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Research Note

Genetic divergence analysis in sesame (*sesamum indicum* L.)

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Abstract
Thirty one germplasm lines of sesame collected from AICRP on Sesame & Niger, Jabalpur and NBPGR Regional Station, Akola were evaluated for genetic divergence using Mahalanobis D^2 analysis. Analysis of variances for dispersion indicates significant differences among the genotypes. Thirty one genotypes were grouped into seven clusters and cluster I (10) was largest, followed by cluster II (8), cluster III (7) and cluster V (3), while clusters IV, VI and VII were solitary. Inter cluster distance ranged from 51.96 (between clusters V and VII) to 423.26 (between clusters II and VII), while maximum intra cluster distance observed within cluster V (48.03). Character oil content contributed maximum (91.83%) towards genetic divergence. On the basis of the inter cluster distance, cluster I, II, III and VII were identified as distant clusters and genotypes *viz.*, S-0434, IC-413209, GRT-8637, NIC-16328, TKG-22, IC-413204, IC-413231, Lalguda local, KMR-116, SI-331517, IC-413208, KMS-5-343, ES-111-284, KMS-5-873, SI-3218 and SI-2973 from these clusters could be used for intercrossing to obtain heterosis and also wider variability.

Key words:
Sesame, genetic distance, yield components

Sesame (*Sesamum indicum* L.) is an important oil seed crop and its seed contains 38-54% oil and 18-25% protein. It is the sixth most important oil seed crop in India having 1.94 mha area with 0.755 mt production and productivity of 389 kg/ha (Anon, 2012). The average productivity is very low as compare to other sesame growing countries and almost stagnant during last few years. In India, the yield plateau and poor productivity can be overcome by commercial exploitation of heterosis and reshuffling of genes to get better recombinants or transgressive segregants by hybridization using suitable parents. Genetic divergence among the parents is an important factor while selecting the parents for hybridization. Rao (1960) and Ramanujam *et al.* (1974) also observed that a cross involving genetically diverse parents is more likely to produce high heterotic effect as compared with lines which are more closely related with each other. While performing selections, more importance should be given to the characters which contribute more towards diversity. Hence, the present study was undertaken to understand the genetic diversity among the 31 germplasm lines and identify the lines for further hybridization.

Thirty one sesame germplasm lines were collected from AICRP on Sesame and Niger, Jabalpur and NBPGR Regional Station, Akola. The study was undertaken at Department of Botany, Pratishthan Mahavidyalaya Paithan during summer 2009 in Randomized Block Design with 3 replications and each plot consisted of 3 m length. Spacing of 30 cm x 15 cm was maintained. All need based practices were followed during the crop growth period in maintaining the good crop stand. Observations were recorded on randomly selected five plants for all 16 quantitative characters *viz.*, days to 50 per cent flowering, days to maturity, plant height (cm), plant height for first capsule (cm), capsule bearing plant height (cm), number of primary branches, internode distance (cm), capsule length (cm), number of nodes on main stem, number of nodes for first capsule, number of capsules on main stem, number of capsule per plant, number of seeds per capsule, 1000 seed weight (g), oil content (%) and seed yield per plant (g). Genetic divergence was analyzed using the Mahalanobis D^2 statistics (1936) and populations were grouped into clusters by following the Tocher's method described by Rao (1952).

Analysis of variance revealed significant differences between 31 genotypes for all the 16 characters studied. Wilk's criteria used to test the aggregate effects of all the 16 traits indicated the significant differences between the genotypes. Similar results were recorded by Kumaresan and Nadarajna (2003).

Thirty one genotypes were grouped into seven clusters (Table 1), maximum ten number of genotypes were grouped into cluster I, followed by eight genotypes in cluster II, seven genotypes in cluster III and three genotypes in cluster V, whereas cluster IV, VI and VII were containing single genotype. The distribution of genotypes into different clusters was based on D^2 values, which ranged from 51.96 to 423.26 (Table 2). Highest inter cluster D^2 value observed in between cluster II and VII (423.26) followed by II and VI (382.17), I and VII (361.34), II and III (324.76), I and VI (320.57), IV and VII (308.30), V and VII (269.65), IV and VI (267.92), I and III (263.30), V and VI (228.75) and III and IV (211.10), whereas lowest observed in between VI and VII (51.96). Highest

intra cluster distance was shown by cluster V (48.03) followed by III (46.99), II (41.26) and I (39.44), where as cluster IV, VI and VII were solitary clusters and showed zero intra cluster distance (Table 2). Solanki and Gupta (2001) and Kumaresan and Nadarajan (2003) also reported the presence of solitary clusters. Intra cluster value indicates the genetic diversity among the genotypes of same cluster. Genotypes for hybridization should be from the clusters showing more genetic distance, as chances are more to obtain heterotic combinations as compared to crosses between genotypes from same cluster. Ramanujam *et al.* (1974) reported that the hybrids between genetically diverse parents were more heterotic. Thiyagu *et al.* (2007) studied the heterosis in genetically diverse lines of sesame. Banerjee and Kole (2011) observed that out of nine heterotic hybrids for oil yield, seven were the results of inter-cluster crossing and two were intra-cluster crosses.

