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Genetic Diversity in Sesame (*Sesamum indicum L.*) Landraces of North East India

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Abstract

The nature and magnitude of genetic divergence was assessed in 20 sesame genotypes of North East India. Based on the relative magnitude of D^2 values, 20 genotypes were grouped into six clusters containing one to twelve genotypes. These clusters consisted of genotypes with different geographical origins indicating no correlation between genetic divergence and geographical divergence. The genotypes of Cluster VI showed maximum genetic divergence with Cluster V and cluster I. The genotypes belonging to cluster VI and cluster V may be selected for hybridization for generating genetic variability. Thus to generate desirable genetic variability the crossing between cluster VI and V genotypes would be useful. It is suggested that hybridization among the genotypes of above said clusters would produce segregants for more than one economic character which can serve as parents of hybrids. Number of capsules per plant followed by oil content, plant height and test weight contributed maximum towards divergence.

Keywords Sesame, D^2 statistic, Cluster, Genetic divergence

Inroduction

Sesame (*Sesamum indicum L.*) is diploid (2n= 26) belongs to Pedaliaceae family. Sesame commonly known as Gingelly, Gergelim, Til (Hindi) is one of the oldest cultivated oilseed crop grown extensively in India. Sesame seeds are highly nutritive (oil 50%, protein 25%) and its oil contains an anti-oxidant called sesamol which imparts to it a high degree of resistance against oxidative rancidity (Ashri, 1989). Due to the presence of potent antioxidant, sesame seeds are known as “the seed of immortality”. In North East an array of local genotypes are in cultivation since long. Though many of them are low yielding but they are valuable with reference to many rare physiological and quantitative traits.

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). Information available on genetic diversity in sesame (*Sesamum indicum* L.) genotypes of North East India is limited. Therefore, the present study was carried out to analyze the genetic diversity in sesame genotypes of North East India to select the potential parents for breeding program.

Materials and Methods:

The present investigation was carried out in the experimental farm of the Department of Genetics and plant Breeding, School of Agricultural Sciences and Rural Development, Medziphema, Nagaland during kharif season of 2016. Seeds of 19 local genotypes and 1 improved variety (Table- 1.) of sesame were collected from northeast and raised in a randomized block design (RBD) in three replications. The sesame seeds were sown on

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20th of June 2016. One-two healthy seeds were dibbled in lines with the help of a small spade manually at 30 cm row to row and 20 cm plant to plant distance. Total plant population of 25 plants per plot was maintained for all the 20 genotypes. All the recommended agronomic practices were followed for raising a good crop. The data were recorded on five randomly sampled plants in each plot for nine quantitative characters *viz.* days to 50% flowering, 80% maturity, plant height, no of primary branches, no of capsules per plant, no of seeds per capsules, test weight, oil content and seed yield. The mean values were subjected to statistical analysis to work out analysis of variance for all the characters as suggested Panse and Sukhatme (1957). The genetic divergence among genotypes was computed by means of Mahalanobis D^2 technique (Mahalanobis, 1936) and the genotypes were grouped into different clusters following Tocher's method (Rao, 1952).

Results and Discussion

Analysis of variance revealed significant variation among the 20 genotypes for all the characters. Several measures of distance have been proposed to suit various objectives of which Mahalanobis's generalized distance (Mahalanobis, 1930, 1936; Rao, 1952) had occupied a unique place in plant breeding. Using this technique, all the genotypes were grouped into 6 different clusters (Table 2). Cluster I has the maximum number of landraces (12) followed by Cluster III (4) and the remaining clusters had one landraces each

The estimates of intra and inter cluster distances have been presented in Table 3. The divergence at inter cluster level was maximum between Cluster V and Cluster VI (D^2= 829.18) indicating wide genetic diversity between these two clusters. Hence, the genotypes of cluster V and cluster VI could be utilized in hybridization program to achieve greater variability in the segregating generations. To achieve higher variability and high heterotic effect, Mishra et al. (2003) and Chaturvedi and Maurya (2005) also recommended that parents should be selected from two clusters having wider inter cluster distance. The divergence at inter cluster level was found to be minimum between Cluster II and Cluster IV (D^2 = 56.57).

