.4252	1.1183	0.5008	2.7023	1.1367	14.1341	0.0000	12.0944	9.3083	0.2528	2.3034
C.D. 1%	8.2607	3.7797	33.6149	1.4785	0.6622	3.5728	1.5029	18.6869	0.0000	15.9902	12.3066	0.3342	3.0453
Min	15.6500	1.9000	44.7000	1.3000	0.7000	1.8000	3.0000	22.4000	1.0000	18.5000	22.6000	2.3667	2.3433
Max	32.8333	6.9333	119.2667	4.6000	1.8000	7.4000	5.3333	68.8000	2.0000	67.8667	72.4000	2.9800	10.8600

Qualitative characters

Two types of Leaf shapes were observed; entire and lobed. Only one accession showed the lobed type of shape whereas the remaining accessions showed entire type.

The Flower colour for all the accessions was found to be white with purple shading.

Six coloured seeds were observed (white, black, brown, grey, light brown, and reddish brown). Among the sixty accessions studied, forty were white, one brown, seven reddish brown, two light brown, four grey, and six were black

Capsule beak was long in all the accessions studied.

Analysis of Variance

ANOVA showed significant differences for all the traits evaluated. The results of ANOVA are presented in Table 3.

Variability

Among the thirteen characters studied, seed yield (29.14%) recorded higher GCV, followed by nodes/main stem (23.82%), while least GCV was recorded for seed weight (4.23%). Highest PCV was recorded by number of branches/plant (48.34%) and the least PCV by seed weight (7.13%) (Table 4).

Table 4: Coefficient of variability for thirteen characters in 60 sesame genotypes

Sl.No	Character	PCV (%)	GCV (%)	ECV (%)
1	Plant height	16.7	7.4	15.02
2	No. of branches/plant	48.3	21.03	43.52
3	No. of leaves/plant	28.6	18.97	21.7
4	Leaf length	23.11	9.68	20.9
5	Leaf width	29.10	5.2	28.6
6	No.of nodes/mainstem	51.3	23.8	45.4
7	Internode length	19.3	4.3	18.8
8	No.of flowers/plant	28.55	20.44	19.93
9	No.of flowers/axil	17.51	17.51	0.0
10	No.of capsules/plant	28.55	22.79	17.20
11	No.of seeds/capsule	24.42	21.64	11.3
12	1000 seed weight	7.12	4.22	5.73
13	Seed yield	38.6	29.14	25.28

The difference between the PCV and GCV values for nodes/main stem was high indicating the influence of environment on these traits. However, the difference between the PCV and GCV values for other characters was low indicating minimum effect of environment.

Table 3 : Analysis of variance for thirteen characters of 60 sesame genotypes

	df	C/P	LL	LW	PH	B/P	IL	N/M	L/P	F/P	SW	SY	N/A	Ns/c
Replicate	2	246.4*	13.12**	0.1615	172.24**	81.39**	3.65**	110.00**	22.3048	168.0608	0.0382	23.79**	0.0000	27.1854
Treatments	59	350.53**	0.7838*	0.1056	25.7461**	5.3167**	0.5738	5.0956**	812.18**	317.63**	0.06**	10.11**	0.0983**	397.9**
Error	118	55.9511	0.4783	0.0959	14.9326	3.1262	0.4942	2.7933	247.2663	76.4144	0.0244	2.0294	0.0000	33.1417

C/P-capsules per plant, B/P-branches per plant, F/P-flowers per plant, Ns/C-number of seeds/capsule, LL-leaf length, IL- internode length, SW-seed weight LW-Leaf width, N/M-nodes per mainstem, SY-seed yield, PH-plant height, L/P-leaves per plant, N/A-number of flowers per axil

**Significant at 1% level

* Significant at 5 % level

Genetic divergence

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistics for yield and its contributing characters. D^2 statistic was carried out following the procedure of Rao (1952).

The distribution of 60 genotypes of sesame into different clusters is presented in Table 4.

