

D² Statistic in sesame (*Sesame indicum* L.)

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Abstract : Sixty seven sesame genotypes were subjected to D² analysis. Observations were recorded for plant height, number of branches/plant, number of capsules/plant, seeds/capsule, 1000-seed weight and seed yield/plant. The genotypes were grouped into 10 clusters. Among the clusters, cluster I had 46 genotypes, cluster III, IV, II and V had 6, 5, 3 and 2 genotypes respectively. The cluster VI, VII, VIII, IX and X were highly divergent from cluster II and cluster I from cluster X. Among characters, plant height followed by number of branches/plant and 1000 seed weight contributed more towards the total divergence. Crosses could be effected between genotypes of the divergent clusters namely B45 (I), Govindapuram local (I), SI 861 (I), Madhavi (II), Chidambaram local (II), SO 317 (II), C0 1 (VII), SO 138 (VIII), SI 11 (IX) and IS 45 (X) to get more heterosis and wide segregants. (*Key Words :* Sesame, Genetic divergence).

Sesame (*Sesamum indicum* L.) is one of the main oil seed crops. The development of new varieties depends largely on the availability of genetic variability in the base material and the extent of variability for the desired character. The nature and magnitude of genetic divergence play an important role in the formulation of successful breeding programme. The genetically diverse parents are likely to produce heterotic effect and desirable segregants. The multivariate D² statistic is a powerful tool in quantifying the degree of divergence among the populations. Thus, the present study was undertaken to ascertain the nature and magnitude of genetic diversity in sesame and to identify genetically divergent genotype to serve as parents in hybridization programme.

Materials and Methods

Sixty seven sesame genotypes were evaluated at Experimental Farm, Annamalai University, Annamalainagar during summer, 1994. The trial was laid out in randomized block design replicated three times. Each entry was sown in a single row of 4m length adopting a spacing of 30 x 30 cm. Recommended cultural practices were followed throughout the crop growth. Observations were recorded on ten randomly chosen plants for six characters namely plant height, number of branches/plant, number of capsules/plant, seeds/capsule, 1000-seed weight and seed yield/plant. Multivariate analysis was done as per Mahalanobis (1936) method and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

Results and Discussion

The analysis of variance showed significant differences among all six characters studied. The D² values ranged from 0.00 to 415.14 and sixty seven genotypes were grouped into 10 clusters (Table 1 & 2). Among the clusters, cluster I had 46 genotypes. The clusters III, IV, II and V had 6, 5, 3 and 2 genotypes. The clusters VI, VII, VIII, IX and X had one genotype each. The intra and inter cluster distance among ten clusters are presented in Table 2. The intra cluster distance ranged from 0.00 to 9.27. The highest intra cluster distance was recorded for cluster V (9.27) followed by IV (8.80). The inter cluster distance ranged from 14.49 (between cluster I and cluster II) to 415.14 (between cluster II cluster X). The highest inter cluster distance was observed between cluster II and cluster X (415.14) followed by between cluster II and IX (377.32), between cluster II and cluster VIII (350.44), between cluster X (315.19) and between cluster II and cluster VII (310.79). Hence, genotypes of these divergent clusters when crossed among them may produce high heterosis. Murthy and Anand (1966) claimed that, there is a positive relationship between the specific combining ability and the degree of genetic diversity in *Linum usitatissimum* (L.). Endang *et al.* (1971) stated that the clustering patterns could be utilized in closing parents for cross combination which are likely to generate the highest possible variability for various economic characters.

The cluster mean of the various characters are presented in Table 3. Cluster II and X recorded high mean values for important yield contributing characters namely number of capsules/plant and seed

yield/plant and cluster VI for all characters. The following genotypes are suggested as parents for hybridization based on their mean and genetic divergence.

