

## Characterization (Diversity Analysis) in Germplasm of Sesame (*Sesamum indicum* L.)

Divya K.<sup>1\*</sup>, Shobha Rani T.<sup>2</sup>, Padmaja D.<sup>3</sup> and Kiran Babu T.<sup>4</sup>

<sup>1</sup>Department of Genetics and Plant Breeding, College of Agriculture,  
PJTSAU, Rajendranagar, Hyderabad, (Telangana), India.

<sup>2</sup>Senior Scientist, Plant Breeding, Agricultural Research Station,  
PJTSAU, Nathanaipally, Medak, (Telangana), India.

<sup>3</sup>Scientist, Plant Breeding, Regional Agricultural Research Station,  
PJTSAU, Polasa, Jagtial, (Telangana), India.

<sup>4</sup>Scientist, Plant Pathology, Agricultural Research Institute,  
PJTSAU, Rajendranagar, Hyderabad, (Telangana), India.

(Corresponding author: Divya K. \*)

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**ABSTRACT:** Diversity reveals the presence of variability in nature which helps in identifying elite genotypes. In the present study, 133 sesame genotypes comprised of mutant breeding lines, indigenous lines, IVT's, AVT's, MLT's, popular varieties and checks were evaluated for the genetic diversity. Considerable amount of diversity was found among the genotypes for all the ten characters studied and cluster analysis grouped the genotypes into nineteen distinct clusters. Cluster I was the largest with fifty-four genotypes and 13 clusters (V, VI, VII, VIII, X, XI, XII, XIII, XV, XVI, XVII, XVIII, XIX) were with one genotype each. The study also revealed that cluster XV has low estimate for phyllody (% incidence) and genotypes from this cluster can be used as donors in resistance breeding programme. The genotypes with specific traits could be selected and used in the crossing programme to improve the yield and disease resistance in sesame.

**Keywords:** genetic diversity, D<sup>2</sup>- statistics, sesame, phyllody, mutant breeding lines and resistance breeding.

### INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the important oilseed crops in India and around the world and is considered as the "Queen of Oilseeds". It is an ancient oil seed crop known to man because of its ease of extraction, great stability, and drought resistance. It has many uses including oil, culinary purposes and in cosmetics etc. Some of the important sesame growing countries are India, China, Sudan, Mexico, Turkey, Burma and Pakistan. In India, sesame is being grown over an area of 16.22 lakh hectares with production of 6.57 lakh tonnes and productivity of 405 kg/ha ([www.indiastat.com](http://www.indiastat.com), 2019-20). Major sesame growing states in India are West Bengal, Madhya Pradesh, Uttar Pradesh, Rajasthan and Gujarat. In Telangana, it is grown over an area of 0.21 lakh hectares with an annual production of 0.13 lakh tonnes and productivity 363 kg/ha ([www.indiastat.com](http://www.indiastat.com), 2019-20). In Telangana state, it is grown as *summer* crop in the districts of Jagtial, Nizamabad, Nirmal, Adilabad, Karimnagar, Khammam, Asifabad and Mahaboobnagar. In recent years, its performance as a catch crop in *rabi* and after *Bt* cotton and turmeric in *summer* season and late *kharif*

(under contingency) particularly in area under cultivation is encouraging.

Sesame seed contains 50-60 % oil and 19-25 % protein with two lignans *i.e.*, sesamin and sesamol, which prevent rancidity and give sesame oil a long shelf life (Ashakumary *et al.*, 1999). But it has been given less attention by the farmers because of poor yield due to non-availability of cultivars that suit diverse agro-climatic conditions and resistant to diseases. So, for the need to identify genotypes with resistance and agronomical superiority diversity present within the available material is assessed (Divya, 2018). This divergence at genetic level among the genotypes play an important role in the selection of parents having wider variability for different characters and ultimately for rational use of genetic resources. It is further important to make inferences about the history of its domestication (Dossa *et al.*, 2016). D<sup>2</sup> analysis is a useful statistical method for analyzing inter-relationships operating between and within the plant populations, under natural and human selections with morphological traits. There were studies also where the genetic level diversity was dissected using marker systems such as amplified fragment length

polymorphism (AFLP), sequence related amplified polymorphisms (SARP), random amplified polymorphic DNA (RAPD) and intersimple sequence repeat (ISSR) (Adu-gyamgi *et al.*, 2019) characterization of genotypes using these molecular markers is playing great role in assisting parental line and breeding strategy, designs and selection (Wu *et al.*, 2014). With this theme of selecting parental lines, the present study was aimed to assess the genetic diversity using yield traits among 133 sesame genotypes comprised of mutant breeding lines, indigenous lines, IVT's, AVT's, MLT's, popular varieties and checks.