Table 4: Distribution of 60 sesame genotypes into different clusters

Cluster no	No. of Accessions	Accessions
I	4	IC14080, IC 52600, IC 43185, IC 96098
II	7	IC 16243, IC 20156, IC 16248, IC43217, IC 52593, IC 23335, IC 14329
III	7	IC 23271, IC 52592, IC 43169, IC 23332,IC 41964, IC 14174, IC 96079
IV	5	IC 16236, IC 41948, IC 41932, IC751, IC52599
V	10	IC 16238, IC 42987, IC 42965, IC 16250, IC 52586, IC 41910, IC 41911, IC 16249, IC 42200,IC 96109
VI	13	IC 14106, IC43177, IC 14135,IC 41966,IC 21705,IC 23321,IC 23341, IC 16225,96113,IC 14155, IC 41978, IC 41953, IC 26303
VII	7	IC 16832, IC 23346, IC 41912, IC 23233, IC 41906, IC31379, IC 43181
VIII	7	IC 23325,IC 52585, IC14163,IC 23327, IC43179, IC41962, IC43179

Average intra and inter cluster distances

The average intra and inter cluster D^2 values are presented in Table 7. Intra cluster values ranged from 10.31 (Cluster II) to 17.32 (Cluster VII) (Fig 2 and 3). From the inter-cluster distances, it can be inferred that highest divergence occurred between Cluster I and VII (64.2), while it was least between Cluster II and Cluster III (16.88) (Table 6).

Table 5 : Cluster means for thirteen characters

	Plant height (cm)	Branches / plt	leaves / Plt	leaf length (cm)	leaf width (cm)	Nodes/ Main stem	Internode length (cm)	Flowers / plt	Capsules / plt	No. of seeds/ capsule	seed weight (gm)	Seed yield (gm)
Cluster I	25.9	4.90	60.95	3.28	0.988	4.55	3.52	39.96	39.43	70.48	2.59	4.80
ClusterII	26.8	4.62	67.47	3.78	1.104	4.66	3.55	39.67	38.89	55.51	2.64	5.17
ClusterIII	23.2	2.45	61.91	2.60	0.930	2.38	3.92	31.63	30.87	60.95	2.81	4.54
ClusterIV	24.0	4.83	80.17	3.57	1.469	4.11	3.78	29.20	27.83	46.43	2.63	3.49
ClusterV	26.5	4.43	79.80	3.48	1.053	3.91	3.56	51.93	51.46	61.29	2.83	8.41
ClusterVI	25.5	3.49	69.66	3.14	1.079	3.00	3.98	41.88	40.77	43.11	2.73	4.84
ClusterVII	24.9	4.47	68.09	3.28	1.067	4.04	4.03	54.10	53.75	36.97	2.67	5.91
ClusterVIII	27.6	4.20	86.85	3.35	1.053	3.74	3.39	54.88	57.54	41.80	2.76	6.43
Mean	25.6	4.06	72.31	3.29	1.082	3.68	3.74	43.86	43.48	50.90	2.72	5.63
TreatMSS	14.7	4.72	571.6	0.87	0.138	4.26	0.46	655.89	772.24	899.52	0.052	17.98
ErrMSS	7.76	1.38	230.22	0.18	0.021	1.35	0.16	31.83	28.61	29.17	0.017	1.40
F Ratio	1.88	3.43	2.48	4.81	6.46	3.14	2.91	20.60	26.98	30.83	3.01	12.8
Probability	0.09	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.01	0.00

