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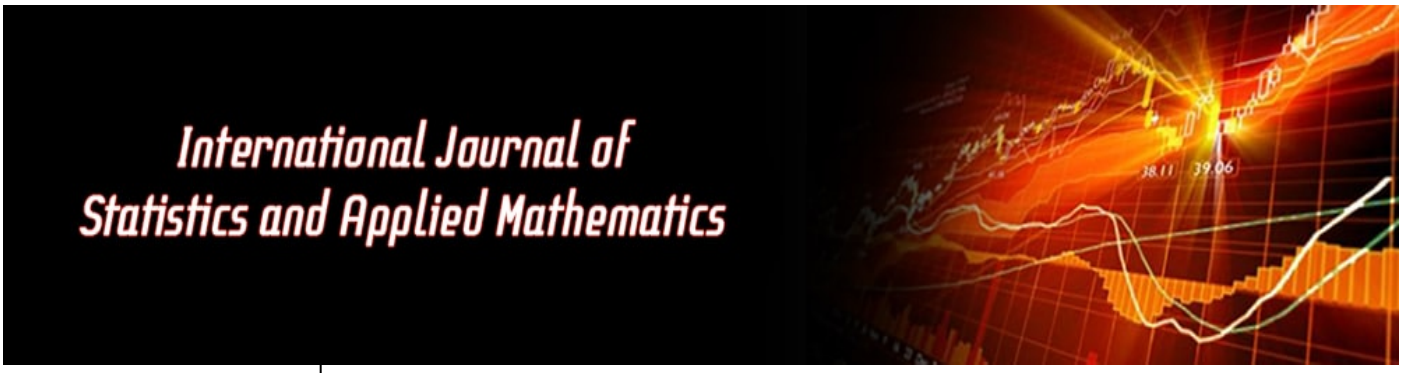

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Genetic Divergence in Sesame (*Sesamum indicum* L.)

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Abstract
The nature and magnitude of genetic divergence was measured in thirty-two sesame (*Sesamum indicum* L.) germplasm lines collected from different parts of NE region were evaluated at Regional Agricultural Research Station Diphu, Karbi Anglong, Assam, India using Mahalanobis's D^2 statistic. The population was grouped into four clusters and the parents from the respective clusters were selected based on their cluster distances and cluster means for hybridization programme. Cluster I was the largest with 24 genotypes followed by cluster II (4), III (3), while cluster IV with one genotype. The study revealed D^2 values from 101.0543 to1145.0130, indicating significant divergence in the genotypes.

Keywords: *Sesamum indicum*, D^2 statistic, genetic divergence

Introduction
Sesame (*Sesamum indicum* (L.) is an important oilseed crop of Assam. Most of the improved varieties of sesame grown in Assam do not have drought tolerant capacity. So, *kharif* sesame suffered most if it is sown a bit late. Development of drought tolerant varieties is inevitable for which identification of suitable parents is necessary. The selection of parents for varietal improvement programme depends on the knowledge of available diversity which is practically difficult to identify the genotypes suitable for the agro climatic conditions of Assam. Therefore, the present study has been undertaken to ascertain the nature and magnitude of genetic diversity among 32 sesame cultivars collected from different parts of North East Region of India.

Materials and Methods
The experimental material comprised of thirty-two genotypes collected from Assam as well as North Eastern Region. These genotypes were grown in randomized block design with three replications at Regional Agricultural Research Station, Diphu during kharif 2018 to 2020. Each plot consisted of 4 rows of 5m length spaced at 30 cm and plants within row at 10 cm. Observations were recorded on ten random plants for eight quantitative characters *viz*., Root length (cm), Root volume (cc), Leaf Relative water Content (RCW) (%),Plant height(cm), Seed Yield/plant (g), Days to maturity (days), No. of capsules/plant, and Seeds/capsule. The data were subjected to Mahalanobis D^2 statistic and genotypes were grouped into different clusters following the Tocher's method as proposed by Rao (1952) [1].

Results and Discussion
The analysis of variance revealed significant difference among 32 genotypes for all the characters under study, indicating considerable variation among the genotypes. The D^2value range from 101.0543 to 1145.0130 reflecting wide diversity among the genotypes. On the basis of D^2estimates, 32genotypes were grouped into four clusters (Table 1). Among theses, cluster I had maximum number of 24 genotypes, followed by cluster II and cluster III with 4 and 3 genotypes respectively. The cluster IV had single genotype. Interestingly, the related genotypes collected from Assam as well as NE region were distributed in different clusters. This results indicated that the genetic divergence is not related to geographical diversity. Similar type of result was reported by Gangadhara Rao (2011) [5] and Gangadhara *et al*. (2012) [6].