## MATERIALS AND METHODS

The experimental material obtained from UAS, Raichur and RARS, Jagtial contains 133 genotypes including national check (TKG-22), Zonal check (Pragathi) and Local check (Swetha til). The genotypes were evaluated during *kharif*, 2017 at Regional Agricultural Research Station, Polasa, Jagtial. The experiment was laid in Randomized Block Design (RBD) with a spacing of 30 × 10 cm in three replications following standard agronomic practices. Observations were recorded from five random plants for every genotype in every replication for yield and its attributing characters such as days to 50 % flowering, days to maturity, plant height (cm), number of branches per plant, number of

capsules per plant, test weight, seed yield per plant (g) and diseases (*Alternaria* and *Cercospora* leaf spot and phyllody). The amount of divergence and clustering was done according to the procedure provided by Mahalanobis D<sup>2</sup> (1936) statistics and Tocher's method (Rao C.R., 1952). The inter and intra-cluster distances were calculated by the formula given by Singh and Chaudhary (1977).

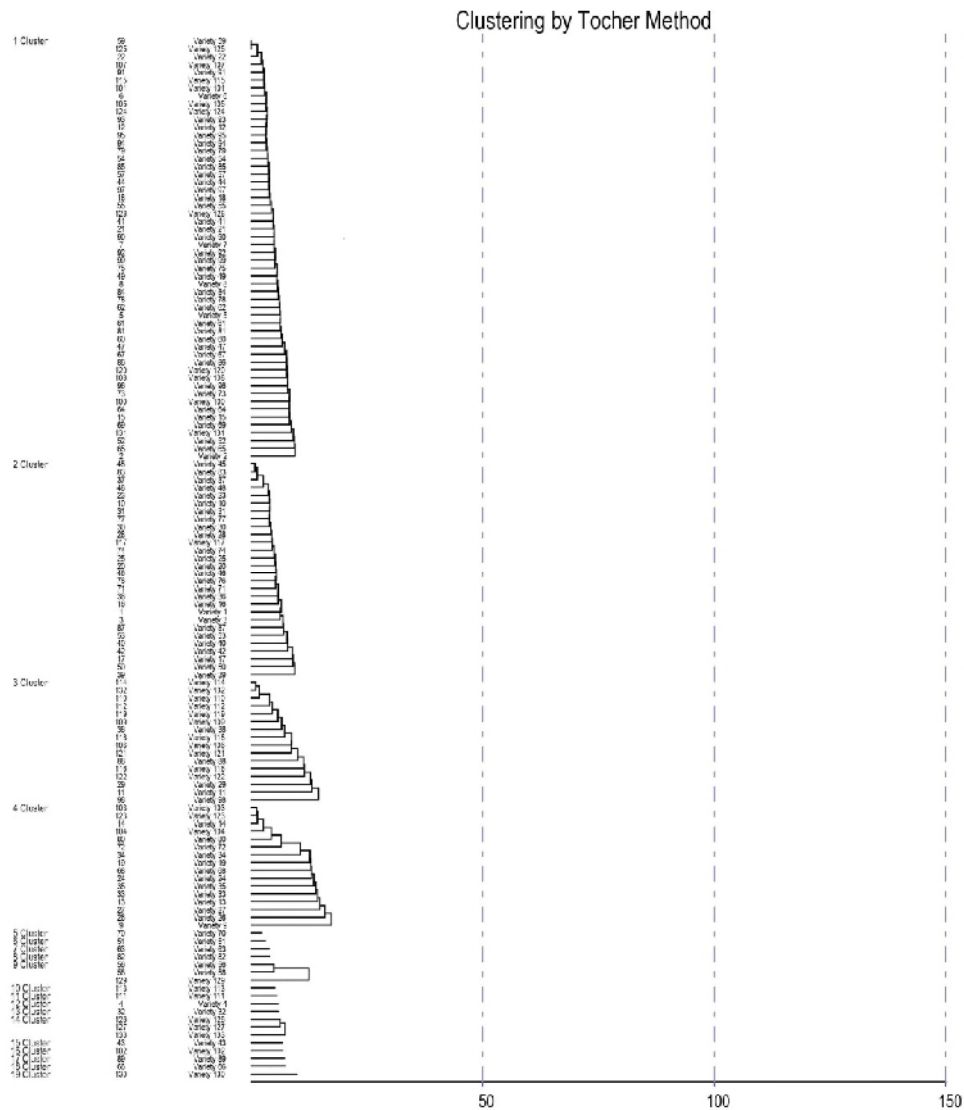
## RESULTS AND DISCUSSIONS

### A. Clustering pattern

Basic understanding of the genetic diversity that exists in the germplasm available is fundamental to a successful breeding programme (Krishna *et al.*, 2018). Based on the D<sup>2</sup> values, the breeding lines were distributed into nineteen clusters with variable number of genotypes revealing the presence of considerable amount of diversity in the material (Table 1, Fig. 1). Cluster I was the largest cluster with 54 breeding lines followed by cluster II with 28 breeding lines, and cluster III & IV with 16 lines each. Other clusters V, VI, VII, VIII, X, XI, XII, XIII, XV, XVI, XVII, XVIII and XIX were solitary. Solitary clusters may be of distinct recombinant or rare segregants (Soundharya *et al.*, 2017; Mohanty *et al.*, 2020). More number of cluster formations is an indication of higher diversity.

