Received: 04 Sep 2022 | Revised: 27 Mar 2023 | Accepted: 28 Mar 2023

Electronic Journal of Plant Breeding

Research Note

Genetic diversity analysis in sesame (*Sesamum indicum* L.)

K. Mukhthambica[1*], R. Bisen[1] and K.T. Ramya[2]

[1]Jawaharlal Nehru Krishi Vishwavidyalaya
[2] Indian Institute of Oilseeds Research
***E-Mail:**mukhthambica1998@gmail.com

Abstract
In the present investigation, 70 genotypes of sesame were characterized for 12 morphological and 14 quantitative characters and subjected to genetic divergence (UPGMA hierarchial clustering) analysis. It revealed that a considerable amount of genetic variability was exhibited for majority of the morphological traits except for locule number per capsule, capsule number per leaf axil and capsule shape. In divergence analysis for both morphological and quantitative characters, 70 genotypes were grouped into seven clusters at the genetic distance of 0.5 using Ward's minimum variance method and Gower's method of genetic distance. Selection of the genotypes present in different clusters having more genetic distance, preferably belonging to different geographical origin may result in more heterotic effects in the hybridization programme. Good recombinants can be obtained by mating between clusters I and VII for genotypes *viz.,* GJT-5, RT-46 with TMV-3, VRI-3, Paiyur 1 as they have maximum genetic distance between them. Most of the characters recorded high mean values in cluster VII. Hence, for improvement of these traits, the genotypes present in cluster VII could be exploited as parents.

Keywords: Sesame, Diversity, Cluster, UPGMA

Sesame (*Sesamum indicum* L.), order Tubiflorae and family Pedaliaceae, is an ancient oilseed crop known to mankind. It is originated and domesticated in India and is widely grown in tropical and sub-tropical regions of the world (Bedigian, 2003). It is commonly called as 'Til.' 'Benni seed' and 'Gingelly'. Sesame is diploid with chromosome number 2n=26 and genomic size of ~369Mb (Zhang *et al*., 2013). It is considered the "Queen of oilseeds" because it has excellent nutritional properties, antioxidant properties and a long shelf life. Sesame oil is used for preparing cosmetics and is the base of many Ayurvedic preparations. Sesame meal is used as feed for poultry and livestock.

Sesame ranks sixth in production among oilseeds, i.e., after soybean, groundnut, cottonseed, sunflower, linseed and rapeseed globally. International demand for sesame is increasing across the globe and has increased nearly 80% since 2000. In 2019, Myanmar was the leading country in production followed by India (FAOSTAT, 2020). In India, among oilseed crops, sesame ranks fourth in area (1,730,000 ha) with a production of 7,46,346 metric tons and productivity of 431 kg/ha. India has a large area under cultivation, but the total production and productivity is quite low (431 kg/ha) as compared to the world's average (512 kg/ ha) (Myint *et al*., 2020). This is because sesame is one of the most neglected oilseed crops grown in marginal lands under poor management. Further, poor yield of the crop is due to the non-availability of improved cultivars for diverse agro-climatic conditions and a poor seed supply system. The existence of variation is a prerequisite for the success of any crop improvement programme for which characterization of agro-morphological traits of germplasm is required. It is simple and requires a relatively lower cost which makes it an interesting tool for studying genetic diversity but it

is subjected to high environmental influence (Banerjee and Kole 2009; Tabatabaei *et al*., 2011). Despite these limitations, it is still widely used for assessing genetic diversity. The genotypes that are genetically distant for traits, contributes genetic divergence, are expected to generate a wide range of genetic variation in recombination breeding and pave the way for greater scope for the recovery of transgressive segregants (Sharma *et al*., 2008). The successful recovery of heterosis has been reported in crosses involving genetically diverse parents (Singh *et al.,* 2007 in mustard; Dong *et al.,* 2003 in soybean; Pasquet *et al.,* 2002 in groundnut; Khan *et al.,* 2013 in linseed; and Yousuf *et al.,* 2011 in rapeseed). The understanding of genetic diversity and phylogenetic relationships among sesame cultivars will be critical in selecting genotypes for crop improvement under adverse conditions. Therefore, an attempt has been made to quantify the magnitude of *inter se* genetic divergence between each pair of test genotypes and identify highly divergent genotypes to tailor desirable gene combinations through recombination breeding.