Substantial variability among the genotypes evolved in the same habitat might be due diversity of their pedigree along with natural and directional selection pressure for certain agronomic traits as reported by Katiyar (1978) [2]. In chickpea. Genetic drift and selection forces under diverse environments could cause greater diversity than geographical distance as reported by Bhatt (1970) [3].

The inter-cluster distances were greater than intra-cluster distances, revealing considerable amount of genetic diversity among the genotypes studied (Table 2). Inter cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum intercluster distance are genetically more divergence and hybridization between genotypes of divergent cluster is likely to produce wide variability with desirable segregant as suggested by Roy *et al* (2021) [4] and Gangadhara *et al*. (2012) [6]. The intra-cluster D^2 values ranged from 86.58863 (cluster II) to 166.8774 (Cluster I). The maximum inter cluster D^2values were recorded seed yield (kg/ha) contributing substantially to total genetic divergence as reflected by their coefficient of variation. The maximum inter cluster distance was observed between Cluster II and Cluster III (1145.0130). The results are in conformity with those of Roy *et al*. (2021) [4] and Gangadhara Rao (2011) [5]. The genotype of cluster IV were earliest in maturity and those of cluster II were also earlyin maturity. The genotypes of Cluster III were highest in root volume along with late maturity whereas genotypes in the Cluster I had no significant parameter. Considerable genetic diversity in sesame. Thus in view of considerable genetic diversity in sesame genotypes, there is sufficient scope for varietal improvement through hybridization between genotypes Longsa local, Zuheboto Local, Nempo Kelok (Taralanso) of cluster III and genotypes Nagaon local, Bahuabheti local, Meghalaya local 1, Nempochindon of cluster II. Crossing among these genotypes is suggested to obtain desirable segregants giving higher yield with drought tolerance.

Table 1: Grouping Of genotypes

Cluster number	Total number of genotypes	Name of the genotypes
I	24	AAUDT 301-4-2 (w), AAUDT 302-3-4 (w), AAUDT 303-1-1 (B), Punjab Til 1, Yisemyonglocal,Salulemang local, Wameken Local, Kensa Local, Akhoya Local, Yoangyimsen local, Lungsha Local, Mongsenyimti Local, Chuchuyimlang, Longkong Local, NempoThepo, ST 1683, NempoCherop, Nemposoksu, Manipur Local, Koliabor local, Merangkong Local, Nempokarju`ng, Meghalaya local 2, NempoKelok(Longnit)
II	4	Nagaon local, Bahuabheti local, Meghalaya local 1, Nempochindon
III	3	Longsa local, Zuheboto Local, NempoKelok(Taralanso)
IV	1	AST 1

Table 2: Inter and intra cluster distance of thirty two genotypes of Sesame

Cluster	Cluster I	Cluster II	Cluster III	Cluster IV
Cluster I	166.8774	262.34629	651.6226	526.3268
Cluster II	262.3463	86.58863	1145.0130	811.0956
Cluster III	651.6226	1145.0130	101.0543	365.6581
Cluster IV	526.3268	811.09560	365.6581	0.0000

Table 3: Cluster means for different clusters

Cluster No	Root length (cm)	Root volume (cc)	Leaf Relative water Content (RCW) (%)	Plant height (cm)	Seed Yield/plant (g)	Days to maturity (days)	No. of capsules/plant	Seeds /capsule
I	8.15	0.25	57.14	104.26	34.26	101.21	42.85	43.76
II	5.54*	0.14*	51.30*	113.53	40.06	93.42	48.17	48.69
III	8.67	0.59**	63.38	95.81*	33.78*	107.52**	41.52*	41.89*
IV	10.24**	0.45	73.44**	116.89**	52.39**	85.33*	53.22**	54.00**
Mean	8.15	0.358	61.315	107.623	40.122	96.87	46.44	47.085
SEM (%)	0.221	0.008	1.474	2.309	3.871	2.074	0.726	2.479
CV (%)	4.834	5.139	4.434	3.805	12.129	7.582	2.873	9.645

*, ** Lowest and highest mean respectively

Conclusion

The crosses among divergent parents are likely to yield desirable combinations. Thus, a crossing programme should be initiated between the genotypes belonging to different clusters. However, two important points are to be kept in mind:

1. Selection of particular cluster from which genotypes are to be used as parent in crossing programme.
2. Choice of particular genotypes from the selected clusters. In this study, the maximum divergence was between genotypes Longsa local, Zuheboto Local, Nempo Kelok (Taralanso) of cluster III and genotypes Nagaon local, Bahuabheti local, Meghalaya local 1, Nempochindon of cluster II. These strains were quite divergent and could be used in hybridization programme on the basis of their greater inter cluster distance and higher cluster mean values.

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