**Table 1: Clustering pattern of sesame (*Sesamum indicum* L.) genotypes based on D<sup>2</sup> values at RARS, Polasa, Jagtial during *kharif*, 2017.**

Cluster	No. of Genotypes	Genotypes
Cluster I	54	10KRE8-2, OSE-560-1, JCS-3280, 30KRDS-1-23, SDSN-15-115, SDSN-15-58, MT-2014-14, SDSN-15-84, 50KRE8-3, SDSN-15-109, JCS-2698, SDSN-15-65, 30KRDS-1-6, SDSN-15-72, SDSN-15-70, Rajasthan Kishore, 196 RK, 82 RIL, Mall-1, R6127-8, SDSN-15-77, 30KRDS-1-16, 223 RK, JLT-408, IISL-3, 30KRDS-1-22, SDSN-15-16, 30KRDS-1, SDSN-15-61, SDSN-15-81, L-3-2, RS Black-108, 30KRDS-1-1, 38 RIL, Mall White, OSC-79, SSD-22, 50KRE8-2, Indi Taluk-1, SSD-7, RS Black VRI-1, 198 RIL, IVTS-2017-02, RT-376, SDSN-15-76, L-2, SDSN-15-83, DS-1, 30KRDS-1-10, II IBL Local (4), TKG-22, 162 RK and DSS-9
Cluster II	28	R6134, 32 RIL, E840KR-3, RS I-Black, 30KRDS-1-25, 30KRDS-1-3, 60KRE8-1-3, RCR-L, 60KRE8-1-2, 30KRDS-1-31, JTS-8, L-3-1, 30KRDS-1-27, 30KRDS-1-20, R6135-7, L-7, II IBL Local (6), E840KR-2, 30KRDS-1-11, 10KRE8-1, 10KRE8-3, CPD Local-2016, 188 RK, IISL-2, IISL-4, 30KRDS-1-14, 73 RK and IISL
Cluster III	16	30KRDS-1-5, 30KRDS-1-71, V-72, SDSN-15-03, SDSN-15-79, SDSN-15-114, RT-378, JLS-710, AT-332, TKG-511, GT-10, TKG-506, PT-10, IVTS-2017-11, JCS-2454 and Pragathi
Cluster IV	16	30KRDS-1-2, 30KRDS-1-7, 30KRDS-1-8, 30KRDS-1-18, 30KRDS-1-26, 30KRDS-1-28, 30KRDS-1-29, 60KRE8-1-5, 60KRE8-1-7, 60KRE8-1-9, II IBL Local (1), L-2, Kanakapur Local, SDSN-15-98, SDSN-15-99 and JCS-2696
Cluster V	1	II IBL Local (5)
Cluster VI	1	82 RK
Cluster VII	1	SC-50
Cluster VIII	1	Indi Taluk-2
Cluster IX	3	N-8, Mall-2 and YLM-11
Cluster X	1	DS-46
Cluster XI	1	AT-314
Cluster XII	1	50KRE8-1
Cluster XIII	1	60KRE8-1-4
Cluster XIV	3	Hima, Rajeswari and Swetha til ©
Cluster XV	1	SGPS-17-15
Cluster XVI	1	SDSN-15-97
Cluster XVII	1	SDSN-15-14
Cluster XVIII	1	RT-273
Cluster XIX	1	YLM-66