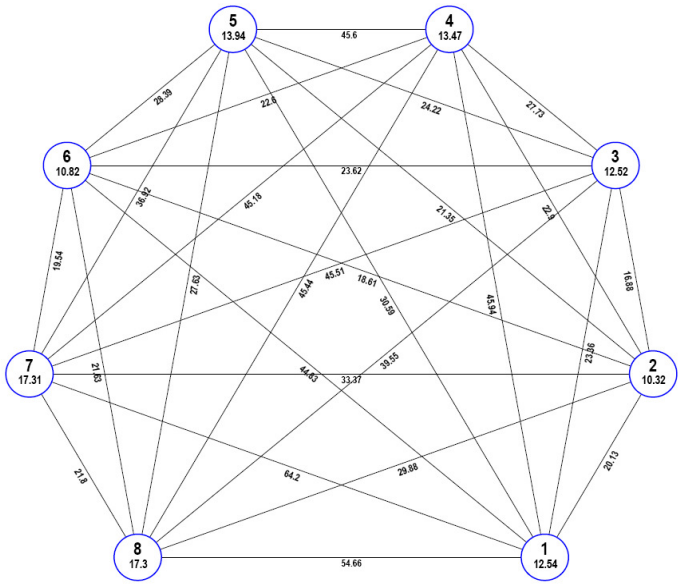

Fig. 2 : Cluster diagram representing diversity for 60 Sesamum genotypes

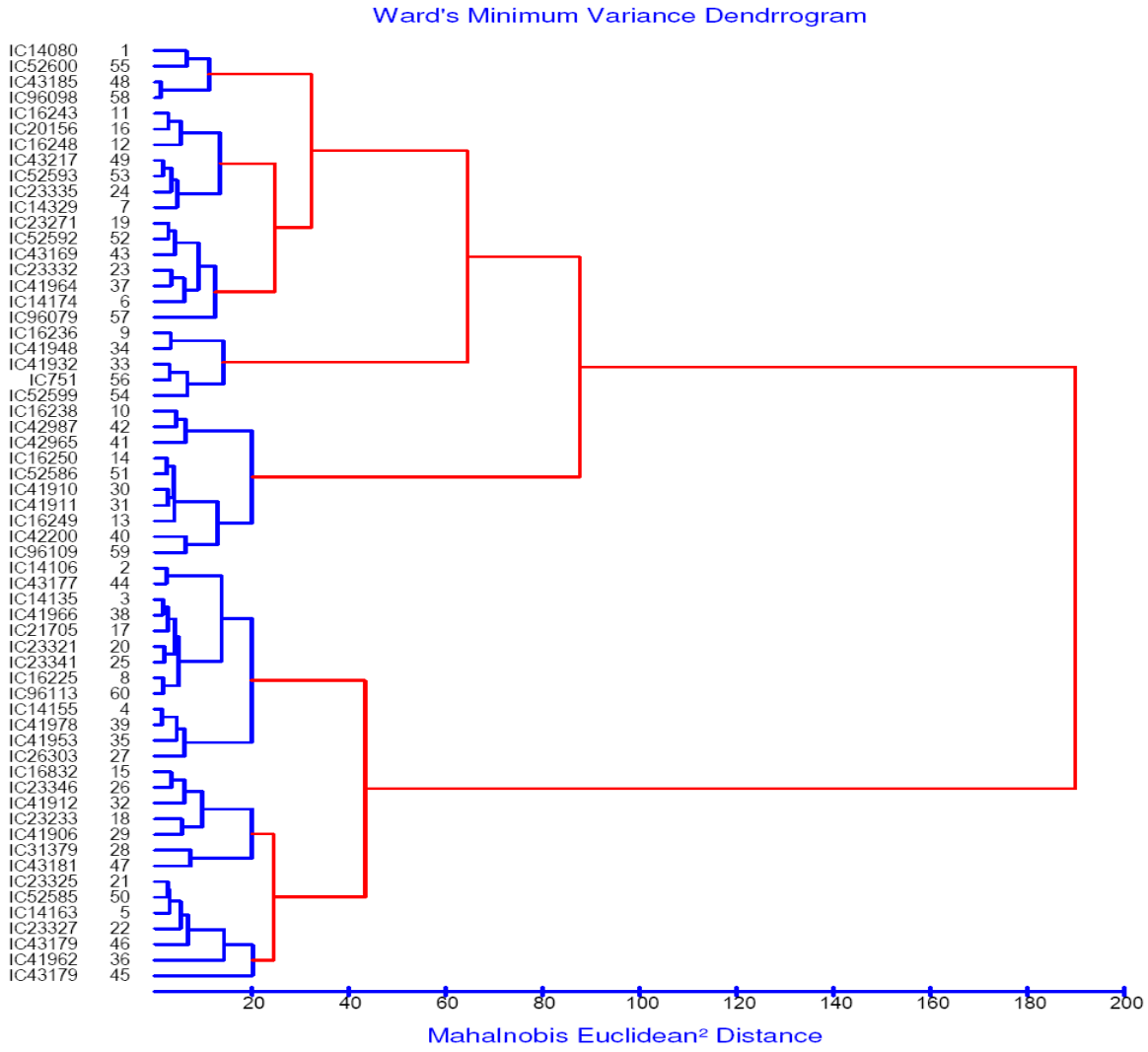

Fig. 3 : Ward's minimum variance dendrogram

Table 6 : Average intra(bold)and inter Euclidean cluster distances

	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	**12.540**	20.131	23.357	45.941	30.589	44.831	64.196	54.660
Cluster II		**10.318**	16.875	22.901	21.350	18.615	33.374	29.877
Cluster III			**12.521**	27.734	24.222	23.623	45.509	39.550
Cluster IV				**13.473**	45.598	22.603	45.176	45.437
Cluster V					**13.940**	28.391	36.924	27.629
Cluster VI						**10.816**	19.537	21.628
Cluster VII							**17.315**	21.796
Cluster VIII								**17.304**

Discussion

The diversity analysis of 60 accessions of *S. indicum* L. carried out by using morphological and the data was analyzed by Cluster analysis. The Ward's minimum variance dendrogram based on morphological characters showed that accessions of same origin did not group in same cluster. The first cluster showed more subclusters than the second cluster thus showing considerable phenotypic variation of morphological characters of *S. indicum*. The phenotypic differences may be due to genetic diversity which may in turn be due to allelic diversity. Genetic variability among Indian sesame accessions is very high as shown both for the morphological (Bisht *et al.,* 1998; Banerjee & Kole, 2006) and molecular markers (Bhat *et al.,* 1999; Laurentin & Karlovsky 2006). The aim of this study was to bring results that could help Indian sesame breeders to select suitable parental material for crossing and increase the efficiency of selection in combination with other diversity data.

As per the character number of flowers per leaf axil which is one of the important characters for plant breeding programs. Most of the varieties (96.6%). observed to have one flower per axil. Only two varieties, IC31379 (Punjab), IC21705 (M.P) of the sixty accessions, bear two flowers per axil as there is not much variation.

As the number of capsules per plant is one of important contributing character to seed yield of sesame (Ibrahim *et al.,* 1983; Osman, 1989), plants with two flowers per leaf axil are important resources for plant breeding programs.