The field experiment was conducted during Summer 2021 at the Research Farm, Indian Institute of Oilseeds Research (IIOR), Narkhoda, Hyderabad, Telangana, India. The plant material used in the experiment comprised of 70 released varieties of sesame except IIOS-1101 (pre-released variety) which were collected from IIOR and AICRP, Sesame and Niger (**Table 1**). The experimental design adopted was Randomized Complete Block design with two replications. Under the present investigation, morphological characterization was done based on the botanical and morphological characteristics of plants and plant parts. The characters under study were based on DUS guidelines with 12 different morphological categories *viz.,* petal color, petal hairiness, branching pattern, stem hairiness, leaf lobes, leaf margin, capsule hairiness, capsule shape, capsule number per leaf axil, capsule arrangement and seed coat color and also 14 quantitative characters like days to emergence, days to 50% flowering, days to flower cessation (completion), days to maturity, length to first capsule (cm), plant height, primary branches per plant, secondary branches per plant, capsule number per plant, number of leaf axils on main stem, capsule length(cm), test weight (g), oil content (%) and seed yield per plant (g). Observations on the above traits were recorded on the five random competitive plants, except for the traits days to emergence, days to 50% flowering, days to flowering cessation (completion), days to maturity, which were recorded on plot basis.

Table 1. Details of the experimental material

1.AKT-101	25.N-32	49.TKG-22
2.AKT-64	26.Nirmala	50.TKG-306
3.Amrit	27. Phule Til-1	51.TKG-308
4.B-67	28. Paiyur	52.TKG-55
5.Chandana	29. PKDS-11	53.TMV-3
6.CUMS-17 (Suprava)	30. PKDS-8	54.TMV-4
7.DS-5	31.Prachi	55.TMV-6
8.DSS-9	32.Pragati	56.TMV-7
9.E-8	33.Punjab Til-1	57.TSS-6
10.GJT-5	34. Punjab Til-2	58. Tarun
11.GT-1	35. Rajeshwari	59. Thilak
12.GT-10	36. Rama	60. Thilottama
13.GT-2	37. RT-103	61.Thilarani
14.GT-3	38. RT-125	62.Uma
15.GT-4	39. RT-127	63.Usha
16.HT-1	40. RT-346	64.VRI-1
17.HT-2	41. RT-351	65.VRI-2
18.Hima	42. RT-372	66.VRI-3
19.IIOS-1101	43. RT-46	67.Vinayak
20.JLT-408	44.Savitri	68.YLM-11
21.JLT-7	45.Shubra	69.YLM-17
22.JTS-8	46.Smarak	70.YLM-66
23.Kanak	47.Swetha Til	
24.Krishna	48.T-78	

The genetic divergence of 70 sesame genotypes were determined by using both morphological and quantitative characters, which were used as input for UPGMA (unweighted pair group method with arithmetic mean) cluster analysis. The UPGMA is a simple agglomerative (bottom-up) hierarchical clustering method attributed by Sokal and Michener (1958). UPGMA clustering is done using Ward's minimum variance method and Gower's method of genetic distance (Gower, 1971). The dendrogram is constructed using R software version 4.1.0.

In the present investigation, 70 sesame genotypes were characterized morphologically as per the DUS guidelines *viz*., petal color (**Fig. 6,7,8**), petal hairiness, branching pattern, stem hairiness, leaf lobes, leaf margin, capsule number per leaf axil (**Fig. 4,5**), capsule hairiness, locule number per capsule, capsule shape, capsule arrangement (**Fig. 1,2,3**), and seed coat color. The categorization of different genotypes on the basis of 12 morphological traits are furnished in **Table 2**.

It revealed that a considerable amount of genetic variability was exhibited for the majority of morphological traits except for locule number per capsule, capsule number per leaf axil and capsule shape, in which 100% of the genotypes have four locule number per capsule while, >90% of genotypes recorded one capsule per leaf axil and broad oblong capsule shape (as presented in **Table 3**). Similar characterization patterns were adopted by Bhoot *et al.* (2019) and Pavani *et al.* (2020).

The choice of parents is of paramount importance in any hybridization breeding programme, but it is a difficult task for a plant breeder. Knowledge about the nature and magnitude of genetic divergence is a prerequisite for an effective hybridization programme. Genetic divergence studies play a vital role in evaluating genotypes for variability, which helps breeder to plan for the selection of genotypes as parents in the breeding programme. Crosses between divergent parents usually produce greater heterosis than those between closely related ones.