**Fig. 1.** Genotypes in clusters using Tocher method.

**B. Intra and Inter cluster distances**

The maximum intra cluster distance was recorded for cluster IV (38.32) followed by cluster IX (37.61). Because of solitary nature clusters V, VI, VII, VIII, X, XI, XII, XIII, XV, XVI, XVII, XVIII and XIX recorded zero as they have only single genotype and were in conformity with Venkatesh *et al.*, (2011); Ahadu (2012); Mohanty *et al.*, (2020). Such intra cluster genetic diversity among the genotypes could be due to heterogeneity, genetic architecture of the populations, past history of the selection in development traits (Furut and Uzun., 2010). The cluster I has minimum intra cluster value of 17.93 indicating that the genetic architecture of genotypes within this cluster was similar (Fazal *et al.*, 2011). The inter cluster distance ranged from 14.81 to 392.03. The highest distance was observed between clusters XIV and XV (392.03), followed by XIV and XVIII (382.37) which indicated that the crossing or hybridization made between the genotypes selected from these clusters may give high heterotic response and thus better segregants (Krishna

*et al.*, 2018; Mohanty *et al.*, 2020). The minimum inter cluster distance is between X and XI (14.81) indicating the close relationship among the genotypes in these clusters (Jadhav and Mohrir, 2012). The average intra and inter cluster distances were presented in Table 2.

**C. Cluster mean**

There were considerable differences among the clusters for most of the characters studied and can be observed with the cluster means (Table 3). The cluster XIX recorded lowest value for days to 50 per cent flowering (43.33) indicating earliness and highest value for seed yield per plant (2.65) were in agreement with Mohanty *et al.* (2020), Sirisha *et al.* (2020). Cluster XIV recorded highest mean for plant height (120.17) while lowest value with cluster XVII for number of capsules per plant (61.00). Cluster XV (30 KRDS-1-8) mean recorded low mean (9.83) for phyllody indicating, the genotype in this cluster can be used as parent in resistance breeding programme.

**Table 2: Average intra (diagonal) and inter cluster distances of sesame (*Sesamum indicum* L.) genotypes at RARS, Poalsa, Jagtial during kharif, 2017.**

