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Research Article

Determination of genetic divergence based on morphological traits in sesame (*Sesamum indicum* L.)

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Abstract
Genetically diverse germplasm is an important source for identification of parental lines having desired traits like high oil content, high seed yield and disease resistance in sesame. In the present study, 90 genotypes have been selected for genetic diversity analysis using Mahalanobis D2 statistics. Data on five quantitative traits namely, plant height (cm), days to 50 per cent flowering, number of capsules plant^{-1}, single plant yield(g) and oil content (%) have been analysed for clustering using Tocher's method. A total of nine clusters were obtained. Of these clusters, cluster IX and V showed highest inter cluster distance indicating that they are the most diverse cluster whereas clusters VIII and II were the least diverse as indicated by the inter cluster distance. Cluster means were highest in cluster IX for number of capsules per plant and single plant yield while it was highest in cluster III for oil content and days to 50 per cent flowering. Based on cluster mean values for desirable traits, genetically diverse genotypes can be used in hybridization programme for oil and yield improvement in sesame.

Keywords
Sesame, diversity analysis, clusters, genetic divergence

Introduction

Sesame is an ancient oilseed crop famous for the medicinal properties of its oil with its origin in India. It is commonly known as "Queen of oilseeds" due to its resistance to oxidation and rancidity. It is also an industrial food crop because of its high nutritional value (Soundharya *et al.*, 2017). The seeds of sesame contain 40 to 63 per cent oil, which contains significant amount of oleic and linoleic acids (Abate and Mekbib, 2015). Even after being such an important oilseed crop in India, its large scale cultivation continues to be hindered by several factors like low oil content of currently available varieties, low seed production of existing varieties, non-availability of varieties suited to different agro-climatic conditions, susceptibility of the crop to untimely rains, lack of phyllody tolerance and non-synchronous maturity. One of the solutions to these problems is the proper utilization of genetic diversity available in sesame germplasm.

Genetic diversity available in any crop forms the basis of crop improvement. The knowledge on nature and magnitude of genetic variability in a crop is important to plan various breeding strategies for crop improvement. Assessment and identification of diverse parents having desired traits is easy with the help of Mahalanobis D2 statistics (1936). Once the parents are identified, they may be used for hybridization in order to transfer the desired traits into the existing cultivars and to develop improved varieties. Keeping these points in view, the present study was carried out to assess the genetic diversity among 90 genotypes for five quantitative traits in sesame germplasm.

Materials and Methods

The experiment was conducted at the research field of Department of Oilseeds, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore during *Rabi* 2017-18. The experimental material comprised of 90 germplasm accessions, collected from Department of Oilseeds, TNAU, Coimbatore and RRS Vridhachalam, Tamil Nadu. These 90 were selected based on oil content (30 genotypes each from high, medium and low oil content based on their *per se* performance). The experimental design was Randomized Block Design (RBD) with two replications wherein each genotype was sown in a row of 4 meter length with inter row spacing of 30 cm and intra row spacing of 10 cm. Sowing was done by dibbling method and all the Recommended package of practices was followed and necessary prophylactic measures were adopted against pests and diseases. Field observations were taken for 5 quantitative traits namely, plant height(cm), days to 50 per cent flowering, number of capsules plant^{-1}, single plant yield (g) and oil

content(%). Oil content was estimated using Pelican Socsplus apparatus. These 90 genotypes were then utilized to assess genetic diversity by Mahalanobis D2 statistics (1936) and grouping of genotypes into different clusters was done according to Tocher's method (Rao, 1952) using GENRES software.

Results and Discussion

Analysis of variance showed significant differences among the 90 genotypes for all the characters taken for the study, indicating the existence of variability among the genotypes for the characters studied. Similar results were obtained by Bandila *et al.* (2011), Menzir (2012), Saha *et al.* (2012), Tripathi *et al.* (2014) & Tanwar and Bisen (2018). Clustering of germplasm was done for five quantitative traits using Mahalanobis D2 statistics. A total of nine clusters were identified with cluster I being the largest having 55 genotypes, followed by cluster IX having 21 genotypes. All the other clusters had two genotypes each.