Morphological characterization

Capsule Arrangement

Fig.1. Opposite

Fig.2. Alternate

Fig.3. Cluster

Capsule number per leaf axil

Fig. 4. One capsule per leaf axil

Fig.5. More than one capsule per leaf axil

Flower petal color

Fig.6. White **Fig.7. Light purple** **Fig.8. Dark purple**

Table 2. Morphological characterization of sesame genotypes

S.No.	Varieties	Petal color	Petal hairiness	Branching pattern	Stem hairiness	Leaf lobes	Leaf margin	Capsule number per leaf axil	Capsule hairiness	Locule number per capsule	Capsule shape	Capsule arrange-ment	Seed coat color
1	AKT-101	2	5	1	1	1	3	1	1	3	3	1	1
2	AKT-64	2	5	2	1	1	3	1	1	3	3	1	1
3	Amrit	1	3	2	1	1	3	1	1	3	3	1	3
4	B-67	2	3	2	5	2	3	1	1	3	3	1	5
5	Chandana	1	5	2	3	2	5	1	3	3	3	1	3
6	CUMS-17	2	3	2	3	2	3	1	3	3	3	1	3
7	DS-5	2	5	1	5	1	3	1	5	3	3	2	1
8	DSS-9	2	5	1	5	1	3	1	5	3	3	2	1
9	E-8	2	3	2	5	1	3	1	5	3	3	1	1
10	GJT-5	2	5	1	3	1	3	9	5	3	3	3	1
11	GT-1	2	3	2	3	1	3	9	3	3	3	3	1
12	GT-10	1	3	2	1	1	3	1	1	3	1	1	5
13	GT-2	2	3	2	1	1	3	9	5	3	3	3	1
14	GT-3	1	5	2	1	1	3	1	3	3	3	1	1
15	GT-4	2	3	2	1	1	3	9	3	3	3	3	1
16	Hima	2	5	2	3	1	3	1	5	3	3	1	1
17	HT-1	2	3	1	1	1	3	1	3	3	3	1	1
18	HT-2	2	5	1	3	1	3	1	3	3	3	1	1
19	IIOS-1101	2	3	2	3	2	5	1	1	3	2	1	1
20	JLT-408	2	5	2	3	2	3	1	3	3	3	2	1
21	JLT-7	2	3	2	3	1	3	1	3	3	3	1	1
22	JTS-8	2	5	2	3	1	3	1	3	3	1	1	1
23	Kanak	1	3	2	5	1	3	1	3	3	1	1	2
24	Krishna	1	5	1	5	1	3	1	3	3	3	1	4
25	N-32	3	3	2	3	1	3	1	3	3	3	2	1
26	Nirmala	2	5	2	3	1	3	1	3	3	3	1	2
27	Phule Til-1	2	5	2	1	1	3	1	3	3	3	1	1

S.No.	Varieties	Petal color	Petal hairiness	Branching pattern	Stem hairiness	Leaf lobes	Leaf margin	Capsule number per leaf axil	Capsule hairiness	Locule number per capsule	Capsule shape	Capsule arrange-ment	Seed coat color
28	Paiyur	1	3	2	1	2	3	1	1	3	1	1	5
29	PKDS-11	2	3	2	1	1	3	1	3	3	3	1	4
30	PKDS-8	3	3	2	1	1	3	1	3	3	3	1	5
31	Prachi	2	3	2	5	1	3	1	3	3	3	1	5
32	Pragati	2	3	2	5	1	3	1	3	3	3	1	1
33	Punjab til-1	2	3	2	3	1	3	1	3	3	3	1	1
34	Punjab til-2	2	3	1	3	1	3	1	3	3	3	1	1
35	Rajeshwari	3	5	2	1	2	5	1	3	3	3	1	1
36	Rama	1	3	2	3	2	3	1	1	3	3	1	3
37	RT-103	3	5	1	1	1	3	1	3	3	3	1	1
38	RT-125	2	3	1	1	1	3	1	3	3	3	1	1
39	RT-127	2	5	1	3	1	3	1	3	3	3	1	1
40	RT-346	2	3	1	1	1	3	1	3	3	3	1	1
41	RT-351	2	5	1	1	1	3	9	3	3	3	3	1
42	RT-372	2	3	1	3	1	3	1	3	3	3	2	1
43	RT-46	3	5	1	5	1	3	1	3	3	3	1	1
44	Savitri	2	3	2	3	1	3	1	3	3	3	1	3
45	Shubra	2	3	2	3	1	3	1	3	3	3	1	1
46	Smarak	2	5	2	3	1	3	1	3	3	3	1	1
47	Swetha til	2	3	2	3	2	5	1	3	3	3	1	1
48	T-78	2	3	2	3	1	5	1	3	3	3	1	1
49	Tarun	2	5	2	3	1	5	1	3	3	3	1	1
50	Thilak	1	5	2	3	2	5	1	3	3	3	1	4
51	Thilothama	2	3	2	3	2	5	1	3	3	3	1	4
52	Thilarani	1	3	2	5	2	5	1	3	3	3	1	4
53	TKG-22	2	5	2	3	1	3	1	3	3	3	2	1
54	TKG-306	2	3	2	3	1	3	1	3	3	3	2	1
55	TKG-308	2	5	2	3	1	3	9	3	3	3	3	1
56	TKG-55	2	5	2	3	1	3	1	3	3	3	2	1
57	TMV-3	2	3	2	3	2	3	1	1	3	3	1	5
58	TMV-4	1	3	2	3	2	3	1	1	3	3	1	4
59	TMV-6	2	3	2	3	2	3	1	1	3	3	1	4
60	TMV-7	3	3	2	3	2	3	1	3	3	3	1	4
61	TSS-6	2	5	2	3	2	3	1	5	3	3	2	1
62	Uma	2	3	2	3	1	3	1	3	3	3	1	2
63	Usha	2	3	2	3	2	3	1	3	3	3	1	3
64	Vinayak	2	3	2	3	1	3	1	3	3	3	1	4
65	VRI-1	1	3	2	3	2	3	1	3	3	1	1	4
66	VRI-2	2	3	2	3	2	3	1	3	3	3	1	4
67	VRI-3	3	3	2	3	2	5	1	3	3	3	1	1
68	YLM-11	1	3	2	3	1	3	1	3	3	3	1	4
69	YLM-17	2	5	2	3	1	3	1	3	3	3	1	4
70	YLM-66	1	3	2	3	1	3	1	1	3	3	1	4

