

## GENETIC DIVERGENCE IN SESAMUM (*Sesamum indicum* L.)\*

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Mahalanobis  $D^2$  analysis was employed to study the genetic diversity in 40 genotypes of sesamum and to know the relative contribution of nine characters to genetic diversity. A wide genetic diversity was noticed among the 40 types tested wherein the genotypes fell into six different clusters. The clustering pattern showed that the geographic diversity need not necessarily be related to the genetic diversity. Genotypes from different ecogeographic regions were grouped in one cluster. Likewise, genotypes from the same ecogeographic region were found scattered in different clusters. The inter-cluster distance study revealed that cluster VI was highly divergent from clusters IV and V. Cluster I recorded the highest cluster mean values for plant height, branch number, capsule number, capsule number on main stem, 1000 seed weight, oil content and seed yield. The ranking analysis disclosed that oil content followed by days to full maturity contributed maximum to genetic divergence.

A wide range of genetic diversity among parents is an essential feature in any hybridization programme. Hence, plant breeders are interested in estimating the relationship between geographical and genetic diversity. Mahalanobis  $D^2$  analysis provides a mean to quantitatively estimate the same and to assess the contribution of different characters to genetic diversity. An attempt of this kind was made in sesamum and the results are discussed.

### MATERIAL AND METHODS

Forty genotypes of sesamum with diverse geographical origin were obtained from the College of Agriculture, Bhubaneswar, Orissa and School of

Genetics, Tamil Nadu Agricultural University, Coimbatore. They were raised in randomised blocks replicated thrice at the Agricultural College and Research Institute, Madurai. Observations on plant height, branch number, capsule number, capsule number on main stem, seed number, 1000 seed weight, days to full maturity, oil content and seed yield per plant were recorded on five randomly selected plants of each genotype in each replication.

The data were subjected to multivariate analysis following Rao (1952). All possible  $\left(\frac{n(n-1)}{2}\right) D^2$  values were worked out by TDC 312 electronic computer, installed at PSG College of Technology, Coimbatore. For deter-

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mining group constellations or clusters, the criterion suggested by Rao (1952) was followed. Inter-cluster distances were worked out taking into consideration of all the component  $D^2$  values among the members of the two clusters in question. Intra-cluster distances were arrived at by taking average of the component types in that cluster. Ranking of component  $D^2$  values, among the nine characters was done as per the method outlined by Singh and Chaudhary (1977).

## RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all the nine characters studied. Wilk's Lambda criterion test also confirmed the significant diversity among types. The  $D^2$  values ranged from 0.7277 to 108.3693. By the application of clustering technique, the forty types were grouped into six different clusters. The number of types included in cluster I, II, III, IV, V and VI were 6, 4, 14, 6, 9 and 1 respectively. In each cluster, the types included were from different geographical origin. Thus, the clustering pattern of the types clearly indicated that the geographic diversity need not necessarily be related to the genetic diversity. This is in consonance with the results of Trehan *et al.* (1974) in sesamum.

The largest cluster, III included four types from Tamil Nadu, four from

Orissa, two each from Australia and Punjab, and one each from Taiwan and West Bengal. Such grouping of genotypes from different locations may be attributed to the free exchange of breeding materials from one place to another (Verma and Metha, 1976) and/or due to the unidirectional selection practised by breeders of different locations (Singh and Bains, 1968). It can also be noted that types from one geographic region were found to be scattered in different clusters. Murthy and Arunachalam (1966) reported that such wide adaptability would be possible due to factors like heterogeneity genetic architecture of the populations past history of selections, developmental traits and degree of general combining ability.

The intra and inter cluster  $D^2$  and  $D$  values among the six clusters are presented in table I. The intra-cluster generalised distance was maximum for cluster III (4.02) and minimum for cluster I (1.97). The highest inter-cluster generalised distance (9.06) was recorded between clusters V and VI, while the clusters I and II were the least divergent (3.04). Cluster IV was highly divergent from clusters IV and V.

The data on the character means for six clusters are summarised in table II. Cluster I recorded the highest mean values for all the characters studied except for days to full maturity and seed number. Maximum clu-

ster mean values for seed number (72.11) and days to full maturity (94.41) were recorded by clusters V and III respectively.

According to Endang *et al.* (1971) the clustering pattern could be utilised in choosing parental combination for prospective breeding programme to generate the highest possible variability in the yield components. In the present study the types in cluster I can be chosen for hybridization programme, as it recorded highest cluster mean values for seven important characters. To select the best type from cluster I, the types in that cluster may be tested in a series of diallel analysis (Chaudhary *et al.*, 1975). For earliness cluster VI (Type T 13) may be included in the breeding programme.

The number of times that each character appeared in first rank and its respective percentage contribution towards genetic divergence is represented in table III. It was observed that oil content contributed the maximum (27.31 per cent) towards genetic divergence followed by days to full maturity (16.28 per cent). Among the nine characters, capsule number on main stem was the least contributor with a share of only 3.33 per cent. Trehan *et al.* (1974) in sesamum reported that plant height contributed the maximum followed by days to full maturity. The  $D^2$  analysis by Yadava *et al.* (1973) in mustard revealed

that oil content contributed the maximum to the genetic diversity,

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Table I Intra and Inter cluster D<sup>2</sup> and D values (within parentheses) for six clusters in sesamum

Cluster	I	II	III	IV	V	VI
I	3.90 (1.97)	9.24 (3.04)	15.47 (3.93)	28.97 (5.38)	46.37 (6.81)	41.10 (6.41)
II		7.67 (2.77)	13.45 (3.67)	17.77 (4.21)	34.42 (5.87)	44.96 (6.70)
III			16.24 (4.03)	17.18 (4.14)	27.93 (5.29)	55.05 (7.42)
IV				8.18 (2.95)	12.39 (3.52)	66.70 (8.16)
V					10.81 (3.29)	82.12 (9.06)
VI						0.0000

Table II : Intra-cluster mean values for nine characters in sesamum.

Cluster	Plant height (cm)	Branch number	Capsule number	Capsule number on main stem
I	108.1	7.3	77.0	27.7
II	90.8	6.0	62.0	19.8
III	91.7	5.9	60.4	24.2
IV	79.2	3.2	39.5	20.5
V	77.8	4.6	46.1	20.9
VI	90.8	1.0	27.6	21.6
Grand Mean	89.7	4.7	52.1	22.5

Continue the Table below

Seed number	1000-seed weight (g)	Days to full maturity	Oil content (per cent)	Seed yield (g)
57.5	3.1	93.6	52.5	13.60
57.4	2.84	88.4	47.4	10.42
62.1	2.82	94.4	48.3	10.24
65.7	2.62	94.0	44.3	6.63
72.1	2.49	92.3	45.7	8.00
70.5	2.49	84.6	50.9	4.59
64.2	2.73	91.2	48.2	8.91

Table III : Relative contribution of nine characters to genetic diversity in sesamum.

Characters	Number of times appearing in first rank	Percentage
Plant height	53	6.79
Branch number	27	3.46
Capsule number	74	9.49
Capsule number on main stem	26	3.33
Seed number	94	12.05
1000 Seed weight	114	14.62
Days to full maturity	127	16.28
Oil content	213	27.31
Seed yield	52	6.67