The average intra and inter cluster D^2 values and D values are given in Table 3. The intra-cluster distance was found to be highest for cluster IX (36.17) followed by cluster I (22.05), indicating that some genetic divergence still existed among the genotypes within each of these clusters. Selection within such clusters might be executed based on maximum mean value for the desirable characters.

The inter-cluster distance was recorded highest between clusters V and IX (38.36) followed by clusters II and VII (37.05) and V and VIII (36.10). This indicates the high divergence between these clusters. When the inter-cluster distance between clusters is higher, the genotypes in those clusters would be more diverse. Genotypes from these diverse clusters may be selected for crossing programme as parents in order to have high heterotic effects in the hybrid combinations. From the results of the present study, it may be inferred that genotypes namely TMV 4-500, Si 241 of cluster V and genotypes namely, ES 345, ES 355-584, KMR 13, KMR 81, KMR 69, RT 49-10 E, SO 557, EC343407, Gopi OP, IS 112, Thilathara, G-10, VRI 2, 52-300, G-43, Rama, ORM 17, 8-78-290, IS 35, G 46 belonging to cluster IX may be used as parents to produce highly heterotic hybrids. The least inter-cluster distance was between cluster VIII and II (7.14) followed by cluster IV and VI (9.45), indicating that the genotypes included in them were closely related.

Cluster means for five quantitative traits have been listed in Table 6. Cluster means for oil content was highest for cluster III (49.53%) followed by cluster IX (42.07%) and cluster I (42.06%). Cluster IX (30.37) showed highest cluster mean values for number of capsules plant^{-1} followed by clusters I (18.94) and III (18.75). For improvement of single plant yield (g), cluster IX (5.79 g) followed by clusters III (3.72 g) and cluster I (3.60 g) possessing high cluster mean values may be used. Since sesame genotypes with dwarf plant height which resist lodging are desirable, cluster VII (28.11) with lowest cluster mean for plant height followed by cluster V (29.27) and cluster III (38.60) need to be chosen. In order to obtain sesame genotypes with early flowering, genotypes with low cluster means for days to 50 per cent flowering, cluster II (35.50), followed by cluster I (36.92) and cluster IX (37.26) should be involved in hybridization programme. In case of improvement for a particular trait, genotypes from those clusters having desirable cluster mean values for that trait may be used as parents for crossing.

The number of times that each of the five characters appeared in first rank and its respective per cent contribution towards genetic divergence was worked out and presented in table 5. By taking first rank 1622 times, single plant yield (g) was found to have highest contribution (40.50%) towards genetic divergence, followed by plant height(cm) (21.85%) and number of capsules plant^{-1} (17.50%). The results were in conformity with Velusami *et al.* (2008) and Tripathi *et al.* (2014) for single plant yield; Mohan (2014) and Soundharya *et al.* (2017) for number of capsules plant^{-1}.

From this study, it is clearly evident that genotypes of cluster IX may be used for improvement of the traits namely, early flowering, number of capsule plant^{-1}, oil content(%) and single plant yield(g) whereas genotypes of cluster III may be selected as parents for dwarf plant height and high oil content. Considering the trait, days to 50 per cent flowering, genotypes from the cluster having lowest cluster mean may be selected as those genotypes will be early flowering genotypes. Here genotypes from clusters I and II will take least number of days for achieving 50 per cent flowering, as indicated by their low cluster mean value.

The promising genotypes from clusters with desirable mean values for different traits may be directly used for adaptation or may be used as parents in future hybridization, depending upon the objective of breeding programme to derive superior transgressive segregants. The present study revealed that selection of parents based on wider inter cluster distance as well as superior mean performance for yield and oil traits will lead to development of F_1 hybrids with better hybrid vigour for desirable traits in sesame.