Note:

Flower petal color- 1-white, 2-light purple, 3-dark purple
Flower petal hairiness- 1-absent, 3-sparse, 5-dense
Plant branching pattern- 1-basal, 2-top
Stem hairiness- 1-absent, 3-sparse, 5-dense
Leaf lobes- 1-slightly lobed, 2-deeply lobed
Leaf margin- 3-weak, 5-strong
Capsule number per leaf axial- 1- one, 9-more than one
Capsule hairiness- 1-absent, 3-sparse, 5-dense
Locule number per capsule- 3-four, 5-six, 7-eight
Capsule shape- 1-tapered, 2-Narrow oblong, 3- Broad oblong, 4-square
Capsule arrangement- 1-alternate, 2-opposite, 3-cluster
Seed coat color- 1-white, 2-grey, 3-light brown, 4-darkbrown, 5-black seed

Table 3. Frequency distribution of for different morphological traits in sesame genotypes

Trait	Classes	Number of genotypes	Frequency (%)
Flower petal color	White	14	20
	Light purple	49	70
	Dark purple	7	10
Flower petal hairiness	Absent	0	0
	Sparse	43	61.4
	Dense	27	38.5
Plant branching pattern	Basal	15	21.4
	Top	55	78.5
Stem hairiness	Absent	17	28.3
	Sparse	43	61.4
	Dense	10	14.3
Leaf lobes	Slightly lobed	49	70
	Deeply lobed	21	30
Leaf margin	Weak	60	85.7
	Strong	10	14.3
Capsule number per leaf axial	One	64	91.4
	More than one	6	8.5
Capsule hairiness	Absent	12	17.1
	Sparse	51	72.9
	Dense	7	10
Locule number/ capsule	Four	70	100
	Six	0	0
	Eight	0	0
Capsule shape	Tapered	5	7.1
	Narrow oblong	1	1.4
	Broad oblong	64	91.4
	Square	0	0
Capsule arrangement	Alternate	55	78.6
	Opposite	9	12.9
	Cluster	6	8.6
Seed coat color	White	41	58.6
	Grey	3	4.3
	Light brown	6	8.6
	Dark brown	14	20
	Black seed	6	8.6

In the present investigation, the genetic divergence of 70 sesame genotypes was determined by using both nominal morphological variables and ordinal variables of quantitative characters, which were used as input for UPGMA (Unweighted Pair Group Method with Arithmetic Average) cluster analysis, in which clustering was done using Ward's minimum variance method and Gower's method of genetic distance was derived. The dendrogram was constructed using R software version 4.1.0.

In the present investigation, 70 genotypes were grouped into 7 clusters based on divergence analysis at a genetic distance of 0.5 (**Fig. 9**). Clustering of genotypes was grouped mainly due to their morphological and quantitative differences. Cluster III and Cluster VI were the largest among all clusters, comprising 15 genotypes each. Clusters II, V, VII, IV and I comprised of 11,9,8,7 and 5 genotypes respectively (**Table 4**). The maximum genetic distance was observed between the genotypes of clusters I and VII; clusters II and VII. So, good recombinants can be obtained by hybridization between lines from the above clusters I. However, the minimum genetic distance was recorded between genotypes of cluster IV and V, followed by cluster II and III.

