



ISSN (E): 2277- 7695

ISSN (P): 2349-8242

NAAS Rating: 5.03

TPI 2020; 9(7): 468-470

© 2020 TPI

[www.thepharmajournal.com](http://www.thepharmajournal.com)

Received: 01-05-2020

Accepted: 03-06-2020

**MH Reddy**

Department of Genetics and  
Plant Breeding, Nagaland  
University, SASRD,  
Medziphema, Nagaland, India

**HP Chaturvedi**

Department of Genetics and  
Plant Breeding, Nagaland  
University, SASRD,  
Medziphema, Nagaland, India

## Genetic diversity in sesame (*Sesamum indicum* L.) genotypes under foothill condition of Nagaland

**MH Reddy and HP Chaturvedi**

### Abstract

The nature and magnitude of genetic divergence were assessed in 16 sesame genotypes. Based on the relative magnitude of  $D^2$  values all the 16 genotypes were grouped in to 5 different clusters. Cluster I had 12 genotypes while remaining clusters II, III, IV and V had one genotype each. The average inter cluster distance was found to be highest between cluster III and IV (79.94) followed by cluster III and V (63.87) and cluster IV and V (62.64) whereas the lowest inter cluster distance was observed between cluster I and II (29.21). The higher inter cluster distance indicated the presence of more diversity among the genotypes included in these clusters. Thus the genotypes of cluster III and IV could be utilized as potential parents and crossing between these genotypes would result in heterotic expression for yield component traits. The relative contribution of different plant characters to the total genetic divergence estimated by  $D^2$  analysis indicated that capsule length contributed the maximum (32.5%) towards genetic divergence followed by number of seeds per capsule (30.83%).

**Keywords:** Sesame,  $D^2$ , cluster, genetic diversity

### Introduction

Sesame (*Sesamum indicum* L.) is diploid ( $2n= 26$ ) belongs to Pedaliaceae family. Sesame seed is highly nutritive (oil 50%, protein 25%) and its oil contains an anti-oxidant called sesamol. Due to the presence of potent antioxidant, sesame seeds are known as “the seed of immortality”. In spite of sesame possessing high nutritional value and resistance to abiotic stress like drought it has low yielding capacity compared to other oilseed crops. Further, sesame has been given less attention by the farmers because of poor yield due to non-availability of cultivars to suit the diverse agro climatic conditions. Hence, development of improved high yielding cultivars adapted to local conditions has become top priority. Germplasm is a valuable source of base population and provides the scope for wider variability. However, to understand the useable variability, grouping or classification of genetic stocks based on minimum divergence or resemblance between them is quite imperative. The nature and magnitude of genetic divergence helps the plant breeder in choosing the right type of parents for higher amount of heterotic expression in F1 and broad spectrum of variability in subsequent segregating generations (Maurya and Singh, 1997) [5]. In general, diverse landraces traditionally are considered important for future food security due to their ability to sustain in changing climate (Huang *et al.*, 2018) [2]. Therefore, the present study was undertaken to assess the nature and magnitude of genetic diversity present in different genotypes of sesame.

### Materials and Methods

The present investigation was conducted with sixteen genotypes (Table- 1) during *kharif* 2018 at the experimental farm of Department of Genetics and Plant Breeding, School of Agricultural Sciences and Rural Development, Nagaland University, Medziphema, Nagaland. The experiment was carried out in randomized block design (RBD) with three replications. Sesame seeds were sowed on 10<sup>th</sup> august 2018. All the recommended agronomic practices were followed for raising a good crop. Data were recorded on five sampled plant in each plot on ten characters *viz.* days to 50% flowering, days to 50% flowering to maturity, plant height, stem height from base to first branch, number of branches per plant, number capsules per plant, capsule length, number seeds per capsule, harvest index and seed yield per plant. The mean values were subjected to statistical analysis to work out analysis of variance for all the characters as suggested Panse and Sukhatme (1957) [7]. The genetic divergence among genotypes was computed by means of Mahalanobis  $D^2$  technique (Mahalanobis, 1936) [3] and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952) [8].