Cluster mean indicates the variation for the quantitative traits among the cluster (Table 3). Considering the seed yield per plant and the major yield attributes, genotypes from cluster I, II, III, IV and V showed higher cluster means along with early flowering and maturity. Genotypes from these clusters should be considered for hybridization for isolating transgressive segregants in later generations of crosses. Cluster VII is solitary and showed low means for seed yield per plant, oil content, 1000 seeds weight and delayed maturity. However higher means for plant height, capsule bearing plant height, number of nodes on main stem, number of capsule per plant and number of capsules on main stem, less internode distance and less number of nodes for first capsule of this genotype may be used as donor for improving these traits.

Analysis of contribution of characters to genetic diversity (Table 4) revealed that oil content contributed highest (91.83%) towards genetic divergence. More important should be given to this character for selection and choice of parents for hybridization. Dikshit and Swain (2000) and Sumathi *et al.* (2008) also reported highest contribution of oil content for divergence. Kumaresan and Nadarajan (2003) reported the higher contribution by 1000-seed weight. Similar results were obtained by Manivannan and Nadarajan (1996) and Salanki and Gupta (2001) for characters contributing to genetic diversity other than oil content and seed yield.

On the basis of the inter cluster distance, clusters I, II, III and VII were identified as more divergent clusters. Genotypes IC-413231, SI-331517, IC-413208 and KMS-5-343 from Cluster-I, IC-413209, TKG-22, IC-413204, KMR-116, ES-111-284 and KMS-5-873 from cluster-II, S-0434, GRT-8637, NIC-16328, Lalguda local and SI-3218 from cluster-III and SI-2973 from cluster-VII could be used for intercrossing to obtain heterosis and also wider variability.

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Table 1. Distribution of genotypes into different clusters

Cluster number	Number of genotypes	Genotypes
I	10	KMS-5-343, KM-40, SI-331517, GJG-30-A, IC-413208, IC-413231, IC-132704, S-0480, IC-413202, IC-132707
II	8	KMR-61, ES-111-2-84, IC-132701, KMR-116, IC-413204, IC-413209, KMS-5-873, TKG-22
III	7	NIC-16328, LALGUDA LOCAL, GRT-8637, S-0434, IS-355, SI-3218, IS-56,
IV	1	KM-9
V	3	KMR-36, IC-132708, GSM-22
VI	1	S-0335
VII	1	SI-2973

Table 2. Intra cluster (in bold) and inter cluster distances (D^2) among seven clusters in sesame

Cluster	I	II	III	IV	V	VI	VII
I	**39.44**	73.17	263.30	61.53	100.70	320.57	361.34
II		**41.26**	324.76	118.75	159.87	382.17	423.26
III			**46.99**	211.10	172.89	69.29	106.98
IV				**0.00**	53.63	267.92	308.30
V					**48.03**	228.75	269.65
VI						**0.00**	51.96
VII							**0.00**

Table 3. Character means in different clusters of sesame genotypes

Cluster	I	II	III	IV	V	VI	VII	Times Ranked 1st	Contri-bution %
Days to 50 per cent flowering	48.05	53.42	50.45	47.00	49.69	52.33	50.94	3	0.65
Days to maturity	84.63	81.10	87.40	84.33	87.78	86.00	88.28	4	0.86
Plant height (cm)	45.93	44.47	51.65	38.66	50.94	57.67	50.83	1	0.22
Plant height for first capsule (cm)	17.48	16.77	19.17	10.90	18.88	22.17	16.33	4	86.00
Capsule bearing plant height (cm)	27.26	25.95	29.07	26.20	31.13	28.67	32.67	3	65.00
Number of primary branches	2.11	2.13	2.46	2.00	2.27	2.00	2.67	3	65.00
Inter node distance (cm)	3.14	2.81	3.34	2.95	3.14	3.19	2.77	0	0.00
Number of nodes on main stem	11.50	10.53	12.06	13.00	14.53	15.67	16.00	4	0.86
Number of nodes for first capsule	5.18	5.00	5.61	2.75	5.21	6.00	4.00	2	0.43
Capsule length (cm)	2.49	2.42	2.36	2.38	2.35	1.58	2.41	0	0.00
Number of capsules per plant	21.29	25.34	23.40	22.80	17.53	11.67	24.00	2	0.43
Number of capsules on main stem	8.95	8.34	10.41	14.80	10.83	9.33	15.00	5	1.08
Number of seeds per capsule	53.14	55.14	57.80	56.00	51.43	67.67	56.67	0	0.00
1000 seed weight (g)	1.62	1.71	1.65	1.47	1.68	1.06	0.80	7	1.51
Oil content (%)	46.57	48.03	40.49	45.20	44.40	38.80	38.20	427	91.83
Seed yield per plant (g)	1.79	2.33	2.34	1.88	1.57	0.84	1.08	0	0.00