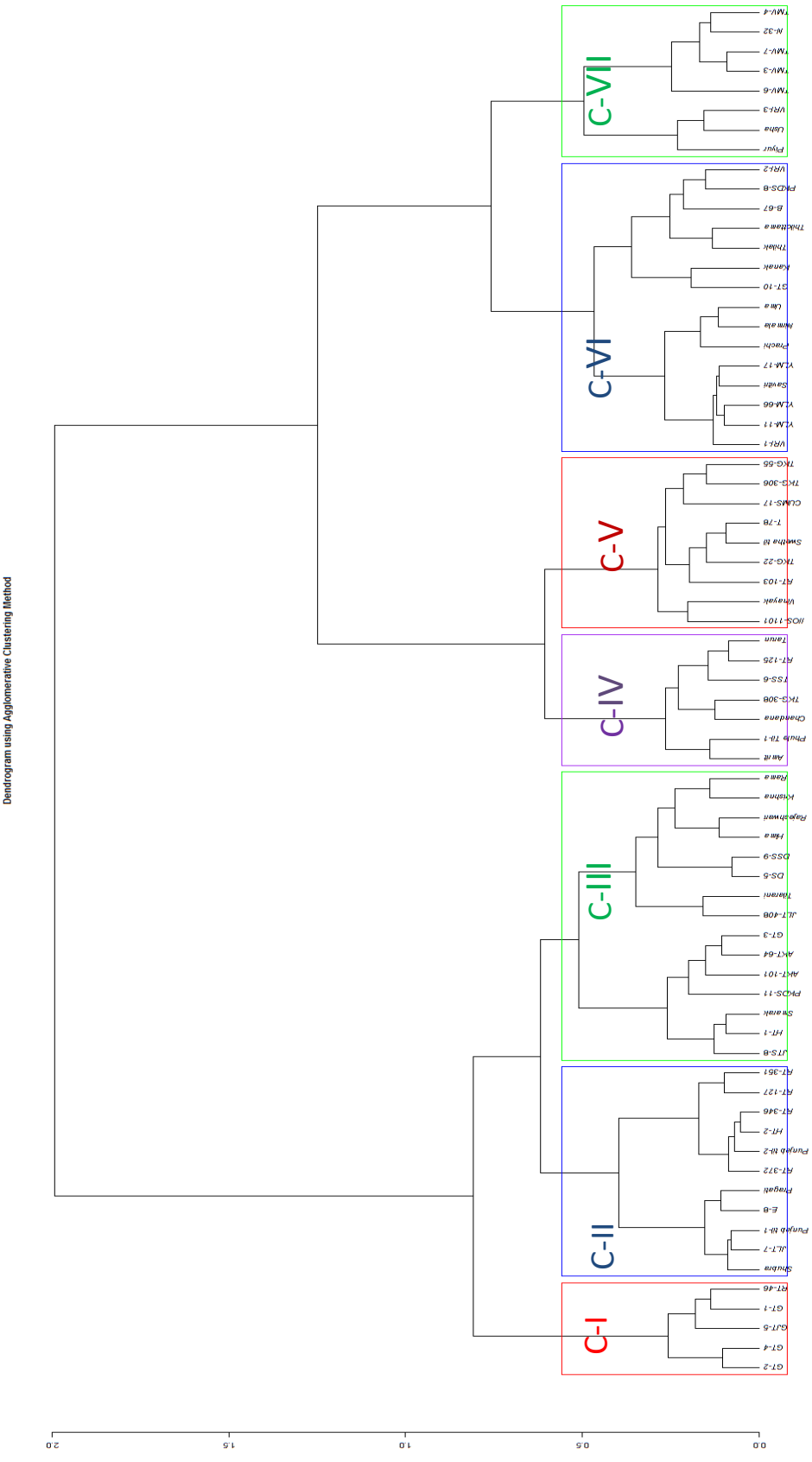

Fig. 9. Agglomerative hierarchical cluster analysis [using the Unweighted Pair Group Method with Arithmetic Mean (UPGMA) procedure] of 70 sesame genotypes using both morphological and quantitative characters at the genetic distance of 0.5.

Table 4. Distribution of sesame genotypes into different clusters

Cluster Number	Number of genotypes	Genotypes
I	5	GJT-5, GT-1, GT-2, GT-4, RT-46
II	11	E-8, HT-2, JLT-7, Pragati, Punjab til-1, Punjab til-2, RT-127, RT-346, RT-351, RT-372, Shubra
III	15	AKT-101, AKT-64, DS-5, DSS-9, GT-3, HT-1,Hima, JLT-408, JTS-8, Krishna, PKDS-11, Rajeshwari, Rama, Smarak,Thilarani
IV	7	Amrit, Chandana, Phule Til-1, RT-125, TKG-308, TSS-6, Tarun
V	9	CUMS-17, IIOS-1101, RT-103, Swetha til, T-78, TKG-22, TKG-306, TKG-55, Vinayak
VI	15	B-67, GT-10, Kanak, Nirmala, PKDS-8, Prachi, Savitri, Thilak, Thilothama, Uma, VRI-1, VRI-2, YLM-11, YLM-17, YLM-66
VII	8	N-32, Paiyur 1, TMV-3, TMV-4, TMV-6, TMV-7, Usha, VRI-3