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV	XV	XVI	XVII	XVIII	XIX
I	<b>17.93</b>	74.55	35.82	45.85	40.80	26.93	41.20	52.18	79.10	90.43	96.81	103.99	37.51	175.54	85.61	134.06	94.98	105.12	160.21
II		<b>18.42</b>	91.99	163.05	35.94	72.17	101.70	69.09	76.84	140.07	150.66	299.45	113.42	362.99	36.06	190.11	154.91	93.45	145.94
III			<b>30.10</b>	62.83	84.43	59.57	43.70	51.61	79.84	52.06	60.08	135.11	46.55	200.00	88.81	98.22	75.67	83.73	122.49
IV				<b>38.32</b>	106.01	67.42	63.64	101.72	134.54	121.95	131.42	60.44	59.22	130.63	158.59	170.34	129.63	171.01	216.07
V					<b>0.00</b>	30.29	94.26	78.72	93.02	166.02	166.08	185.99	74.88	266.29	77.81	209.91	151.46	136.20	214.25
VI						<b>0.00</b>	52.52	66.42	101.71	124.16	124.03	115.70	46.88	222.26	89.77	153.85	120.02	116.35	186.42
VII							<b>0.00</b>	30.34	99.10	62.60	100.84	148.59	69.13	231.22	68.64	91.90	94.55	56.22	102.19
VIII								<b>0.00</b>	68.31	39.07	63.74	209.61	53.45	264.18	51.54	52.65	42.45	19.89	75.87
IX									<b>37.61</b>	107.49	129.30	238.90	110.44	206.62	82.50	161.02	137.58	103.01	82.10
X										<b>0.00</b>	14.81	216.07	65.79	280.90	110.92	18.34	27.56	33.94	71.19
XI											<b>0.00</b>	208.09	48.47	286.01	142.84	32.46	19.14	69.67	130.11
XII												<b>0.00</b>	105.05	85.40	319.46	250.22	197.33	306.37	363.68
XIII													<b>0.00</b>	183.58	127.86	92.03	44.47	107.11	189.07
XIV														<b>25.21</b>	392.03	337.67	272.92	382.37	359.03
XV															<b>0.00</b>	160.70	152.32	60.28	90.82
XVI																<b>0.00</b>	21.43	38.74	104.68
XVII																	<b>0.00</b>	62.00	149.11
XVIII																		<b>0.00</b>	47.86
XIX																			<b>0.00</b>

**Table 3: Cluster means for yield and yield attributing traits using Tocher's method in sesame (*Sesamum indicum* L.) genotypes at RARS, Polasa, Jagtial during kharif, 2017.**

	Days to 50 per cent Flowering	Days to Maturity	Plant height (cm)	Number of Branches per Plant	Number of Capsules per Plant	Test weight (g)	Seed Yield per Plant (g)	Alternaria leaf spot PDI (%)	Phyllody (% incidence)	Cercospora leaf spot PDI (%)
Cluster I	55.41	86.71	90.62	4.82	16.52	2.16	2.21	90.28	79.88	95.44
Cluster II	42.73	74.13	86.71	4.57	17.09	2.08	2.40	90.81	78.18	94.84
Cluster III	55.83	86.21	117.30	5.28	24.35	2.70	3.94	81.46	74.43	88.00
Cluster IV	61.92	93.40	96.43	5.31	16.56	2.10	2.12	89.94	55.15	94.16
Cluster V	48.33	80.00	66.00	4.00	11.00	1.06	0.26	98.00	100.00	100.00
Cluster VI	54.00	84.67	56.50	1.67	13.67	2.61	1.84	80.67	90.67	90.00
Cluster VII	57.67	86.33	81.60	5.67	14.00	2.95	5.26	90.00	57.67	100.00
Cluster VIII	51.33	84.33	72.80	6.67	36.00	2.47	5.60	98.67	64.67	100.00
Cluster IX	42.67	86.11	113.20	5.56	20.89	2.54	4.18	85.89	60.11	87.78
Cluster X	55.67	86.33	118.70	5.67	49.00	2.56	7.49	78.00	67.33	84.00
Cluster XI	56.33	86.33	120.20	5.00	58.67	2.99	6.12	73.00	84.33	85.00
Cluster XII	69.33	102.67	92.50	2.00	12.00	1.72	0.82	97.50	92.00	100.00
Cluster XIII	57.67	89.67	76.85	6.00	42.00	1.79	2.57	75.00	84.67	100.00
Cluster XIV	60.89	110.33	120.17	7.33	11.11	1.96	1.29	94.44	81.00	100.00
Cluster XV	44.00	74.00	85.90	4.00	21.67	2.90	4.38	94.00	9.83	98.00
Cluster XVI	57.00	87.67	93.10	3.67	57.00	2.53	8.66	95.00	90.67	100.00
Cluster XVII	57.33	88.67	90.00	6.00	61.00	2.50	5.97	100.00	94.33	100.00
Cluster XVIII	49.33	79.67	82.05	5.00	39.67	2.29	7.94	89.67	68.67	91.00
Cluster XIX	43.33	83.00	115.50	4.67	32.00	2.65	9.40	71.67	22.67	65.33