The cluster means of all the six clusters are presented in Table 4. Cluster IV showed highest mean value for plant height, number of primary branches, test weight and seed yield per plant. Cluster VI showed highest mean value for days to 50% flowering, 80% maturity, no of capsules per plant, no of seeds per capsules and oil content. 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. Hence, genotypes from cluster IV and VI could be directly used for final field evaluation in advanced breeding experiments.

The contribution of each character to the D^2 values or divergence is presented in Table 5. Among the different characters studied number of capsules per plant contributed maximum (67.89%) towards divergence, followed by oil content (10.53%), plant height (7.37%) and test weight (6.32%). This was in agreement with the findings of Soniasabanam et al. (2018) for test weight, plant height and number of pods per plant; Zhimomi et al. (2019) for test weight and oil content. The present study suggests that the genotypes of cluster V (AST- 1) and cluster VI (Yisemyong local) could be utilized in hybridization program to achieve greater variability in the segregating generations.

Table 2. Clustering pattern of 20 genotypes of sesame on the basis of genetic divergence

Cluster number	Number of genotypes	Genotypes included
I	12	Wameken Local, Manipur Local, Kensa Local, Merangkong Local,Mopongchuket Local, Longkong Local, Akhoya Local, Kashanyu Local, Zunheboto Local, MeghalayaLocal 2, Salulemang Local and Chuchuyimlang Local
II	1	Mongsenyimti Local
III	4	Yoangyimsen Local, Lungsha Local, Longsa Local and Punjab Til No 1
IV	1	Meghalaya Local 1
V	1	AST – 1
VI	1	Yisemyong local

Table 3. Average intra and inter- cluster distance

Cluster	I	II	III	IV	V	VI
I	80.99	164.21	346.58	171.87	151.89	718.39
II		0.00	125.17	56.57	162.12	282.14
III			67.65	194.64	497.72	181.08
IV				0.00	203.09	371.04
V					0.00	829.18
VI						0.00

Table 4. Cluster wise mean values of 9 characters in sesame

	Plant height	No of primary branches	No of capsules per plant	No of seeds per capsules	50% flowering	80% maturity	Test weight	Oil content	Seed yield/ plant
Cluster I	72.44	77.78	239.39	9.68	127.58	80.47	1.56	44.76	131.72
Cluster II	63.67	74.33	202.07	9.93	196.07	79.20	1.53	47.80	171.67
Cluster III	75.17	80.83	233.50	12.02	255.43	82.33	1.49	40.12	150.00
Cluster IV	76.33	88.33	223.8	10.47	186.93	70.00	2.47	46.27	228.00
Cluster V	45.00	78.67	176.33	9.47	109.53	79.87	1.27	47.80	145.67
Cluster VI	65.67	75.33	244.27	16.53	322.80	84.80	2.20	52.73	186.33

Table 5. Contribution of each character to divergence

Sl. No.	Characters	Times ranked first	Percent contribution
1	Days to 50% flowering	4	2.11 %
2	Days to maturity	-	0 %
3	Plant height	14	7.37 %
4	Number of primary branches	-	0 %
5	Number of capsules per plant	129	67.89 %
6	80 % maturity	9	4.74 %
7	Test weight	12	6.32 %
8	Oil content	20	10.53 %
9	Seed yield per plant	2	1.05 %

Table- 1. List of genotypes along with their local names

Sl. No.	**Treatments**	**Genotype name**	**Place of collection**
1	T1	Pubjab Til no 1	Punjab
2	T2	AST – 1	Assam
3	T3	Salulemang Local	Salulemang
4	T4	Yisemyong local	Yisemyong
5	T5	Yoangyimsen Local	Yoangyimsen
6	T6	Longsa Local	Longsa
7	T7	Kashanyu Local	Kashanyu
8	T8	Zunheboto Local	Zunheboto
9	T9	Longkong Local	Longkong
10	T10	Wameken Local	Wameken
11	T11	Kensa Local	Kensa
12	T12	Lungsha Local	Lungsha
13	T13	Chuchuyimlang Local	Chuchuyimlang

14	T14	Merangkong Local	Merangkong
15	T15	Akhoya Local	Akhoya
16	T16	Mopongchuket Local	Mopongchuket
17	T17	Mongsenyimti Local	Mongsenyimti
18	T18	Meghalaya Local – 1	Meghalaya
19	T19	Meghalaya Local – 2	Meghalaya
20	T20	Manipur Local	Manipur

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