In cluster I, the highest cluster mean values were recorded for capsule length and oil content, whereas in cluster II, the highest cluster mean values were recorded for days to emergence and test weight. In clusters III, IV and V, none of the characters recorded the highest cluster mean value. In cluster VI, the highest cluster mean value was recorded for days to maturity and primary branches per plant, whereas in cluster VII, the highest cluster mean value was recorded for the following characters *viz.,* days to 50% flowering, days to flower session, length to first capsule, plant height, secondary branches per plant, capsule number per plant, number of leaf axils in main stem and seed yield per plant. Most of characters recorded high mean values in cluster VII. Hence, to breed for these characters selection of the genotypes in cluster VII could yield desirable results (**Table 5)**.

The clustering pattern indicated that out of the 70 genotypes, only 50% of genotypes were clustered according to geographical origin (**Table 6)**. The genotypes belonging to Gujarat state (GJT-5, GT-1, GT-2, GT-3, GT-4, GT-10) were grouped in one cluster (cluster I) except for genotypes like GT-3 (cluster III) and GT-10 (cluster VI) due to their white petal color, one capsule per leaf axil, and alternate capsule arrangement. GT-3 is different from others in its dense petal hairiness, while GT-10 has a tapered capsule shape and a black seed coat color. The genotypes belonging to Rajasthan state (RT-46, RT-372, RT-351, RT-346, RT-127, RT-125 and RT-103) were grouped in one cluster (cluster II) except for genotypes like RT-46, RT-125 and RT-103. RT-46 and RT-103, which are different due to their dark purple petal color. RT-46 is different due to dense stem hairiness, while RT-125 has sparse petal hairiness.

Table 5. Cluster mean values for fourteen traits in sesame genotypes

Character	ClusterI	ClusterII	ClusterIII	ClusterIV	ClusterV	ClusterVI	ClusterVII
Days to emergence	5	6.5	5.3	5.5	6.2	5.6	5.5
Days to 50% flowering	42	41.8	41.9	40.9	44.7	45.9	48.4
Days to flower session(completion)	67.5	68.4	69.9	69.1	71.5	72.3	79.5
Days to maturity	93	94.1	95	93.3	93.6	99.6	98.8
Length to first capsule (cm)	20.6	19.8	23	18.2	21.3	27.7	38.3
Plant height	88.7	82.5	88.9	84.6	87	100.7	111.3
Primary branches per plant	4.8	4.4	4.8	4	5.6	6.3	6.1
Secondary branches per plant	2.4	0.4	3.6	0	2.2	4.6	6.6
Capsule number per plant	55.2	71.5	78.6	75.3	80.1	77.2	155.8
Number of leaf axils on main stem	47.2	84	90.8	87.9	93.9	89.7	169.9
Capsule length(cm)	2.8	2.6	2.6	2.7	2.6	2.5	2.6
Test weight (g)	3.6	3.7	3.3	3.3	3.4	3.2	3.3
Oil content (%)	49.3	48.5	48.6	48.2	48.1	46.6	47.6
Seed yield per plant (g)	6.3	6	7.4	6.1	6	7.3	8.5

Table 6. Clustering of genotypes in accordance to geographical origin

Geographical origin	Genotypes	Cluster
Gujarat	GT-2, GT-4, GT-1, GJT-5	Cluster I
	GT-10	Cluster VI
	GT-3	Cluster III
Rajasthan	RT-372, RT-351, RT-346, RT-127	Cluster II
	RT-125	Cluster IV
	RT-46	Cluster I
	RT-103	Cluster V
Maharashtra	AKT-64, JLT-408, AKT-101	Cluster III
	Phule Til-1	Cluster IV
	JLT-7	Cluster II
Madhya Pradesh	TKG-306, TKG-22, TKG-55	Cluster V
	JTS-8, PKDS-11	Cluster III
	TKG-308	Cluster IV
	N-32	Cluster VII
	PKDS-8	Cluster VI
Andhra Pradesh	YLM-66, YLM-17, YLM-11	Cluster VI
	Hima, Rajeshwari	Cluster III
	Chandana	Cluster IV
	Swetha Til	Cluster V
Uttar Pradesh	Tarun	Cluster IV
	Pragati	Cluster II
	T-78	Cluster V
West Bengal	Savitri, B-67	Cluster VI
	CUMS-17	Cluster V
	Rama	Cluster III
Tamilnadu	TMV-7, TMV-6, TMV-4, TMV-3, VRI-3, Paiyur	Cluster VII
	VRI-1, VRI-2	Cluster VI
	TSS-6	Cluster IV
Bihar	Krishna	Cluster III
Karnataka	DS-5, DSS-9	Cluster III
	E-8	Cluster II
Kerala	Thilothama, Thilak	Cluster VI
	Thilarani	Cluster III
Punjab	Punjab Til-1, Punjab Til-2	Cluster II
Odisha	Kanak, Nirmala, Uma, Prachi	Cluster VI
	Usha	Cluster VII
	Vinayak	Cluster V
	Amrit	Cluster IV
	Smarak	Cluster III
	Shubra	Cluster II
Haryana	HT-1	Cluster III
	HT-2	Cluster II
Telangana	IIOS-1101	Cluster V

