



Studies on genetic divergence for yield and yield attributing traits in sesame (*Sesamum indicum* L.) germplasm

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Abstract : One hundred and thirty one germplasm accessions were used to assess the nature of genetic diversity in sesame, *Sesamum indicum* L. cass by using Mahalanobis D^2 statistics using all the six characters studied. Seed yield, plant height and seeds per capsule were observed to be the major contributors to the genetic divergence in the germplasm. Grouping of genotypes into clusters using Tocher's method resulted in formation of eight clusters. Maximum intracluster distance was shown by cluster IV while cluster II and VI showed highest inter cluster distance suggesting wide diversity and by utilization of these accessions from these clusters desirable segregants may be evolved through hybridization. Cluster VII exhibited highest means for seed yield and number of capsules per plant. Cluster VIII exhibited highest means for plant height and number of branches per plant. Seed yield contributed maximum to the diversity which is given greater importance in selection of potential parents.

Key Words : Cluster, Genetic diversity, Genotypes, Sesame, D^2 statistic

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INTRODUCTION

Sesame (*Sesamum indicum* L.) is an important oilseed crop with 45-54 per cent oil and 20-25 per cent protein. It is rich in minerals too, as it contains good amount of calcium and phosphorus and high level of unsaturated fatty acids. It is cultivated both in tropical and subtropical region. Among the sesame growing countries in the world, India ranks first in area (17.5 lakh hectares) and production (7.39 lakh tones). The success of any crop improvement breeding programme essentially depends on the nature and magnitude of genetic variability present in the crop. Greater success can be achieved through judicious choice of parents for hybridization based on genetic divergence. Therefore, the present investigation was carried out to have detailed knowledge of genetic diversity among the diverse genotypes in sesame, the basis of which would help in selection of superior and desirable genotypes to utilize them in the breeding programme. Crosses between divergent parent usually produce greater heterosis

than those between closely related ones (Moll and Stuber, 1971).

MATERIALS AND METHODS

The material for the present investigation consisted of 131 germplasm lines of sesame obtained from Project Coordinating Unit, All India Coordinated Research Project on Sesame and Niger, Jabalpur, Madhya Pradesh. They were grown at Main Agricultural Research Station, University of Agricultural Sciences, Dharwad, in a augmented unreplicated design during *Kharif* 2009 and 2010. Each line was sown in two row of 4 m length with a spacing of 30 cm x 15 cm, recommended dose of fertilizers and agricultural practices were applied to raise the crop.

Five plants were chosen randomly in each strain to record observations on six characters *viz.*, seed yield (kg/ha), number of capsule per /plant, plant height (cm), number of branches / plant, days to flowering and days to maturity. Of the several

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methods available, Mahalanobis' generalize distance estimated by D^2 statistic is a unique tool for discriminating population considering a set of parameters together rather than inferring from indices based on morphological similarities and polygenic relationship. The mean data of two seasons was subjected to statistical analysis using Mahalanobis' D^2 statistic to assess genetic divergence. The germplasm lines were grouped on the basis of minimum generalized distance using the Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

Wide variation (186-548 kg/ha) was observed in seed yield in evaluated sesame lines (Table 5), suggesting considerable levels of genetic diversity. Number of capsule per plant in sesame genotypes ranged from 12-45. Plant height ranged from 66-131 cm. Number of branches ranged from 2.1 – 3.8. Days to first flowering of the genotypes ranged from 32-43 and days to maturity ranged from 80-96.

The phenotypic coefficient of variability (PCV) was

higher than genotypic coefficient of variability (GCV) for all the traits under the study indicating traits were not much influenced by environmental factors. Johnson *et al.* (1955) suggested that traits with high heritability coupled with high genetic advance would respond to select better than those with high heritability and low genetic advance. Heritability is not an exact parameter because it could be high when genetic advance is very low (Table 5). However expected genetic gain can be high only if the genetic variance is high (Allard, 1960). Burton and Davane (1953) suggested that GCV along with heritable estimates would give a better picture of the amount of progress expressed by phenotypic selection.

Seed yield (kg/ha) and number of capsules per plant had high PCV and GCV. High GCV and PCV estimates were observed for seed yield per plant, number of branches per plant and number of capsules per plant, in a study conducted by Solanki and Deepak (2003). Plant height showed medium PCV and GCV values. Days to 50 per cent flowering and days to maturity had low GCV and PCV values. These findings are in

Table 1 : Distribution of 131 sesame genotypes into different clusters

Clusters	Genotype included in the cluster	Number of genotypes
I	NIC-8368, RTS-151, IS-3166, NIC-8423B, S-622, ES-35B, IS-31310, S-0440, IC-413234, IC-413211, NIC-8202, ES-31, IS-1547A, KMS-349, NIC-8393, NIC-805, IS-294, RTS-15, IS-423C, IS-780, B-203, ES-131-84, S-0622A, KMR-87, RTS-175-1, GRT-83126A, IC-9615, JLC-1B(46), IS-167, S-615-8A, NIC-174, KMS-5366, IS-2, IC-413204, 060-7115, IS-77A, IS-80A, SI-3280, NIC-17283, ES-303446, IS-1865B, NIC-8392, RMR-26, IS-184, JRT-85-76, IS-85/1, IS-723A, IS-562A, IS-191A, IS-1547A, IS-101-1B, RTS-175-1, SI-1248, KMS-5380, GRT-8623A, B-203, S-02-23, IS-101-184, IS-178A, GKT-8336, NIC-8279, IS-562B, IS-621, T-16, S-0580A, IS-157A, IS-130, ST-1184A, RTS-151-11, OMT-4A, S-02-53B, IS-562B, UMA, IS-101-8B, IS-112, ES-131-84B, GRT-8576, NIC-17274, S-05-23B, GRT-83126, ES-131-184-B, TR-352, NIC-7817, KIS-304B, IC-20483, IC-847, RM-111, IS-859, T-1-6, IS-153A, IS-102-184, S-0223, IS-191B, OLT-5, IC-56149, GM-139, IS-124	97
II	ES-234-1-84, S-0325, TKG-357, GRT-8351B, KMR-18B, IC-413205, IS-390, ES-22B, NIC-80, BJP local, RT-352	11
III	ES-10A, Kanaka, IS-299A, S-0268B, IC-413205, IC-413234	6
IV	41-3200, IS-413229, KMS-4-244, DS-1-4, IS-93B, DS-1, IC-413808, NIC -9824	8
V	KIS-375	1
VI	IC-413209, NIC-7939, IC-413210, GM-36-2-1, GM-36-2	5
VII	RT-54, IC-4132	2
VIII	NIC-9824	1