Characters	Genotypes
Plant height	Mdhavi (II), IS 45 (X)
Number of branches/plant	B 45 (I), Madhavi (II)
Number of capsules/plant	B 45 (I), Govindapuram local (I), S 0317 (II)
Seeds/capsule	CO 1 (VII), S 0138 (VIII)
1000-seed weight (g)	SI 861 (I)
Seed yield/plant	B 45 (I), Madhavi (II), S 0317 (II), Chidambaram local (II)

The ranking technique was adopted to rank the characters in the order of contribution to total genetic divergence (Murthy *et al.*, 1965). The contribution towards the total divergence are presented in Table 3. The highest contributor was plant height, followed by number of branches/plant and 1000-seed weight. Manivannan and Nadarajan

(1996) also reported that plant height followed by number of branches/plant were the highest contributors to the total divergence. It indicated the major role of these characters in differentiating at inter cluster level.

To conclude, the clusters VII, VIII, IX and X were highly divergent from cluster II and cluster I from cluster X. Hence, crosses could be effected between the genotypes of these clusters namely B 45 (I), Govindapuram local (I), SI 861 (I), Madhavi (II), Chidambaram local (II), S 0317 (II), CO 1 (VII), S 0138 (VIII), SI 11 (IX) and IS 45 (X) to get more heterosis and wide segregants.

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Table 1. Distribution of sesame genotypes into different clusters

Clusters	No. of genotypes	Genotypes
I	46	S 0609, SI 320, RJS 225, S 0573, SI 1412, GOWARI, SI 75, SI 853, S 0624-4, RAJESWARI, IS 1470, SI 264-1, GENE 9101-1, Govindapuram local, ES 14, GENE 9114, TN 63, S 0308, S 0589, SI 587, TMV 6, TN 8454, RJS 2, S 0596, IS 287, TN 8467-1, IS 553-1, Vallampadugai local, S 0584, GENE 9115, DPI 1525, B 45, S 0160, BS 6-1, IS 1234, GVN-2, DORS 102, BS 14, SI 3272, IS 356, IS 378, SI 3275, SI 858, SI 59, IS 424, SI 861,
II	3	Chidambaram local, S 0317, MADAHVI
III	6	Annamalai 1, S 0626-2, S 0606, IS 187-1, SI 263-2, SI 1672.
IV	5	Kayamkulam 2, PAIYUR 1, TC 25, S 0139, IS 305.
V	2	BS 49, S 0440.
VI	1	TMV 5
VII	1	CO 1
VIII	1	S 0138
XI	1	SI 11
X	1	IS 45

Table 2. Intra (in diagonal) and inter cluster D² Values of clusters in sesame genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X
I	7.67	14.49	19.18	35.32	100.02	217.48	238.27	258.97	282.13	315.19
II		6.45	18.43	42.36	130.90	283.23	310.79	350.44	377.32	415.14
III			7.44	14.99	52.39	132.81	150.97	173.65	204.65	242.02
IV				8.80	19.03	68.52	87.00	121.86	143.07	185.06
V					9.27	33.27	64.63	84.98	115.83	135.24
VI						0.00	3.27	55.45	94.01	162.06
VII							0.00	30.87	49.47	91.40
VIII								0.00	29.98	80.45
IX									0.00	40.75
X										0.00

Table 3. Cluster means and contribution to total divergence for different characters in sesame genotypes.

Clusters	Plant height (cm)	Number of branches/plant	Number of capsules/plant	Seeds/pod	1000-seed weight (g)	Seed yield/plant (g)
I	79.69	3.78	62.20	53.73	3.18	7.68
II	94.47	7.48	183.57	55.48	3.25	24.97
III	54.89	4.32	47.01	57.17	2.48	3.98
IV	60.21	0.37	16.96	35.48	2.16	0.71
V	80.88	3.22	63.77	51.01	3.75	0.50
VI	96.83	7.09	60.10	75.50	3.75	19.87
VII	77.96	1.55	38.68	76.67	2.91	4.50
VIII	60.13	0.39	38.35	62.00	2.35	4.83
IX	71.96	0.78	39.35	62.00	2.35	4.63
X	131.76	5.72	221.05	64.04	3.55	10.10
Contribution towards total divergence	23.3	18.8	12.9	14.7	15.8	14.4

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