The genotypes belonging to Maharashtra (JLT-7, JLT-408, AKT-101, AKT-64 and Phule Til-1) were grouped in cluster III except for genotypes like Phule Til-1 (cluster IV) and JLT-7 (cluster II). The similarity between genotypes is due to their light purple petal color, dense petal hairiness, weak leaf margin, one capsule number per leaf axil, four locule number per capsule, broad oblong capsule shape and white seed coat color. The genotypes belonging to Madhya Pradesh state (JTS-8, TKG-306, TKG-22, TKG-308, TKG-55, PKDS-11, PKDS-8) are clustered in cluster V except for genotypes JTS-8, TKG-308, PKDS-8 and PKDS-11. PKDS-8 and PKDS-11 are different due to the absence of stem hairiness. JTS-8 is different due to its tapered capsule shape, while PKDS-8 has dark purple petal color and TKG-308 has more than one capsule number per leaf and a clustered capsule arrangement.

The genotypes belonging to Andhra Pradesh (Swetha Til, Hima, Chandana, YLM-66, YLM-17, YLM-11, Rajeshwari) were grouped in Cluster VI except for genotypes Rajeshwari, Swetha til, Chandana and Hima. The similarity of genotypes in cluster VI is due to their top branching pattern, sparse stem hairiness, slightly lobed leaf lobes, weak leaf margin, one capsule number per leaf axil, four locule number per capsule, broad oblong capsule shape, alternate capsule arrangement and dark brown seed coat color. The genotypes belonging to West Bengal (Savitri, B-67 and Rama) were grouped in cluster VI except for genotype Rama. The similarities of genotypes are due to light purple petal color, sparse petal hairiness, top branching pattern, weak leaf margin, one capsule number per leaf axil, four locule number per capsule, broad oblong capsule shape and alternate capsule arrangement.

The genotypes belonging to Tamil Nadu (Paiyur 1, TMV-7, TMV-6, TMV-4, TMV-3, TSS-6, VRI-1, VRI-2 and VRI-3) were grouped in cluster VII, except for genotypes like TSS-6 (cluster IV), VRI-1 and VRI-2 (cluster VI). The similarities among genotypes are due to sparse petal hairiness, top branching pattern, deeply lobed leaf lobes, one capsule number per leaf axil, four locule number per capsule and alternate capsule arrangement. The genotypes belonging to Odisha (Amrit, Smarak, Shubra, Kanak, Usha, Nirmala, Uma, Vinayak, and Prachi) are grouped in cluster VI except the genotypes like Smarak, Shubra, Amrit, Usha and Vinayak. The similarities among genotypes in cluster VI are due to their top branching pattern, slightly lobed leaf lobes, weak leaf margin, one capsule number per leaf axil, four locule number per capsule, sparse capsule hairiness and alternate capsule arrangement.

The genotypes belonging to Kerala (Thilothama, Thilak and Thilarani) were grouped in cluster VI except for genotype Thilarani because it has dense stem hairiness. The above-mentioned genotypes belonging to different states may most probably differ for quantitative characters. The genotypes belonging to Karnataka (DS-5, DSS-9) and Bihar (Krishna) were grouped in cluster III and the genotypes of Punjab (Punjab Til-2, Punjab Til-1) were grouped in cluster II. The genotypes belonging to other states were grouped in different clusters , which might be due to difference in both morphological and quantitative characters.

Hence, selection of genotypes present in different clusters having more genetic distance, preferably belonging to different geographical origin may result in more heterotic effects in hybridization programme. Similar, diverse clustering pattern in sesame were reported by Swathy *et al*. (2018), Bhattacharjee *et al*. (2019) and Ramya *et al.* (2020).

From the present investigation, it is clear that there is a considerable amount of genetic variability for majority of the morphological traits except for locule number per capsule, capsule number per leaf axil and capsule shape. High heterotic effects in hybridization programme can be obtained on mating between the clusters I and VII for genotypes *viz.,* GJT-5, RT-46 with TMV-3, VRI-3 and Paiyur 1.

ACKNOWLEDGMENTS

The research was supported by The Indian Council of Agriculture Research (ICAR) - Indian Institute of Oilseeds Research, Hyderabad.