Table 2 : Intra cluster (Diagonal) and inter cluster distances for eight clusters in sesame germplasm

Clusters	I	II	III	IV	V	VI	VII	VIII
I	38.04	60.95	69.13	145.53	62.93	346.27	237.26	78.29
II		37.36	112.07	191.35	64.41	393.59	284.36	86.57
III			37.92	89.82	89.84	288.50	178.96	91.33
IV				42.54	160.26	209.65	100.80	154.43
V					0.00	361.26	251.41	34.0
VI						69.94	118.08	351.46
VII							33.28	241.98
VIII								0.00

accordance with the studies by Kandaswamy *et al.* (1990), and Shadakshari *et al.* (1995). Higher genetic advance was observed for seed yield (kg/ha) followed by plant height and number of capsules per plant. Days to 50 per cent flowering showed medium genetic advance. Number of branches per plant and days to maturity had lower genetic advance.

Based on D² values, 131 genotypes were grouped in eight clusters (Table 1), indicating the presence of large amount of diversity among the genotypes. The maximum number of genotypes (97) were included in cluster I followed by cluster II (11). Cluster III consisted of six genotypes, cluster IV has eight, cluster V is solitary, cluster VI has 4 genotypes, cluster VII has 2 genotypes and VIII is solitary (Fig. 1).

Minimum intra-cluster distance (0.00) was observed in cluster V and VIII (Table 2). Maximum inter-cluster distance

(393.59) was found between clusters II and VI followed by the distance between V and VI.

Cluster VI had high yielding genotypes followed by cluster VII (Table 3). Genotypes in the cluster VIII had maximum number of capsules per plant followed by VII. Taller genotypes were found in the cluster VIII followed by cluster V. The genotypes in the cluster VIII had more number of branches followed by cluster VII.

Genotypes in the clusters V and II were early flowering genotypes and those of clusters II, III and VII were early maturing.

Seed yield contributed maximum to the diversity followed by plant height and number of capsules per plant (Table 4).

Maximum diversity was observed between cluster II and VI suggesting that the accessions belonging to these clusters

Table 3 : Mean values of eight clusters of sesame germplasm for six characters

Clusters	Seed yield (kg/ha)		Number of capsules/plant		Plant height (cm)		Number of branches /plant		Days to 50% flowering		Days to maturity		Score	Rank
I	157.60	(5)	26.21	(7)	104.96	(8)	2.93	(6)	39.29	(4)	89.22	(4)	34	6
II	109.55	(8)	25.16	(8)	112.13	(6)	3.04	(5)	38.55	(6)	87.55	(6)	39	8
III	215.83	(4)	30.55	(3)	112.03	(7)	2.83	(8)	39.17	(5)	87.17	(8)	35	7
IV	296.88	(3)	26.76	(5)	121.39	(4)	3.09	(4)	40.75	(2)	89.38	(3)	21	4
V	144.00	(7)	30.20	(4)	160.10	(2)	2.90	(7)	38.00	(7)	88.00	(5)	32	5
VI	499.80	(1)	26.38	(6)	116.16	(5)	3.10	(3)	40.80	(1)	89.40	(2)	18	2
VII	392.00	(2)	33.00	(2)	122.50	(3)	3.25	(2)	40.00	(3)	87.50	(7)	19	3
VIII	157.00	(6)	59.50	(1)	170.50	(1)	3.50	(1)	40.00	(3)	92.00	(1)	13	1

Number in parenthesis indicate relative grade/score for each character across 14 clusters

Table 4 : Percentage contribution of each character towards genetic divergence in sesame germplasm

Sr. No.	Source	Times ranked 1st	Per cent contribution
1.	Seed yield kg/ha	6182	72.60
2.	No. of capsules/plant	146	1.71
3.	Plant height (cm)	2149	25.24
4.	Number of branches /plant	0	0.00
5.	Days to first flowering	5	0.06
6.	Days to maturity	33	0.39

Table 5 : Mean, range, coefficient of variation, heritability and genetic advance for six characters in sesame germplasm

Character	Range	Mean ± SE	PCV	GCV	h ²	GA as % of mean
Seed yield(kg/ha)	186-548	186± 1.71	45.4	45.3	99.9	93.4
Number of capsules/plant	12-45	26.9 ± 9.03	40.0	21.2	28.1	23.2
Plant height (cm)	66-131	83.9 ± 1.73	17.18	17.11	99.1	35.0
Number of branches/plant	2.1-3.8	2.9± 4.28	14.59	13.7	0.89	2.6
Days to first flowering	32-43	36.8 ± 0.19	5.0	4.9	99.0	10.2
Days to maturity	80-96	87.9± 1.39	3.9	3.6	84.2	6.8

PCV - Phenotypic coefficient of variability

GCV - Genotypic coefficient of variability

h² -Heritability

GAM - Genetic advance as % of mean