**Corresponding Author:**

**HP Chaturvedi**

Department of Genetics and  
Plant Breeding, Nagaland  
University, SASRD,  
Medziphema, Nagaland, India

**Table 1:** List of genotypes used under investigation

S. No.	Genotypes	Procurement Location
1	TKG – 21	JNKVV, Jabalpur
2	GT – 10	JNKVV, Jabalpur
3	GT – 3	JNKVV, Jabalpur
4	TKG – 22	JNKVV, Jabalpur
5	TKG – 53	JNKVV, Jabalpur
6	Nempo Karjung	AAU, Experimental centre, Diphu
7	Nempo Thepo	AAU, Experimental centre, Diphu
8	Nempo Soksu	AAU, Experimental centre, Diphu
9	Bahubheti Local	AAU, Experimental centre, Diphu
10	ST-1683	AAU, Experimental centre, Diphu
11	Nempo Charap	AAU, Experimental centre, Diphu
12	Kensa	Ngaland
13	Youngyimsen	Ngaland
14	Meghalaya (Local)	Meghalaya
15	Chuchuyimlang	Naagaland
16	Yisemyong	Nagaland

### Results and Discussion

The analysis of variation revealed significant differences among the genotypes for all characters (Table- 2).  $D^2$  statistic is a useful tool to measure genetic divergence among

genotypes in any crop. The study of  $D^2$  (genetic divergence) of 16 genotypes was done through Mohalanobis  $D^2$  statistic as described by Rao (1952)<sup>[8]</sup>.

**Table 2:** Analysis of Variance for 10 characters in sixteen genotypes of sesame

Source of variation	DF	Sum of mean squares									
		Days to 50 per cent Flowering	Days to 50% flowering to maturity	Plant height	Number of branches per plant	Stem height from base to first branch	Number of capsules per plant	Capsule length (cm)	Number of Seeds per capsule	Harvest index (g)	Seed yield per plant (g)
Replication	2	33.83	18.52	6.31	0.25	65.60	153.17	0.02	4.11	18.27	1.95
Treatment	15	278.15*	107.26*	359.12*	1.51*	421.01*	124.69*	0.09*	331.44*	117.12*	1.41*
Error	30	23.19	8.43	25.31	0.20	81.54	50.77	0.002	13.15	17.71	0.53

### Clustering pattern of 16 genotypes

Based on the relative magnitude of  $D^2$  values all the 16 genotypes were grouped in to 5 different clusters (Table- 3). Cluster I had 12 genotypes which include TKG- 21, GT- 10, nempo thepo, nempo soksu, bahubheti local, ST- 1683,

nempo chrap, kensa, young yimsen, Meghalaya local, chuchuyimlang, yisemyong. This cluster has the highest number of genotypes while remaining clusters II, III, IV and V have one genotype each.

**Table 3:** Clustering pattern of 16 sesame genotypes on the basis of genetic divergence

Cluster Number	Number of Genotypes	Genotypes
Cluster I	12	TKG- 21, GT- 10, nempo thepo, nempo soksu, bahubheti local, ST- 1683, nempo chrap, kensa, young yimsen, Meghalaya local, chuchuyimlang, yisemyong
Cluster II	1	TKG- 53
Cluster III	1	Nempo karjung
Cluster IV	1	TKG- 22
Cluster V	1	GT- 3

### Average intra and inter clustering pattern of 16 genotypes

The estimates of intra and inter cluster values have been reported in the table 4. The average inter cluster distance was found to be highest between cluster III and IV (79.94) followed by cluster III and V (63.87) and cluster IV and V (62.64) whereas the lowest inter cluster distance was observed between cluster I and II (29.21). The higher inter cluster distance indicated the presence of more diversity among the genotypes included in these clusters. The minimum inter cluster distance indicated close relationship among the genotypes of these clusters and had a maximum of similar gene complexes among them. The maximum inter-cluster

distance suggested wide diversity among the genotypes between the groups. The promising genotypes from these clusters could be utilized as potential parents and crossing between these genotypes would result in heterotic expression for yield component traits. It is suggested that the crosses between selected varieties from widely separated clusters are most likely to give desirable recombinants. To achieve higher variability and high heterotic effect, Mishra et al. (2003)<sup>[4]</sup> and Chaturvedi and Maurya (2005)<sup>[1]</sup> also recommended that parents should be selected from two clusters having wider inter cluster distance.