REFERENCES

Banerjee, P.P. and Kole, P.C. 2009. Analysis of genetic architecture for some physiological characters in sesame (*Sesamum indicum* L.). *Euphytica,* **168**: 11-22. [Cross Ref]

Bedigian, D. 2003. Evolution of sesame revisited: domestication, diversity and prospects. *Genetic Resources and Crop Evolution,* **50**: 779–787. [Cross Ref]

Bhattacharjee, M., Iqbal, A., Singh, S., Nath, D., Prakash, S.H. and Dasgupta, T. 2019. genetic diversity in sesame. *Bangladesh Journal of Botany*, **48**(3): 497-506. [Cross Ref]

Bhoot, H.V., Sharma, L.K., Kulkarni, G.U., Ravat, U. and Rathva, S. 2019.Characterization of sesame genotypes through morphological characters. *Journal of Pharmacognosy and Phytochemistry,* **8**(3): 3132-3138.

Dong, Y.S., Zhao, L.M., Liu, B., Wang, Z.W., Jin, Z.Q. and Sun, H. 2003. The genetic diversity of cultivated soybean grown in China. *Theoretical and Applied Genetics,* **108**(5): 931-936. [Cross Ref]

Food and Agricultural Organisation. QCL Crops and livestock products 2020. Available from: https://www.fao.org/faostat/en/#data/QCL

Gower, J.C. 1971. A general coefficient of similarity and some of its properties. *Biometrics,* **27**:857–871. Available from: http://dx.doi.org/10.2307/2528823. [Cross Ref]

Khan, M.A., Mirza, M.Y., Amjad, M., Nawaz, N., Nawaz, M.S. and Baig, D. 2013. Assessment of genetic diversity in germplasm of linseed. *Pakistan Journal of Agricultural Research*, **26**(3): 23-25.

Myint, D., Gilani, S.A., Kawase, M and Watanabe, K.N. 2020. Sustainable sesame (*Sesamum indicum* L.) production through improved technology: An overview of production, challenges and opportunities in Myanmar. *Sustainability (MDPI)*, **12:** 3515. [Cross Ref]

Pasquet, R.S., Mergeai, G. and Baudoin, J.P. 2002. Genetic diversity of the African geocarpic legume Kersting's groundnut, *Macrotyloma geocarpum* (Tribe-Phaeoleae, Family: Fabaceae). *Biochemical Systematics and Ecology,* **30**(10): 943–952. [Cross Ref]

Pavani, K., Ahamed, M., Ramana, J.V. and Sirisha, A.B.M. 2020. Morphological characterization of sesame (*Sesamum indicum* L.) genotypes using DUS descriptors. *Journal of Plant Development Sciences,***12**(6): 349-354.

Ramya, K.T., Lal, J.J., Swamy, H.H.K. and Ratnakumar, P. 2020. Morphological characterization of sesame germplasm. *Journal of Oilseeds Research*, **37**.

Sharma, A., Gupta, K.R. and Kumar, R. 2008. Genetic divergence in basmati rice (*Oryza sativa* L.) under irrigated ecosystem. *Crop Improvement,* **35**(1):8-10.

Singh, V., Bhajan, R. and Kumar, K. 2007. Genetic diversity in Indian mustard (*Brassica juncea* L.Czern and Coss). *Progressive Agrilculture,* **7**(1-2): 105-109. [Cross Ref]

Sokal, R. and Michener, C. 1958. A statistical method for evaluating systematic relationships. *University of Kansas Science Bulletin*, **38**: 1409-1438.

Swathy, V., Ameena Premnath, Viswanathan, P.L., Raveendran, M. and Manonmani, S. 2018. Determination of genetic divergence based on morphological traits in sesame (*Sesamum indicum* L.). *Electronic Journal of Plant Breeding*, **9**(2): 747 – 752. [Cross Ref]

Tabatabaei, I., Pazouki, L., Bihamta, M.R., Mansoori, S., Javaran, M.J. and Niinemets, U. 2011. Genetic variation among Iranian sesame (*Sesamum indicum* L.) accessions vis-à-vis exotic genotypes on the basis of morpho-physiological traits and RAPD markers. *Australian Journal of Crop Sciences,* **5**:1396–1407.

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. [Cross Ref]

Yousuf, M., Ajmal, S.U., Munir, M. and Ghafoor, A. 2011. Genetic diversity analysis for agro-morphological and seed quality traits in rapeseed (*Brassica campestris* L.). *Pakistan Journal of Botany,* **43**(2): 1195-1203.

Zhang, H., Miao, H., Wei, L., Li, C., Zhao, R. and Wang, C. 2013. Genetic analysis and QTL mapping of seed coat color in sesame (*Sesamum indicum* L.). *PLOS One,* **8**: 63898. [Cross Ref]