Observed data revealed that variation was least for qualitative characters like leaf shape, flower colour, seed colour and type of capsule beak. And only one flower colour *i.e.* white with purple shading is observed which is similar in Indian sesame collection.

The analysis of variance revealed significant difference among the genotypes for each character, indicating the existence of variability among the genotypes for the character studied.

The cluster analysis based on agro-morphological traits assigned the sixty sesame germplasm accessions into eight main clusters. A dendogram grouped the sesame accessions into individual groups. As per the cluster analysis, the germplasm was not separated based on geographical origin and result is in agreement with findings of Dixit and Swain (2000) and Gupta *et al.* (2001). Some ecological conditions may also lead to gene flow between populations from different geographical origins.

Sixty genotypes were grouped into eight clusters based on D^2 values. The pattern of group constellations proved that significant amount of variability existed. It is noted that some genotypes representing differences in their origin were grouped in the same cluster. This indicates the absence of relationship between genetic diversity and geographic diversity. Similar results have been reported by Ganesh and Thangavelu (1996), Manivannan and Nadarajan (1996), Swain and Dikshit (1997), Johnjoel *et al.* (1998) and Gupta *et al.* (2001).

The number of seeds per capsule contributed highest towards the divergence followed by number of capsules per plant. All other characters showed negligible contribution. Alarmelu and Ramanathan (1998) and Sudhakar *et al.* (2006) recorded similar observations.

There was a wide range of variation in the cluster mean values for most of the characters under study. Therefore a crossing program should be initiated between the genotypes belonging different clusters. The greater the distance between two clusters, the wider the genetic diversity among the parents to be included in hybridization program.

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