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Table 1. Analysis of variance (ANOVA) for quantitative traits in sesame genotypes

Source	df	Plant height (cm)	Number of capsules plant^{-1}	Days to 50% flowering	Oil content (%)	Single plant yield (g)
Replication	1	1.10	0.55	0.032	2.81	0.001
Treatment	89	281.04**	266.33**	12.19**	54.85**	107.94**
Error	89	1.18	1.57	0.69	1.94	0.15

Table 2. Distribution of genotypes into clusters based on D2 analysis in sesame genotypes

Cluster number	Number of genotypes	Name of genotypes in each cluster
Cluster I	55	NIC 16288, EO 61, KMS 4-393, Si 1578, Si 2186, Si 1760-1, ES71, ES-15, RT 46, IC 110062, KMR 87, EC 383284, ESG 542, ES 13, BS 496, BO 42, KM 6, DCB 1810, PS 9104, OMT 21, JLSC 96, TKG 105, TKG 67, Si 769-2, Si 2143, Si 97, Si 2630, Si 3012, Si 490, Si 930, Si 3216, Si 173, Si 983/1, Si 2289, Si 608, Si 2595-2, Si 1771, Si 1868, Si 1065, Si 328, Si 1659, Si 1760-1, Si 3278/2, Si 7178, Si 4721, Si 1885, Si 43, B 203, IS 99, IS 1516, IS 4996, IS 16, IS 52, NIC 8223, ES 25
Cluster II	2	IC 204495, GT 2
Cluster III	2	IC 1994-29A, Gowri
Cluster IV	2	KMS 342, Si 14-96-1
Cluster V	2	TMV 4-500, Si 241
Cluster VI	2	TMV 3, NAE 7911
Cluster VII	2	EC 89111, NIC 8252
Cluster VIII	2	IC 205 206, Paiyur 1
Cluster IX	21	ES 542/1, ES 345, ES 355-584, KMR 13, KMR 81, KMR 69, RT 49-10 E, SO 557, EC343407, Gopi OP, IS 112, Thilathara, G-10, VRI 2, 52-300, G-43, Rama, ORM 17, 8-78-290, IS 35, G 46

Table 3. Average inter and intra cluster D2 values and D values in sesame genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**486.22** **(22.05)**	724.31 (26.91)	294.64 (17.17)	471.96 (21.73)	626.54 (25.03)	406.91 (20.17)	496.44 (22.28)	724.81 (26.92)	971.5 (31.17)
II		**7.37** **(2.72)**	707.32 (26.6)	288.83 (17)	1454.73 (38.14)	583.71 (24.16)	1373 (37.05)	50.94 (7.14)	1057.75 (32.52)
III			**23.7** **(4.87)**	437.01 (20.91)	419.21 (20.48)	316.56 (17.8)	225.3 (15.01)	722.98 (26.89)	797.84 (28.25)
IV				**27.13** **(5.21)**	572.99 (23.94)	89.29 (9.45)	651.61 (25.53)	188.24 (13.72)	1053.53 (32.46)
V					**29.54** **(5.44)**	248.2 (15.75)	91.71 (9.58)	1302.96 (36.1)	1471.7 (38.36)
VI						**37.86** **(6.15)**	330.26 (18.17)	466.69 (21.6)	1082.82 (32.91)
VII							**52.17** **(7.22)**	1297.98 (36.03)	1216.02 (34.87)
VIII								**54.92** **(7.41)**	1121.03 (33.48)
IX									**1308.49** **(36.17)**

Table 4. Percentage contribution of each character to genetic diversity in sesame genotypes

Character	**Number of first rank**	**Per cent contribution**
Days to 50% flowering	139	3.47
Plant height (cm)	875	21.85
Number of capsules plant^{-1}	701	17.50
Oil content (%)	668	16.68
Single plant yield (g)	1622	40.50
Total	**4005**	**100.00**

Table 5. Cluster means for each quantitative character in sesame genotypes

Character/ Cluster	Days to 50% flowering	Plant height (cm)	Number of capsules per plant	Oil content (%)	Single plant yield (g)
I	36.92	42.00	18.94	42.06	3.60
II	35.50	62.81	16.50	41.59	2.89
III	39.50	38.60	18.75	49.53	3.72
IV	38.50	52.28	10.50	31.68	2.10
V	38.50	29.27	6.75	34.20	1.26
VI	38.25	43.57	9.33	31.97	1.49
VII	38.00	28.11	13.50	40.81	2.62
VIII	38.25	63.22	14.33	36.84	2.95
IX	37.26	45.84	30.37	42.07	5.59