**Table 4:** Average inter and intra cluster distances of 16 sesame genotypes.

Cluster number	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V
Cluster I	18.90	29.21	41.33	43.16	61.89
Cluster II		0.00	45.21	41.38	32.11
Cluster III			0.00	79.94	63.87
Cluster IV				0.00	62.64
Cluster V					0.00

**Cluster wise mean values of 10 characters in sesame**

Cluster wise mean values for all the characters have been listed in the table 5. Cluster I Showed maximum mean value for days to 50% flowering; stem height from base to first branch and number of branches. Cluster III showed maximum mean values for characters days to 50% flowering to maturity and number of capsules per plant. Cluster IV showed

maximum mean value for capsule length, number of seeds per capsule and harvest index. Cluster V for characters plant height and seed yield per plant. Cluster based mean estimations are useful in targeting the genotypes for breeding programme, as they prevent the tedious efforts of screening the inferior germplasm lines.

**Table 5:** Cluster wise mean values for 10 characters in 16 sesame genotypes

Cluster/ Character	Days to 50% flowering	Days to 50% flowering to maturity	Plant height (cm)	Number of branches	Stem height from base to first branch (cm)	Number of capsules per plant	Capsule length (cm)	Number of seeds per capsule	Harvest index (%)	Seed yield per plant (g)
Cluster I	50.47	47.42	97.56	2.62	46.49	31.04	2.50	71.24	39.94	3.31
Cluster II	40.67	47.00	90.59	1.73	26.83	23.20	2.61	53.04	38.27	4.01
Cluster III	32.67	59.67	109.73	2.47	39.80	36.97	2.10	48.24	37.67	4.30
Cluster IV	31.00	59.67	81.43	1.67	36.23	23.87	2.76	78.98	55.00	2.68
Cluster V	31.67	59.00	123.53	2.00	35.74	33.53	2.73	53.41	34.00	4.67

**Contribution of each character to genetic divergence**

The characters capsule length (32.5%) and number of seeds per capsule (30.83%) contributed maximum towards the divergence. The corresponding details are furnished in the table 6. Similar findings were reported by Parameshwarappa *et al.* (2012) [6].

The present study suggests that the genotypes of cluster III (Nempo karjung) and cluster IV (TKG- 22) could be utilized in hybridization program to achieve greater variability in the segregating generations.

**Table 6:** Contribution of each character of sesame towards the divergence

S. No.	Source	Times Ranked First	Contribution (%)
1	Days to 50% flowering	5	4.17
2	Days to 50% flowering to maturity	4	3.33
3	Plant height (cm)	12	10.00
4	Number branches	14	11.67
5	Stem height from base to first branch (cm)	2	1.67
6	Number of capsules per plant	13	00
7	Capsule length (cm)	39	32.5
8	Number of seeds per capsule	37	30.83
9	Harvest index (%)	1	0.83
10	Seed yield per plant (g)	6	5.00

**References**

1. Chaturvedi HP, Maurya DM. Genetic divergence analysis in rice (*Oryza sativa* L.). *Advances Pl. Sciences*. 2005; 18(1):349-353.
2. Huang L, Zhang R, Huang G, Li Y, Melaku G, Zhang S *et al.* Developing superior alleles of yield genes in rice by artificial mutagenesis using the CRISPR/ Cas9 system. *The Crop Journal*. 2018; 6:475-481.
3. Mahalanobis PC. On the generalized distance in statistics. *Proceedings of the National Institute of Science of India*. 1936; 2:49-55.
4. Mishra LK, Sarawgi AK, Mishra RK. Genetic diversity

for morphological and quality traits in rice (*Oryza sativa* L.). *Advances Pl. Sciences*. 2003; 16(1):287-293.

5. Maurya DM, Singh DP. Genetic Divergence in rice. *Ind. J Genet*. 1977; 37:395-402.
6. Parameshwarappa SE, Palakshappa MG, Shinde GG. Studies on genetic divergence for yield and yield attributing traits in sesame (*Sesamum indicum* L.) germplasm. *International Journal of Agricultural Sciences*. 2012; 8(2):441-444.
7. Panse VG, Sukhatme PV. *Statistical methods for agricultural workers*. Indian Council of Agricultural Research, New Delhi, 1957.
8. Rao CR. *Advanced statistical methods in biometrical research*. John Wiley and Sons Inc., New York, USA, 1952.