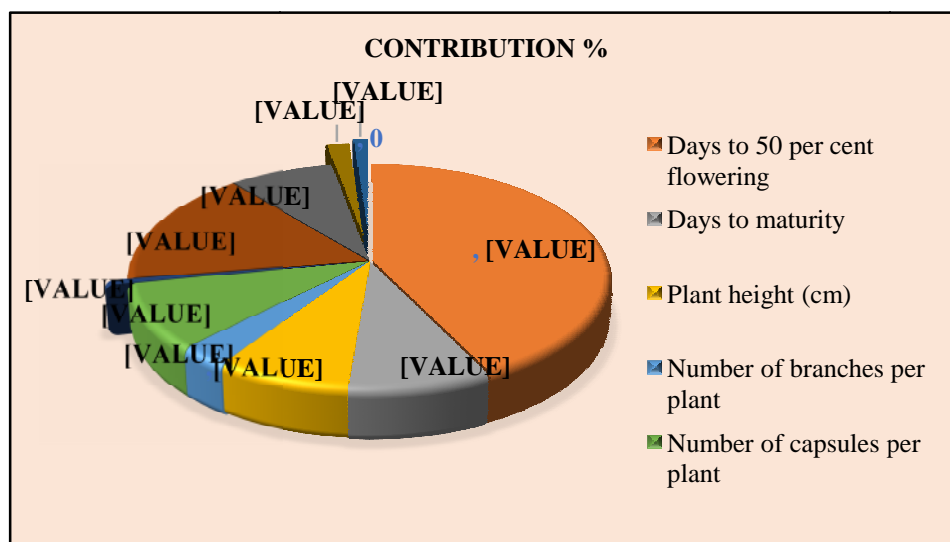
**D. Contribution towards genetic divergence**

Days to 50 per cent flowering (42.74 per cent) has shown the maximum contribution towards genetic divergence followed by seed yield per plant (16.61 per cent) and test weight contributing very low amount of divergence (0.62 per cent) were on par with the results

of Narayan and Murugan (2013); Rajani Bisen *et al.*, (2013) for yield contributing traits. Relative contribution of the parameters towards diversity was presented in Table 4 and the percent was depicted in the form of pie-diagram (Fig. 2).

**Table 4: Relative contribution (%) of yield and yield attributing traits in sesame (*Sesamum indicum* L.) genotypes at RARS, Polasa, Jagtial during *kharif*, 2017.**

Sr. No.	Character	Times ranked 1 <sup>st</sup>	Contribution %
1.	Days to 50 per cent flowering	3752	42.74
2.	Days to maturity	754	8.58
3.	Plant height (cm)	708	8.07
4.	Number of branches per plant	259	2.98
5.	Number of capsules per plant	829	9.44
6.	Test weight (g)	55	0.62
7.	Seed yield per plant (g)	1457	16.61
8.	Phyllody (% incidence)	704	8.03
9.	Alternaria leaf spot PDI (%)	159	1.78
10.	Cercospora leaf spot PDI (%)	101	1.15



**Fig. 2.** Relative contribution (%) of yield and yield attributing traits in sesame (*Sesamum indicum* L.) genotypes at RARS, Jagtial during *kharif*, 2017.

**CONCLUSION**

Genetic diversity has direct relation in creating variability through hybridization. The genotypes from diverse clusters like XIV & XV; XIV & XVIII having high inter-custer distances should be used rather than the genotypes of clusters having low divergence to create variability and to identify heterotic cross combinations for harvesting hybrid vigour, also for utilisation in the hybridization programme (Narayanan and Murugan., 2013). In breeding programmes, parents having high yield potential with wide genetic diversity are likely to yield superior transgressive segregants within short period (Maurya and Singh, 1977). Such genotypes can also be utilised in heterosis breeding to

develop high yield recombinants (Mohanty *et al.*, 2020). In addition, by using marker systems as a part of biotechnological tool efficiency in identifying the transgressive segregants or recombinants can be improved.

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**Conflict of interest.** None.

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