D^2 ANALYSIS FOR ESTIMATING GENETIC DIVERGENCE IN SESAME GENOTYPES (*Sesamum indicum* L.)

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ABSTRACT

Sesame is an important traditional oilseed crop cultivated throughout India. Genetic divergence was studied based on Mahalanobis D^2 statistic and grouping of cluster was done among the 30 genotypes for ten quantitative traits following Tocher's method. The analysis of variance showed significant difference among the genotypes for all the characters studied. The genotypes were categorised into eight clusters based on the genetic distance and mean of different characters. The clustering pattern indicated that there is no association between geographical distribution of genotypes and genetic divergence. The minimum intra-cluster distance (D =5.75) was observed in cluster II and the maximum distance and the maximum inter cluster distance was observed between the clusters III and VIII. Cluster VIII recorded maximum cluster mean for the characters namely plant height at maturity, number of branches, number of capsules per plant, capsule breadth, number of seeds per capsule, 1000 seed weight and seed yield per plant. The characters viz., days to 50% flowering contributed the maximum (39.31%) for the genetic divergence followed by seed yield per plant (20.68%) and 1000 seed weight (15.63%). The genotype VRI 1registered maximum mean among all the quantitative traits followed VRI 1, GT 10 and VRI 2 hold great potential for improving and stabilizing the seed yield.

Key words: sesame, D^2 analysis, Genetic divergence.

INTRODUCTION

Sesame (*Sesamum indicum* L.) 2n = 22, Fabaceae is an important oilseed crop which is widely cultivated and consumed throughout India. Genetic improvement mainly depends upon the amount of genetic variability present in the base population and serves as a valuable source for providing wide variability. Genetic diversity is an important factor and also a prerequisite in any hybridization programme. Inclusion of diverse parents in hybridization programme serves the purpose of combining desirable recombination.

Multivariate analysis of means of Mahalanobis D^2 statistic is a powerful tool in quantifying to degree of divergence at genotypic level. Therefore, an attempt has been made in the present investigation with a view of estimate genetic divergence among a set of thirty genotypes of sesame.

MATERIALS AND METHODS

The study was conducted at Plant Breeding Farm, Annamalai University, Chidambaram. The 30 genotypes were raised in randomized block design (RBD) with three replications. Each genotype was sown in a plot consisting of two rows of 4.5 m in length with a spacing of 30 × 15 cm. Recommended agronomic and plant protection measures were followed by raise a healthy crop. Observations were recorded on five randomly selected plants per replication for quantitative traits namely days to 50 per cent flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, capsule breadth, number of seeds per capsule, 1000 seed weight and seed yield per plant. The data were subjected to Mahalanobis D^2 statistics as per Mahalanobis (1936) method and genotypes were grouped into different clusters following Toucher's method suggested by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant differences between sesame genotypes for all the characters studied. All the thirty genotypes were grouped into eight clusters (Table 1). The maximum number of genotypes were included in the cluster III (8 genotypes), followed by cluster IV (7 genotypes), cluster VI (4 genotypes), cluster I and V (3 genotypes), cluster II and VII (2 genotypes) and cluster VII (1 genotype solitary). The pattern of group constellations indicated that significant variability existed among the genotypes as observed from the clusters. The clustering pattern in the present study indicates that the genotypes from different sources clustered together showing that there was no association between clustering pattern and geographic distribution of genotypes. Similar findings were reported by Ganesan and Thangavelu (1996), Manivannan and Nadarajan (1996) and Gupta *et al.* (2001).

The intercluster III and VIII (38.25) followed by cluster III and VI (34.25). The minimum inter-cluster distance was found between cluster V and VII (11.41). Hybridization among the genotypes between cluster VIII and III is likely to produce heterotic hybrid and transgressive segregants.

Cluster VIII showed maximum cluster mean for six characters *viz.,* plant height, number of capsules per plant, capsule breadth, number of seeds per capsule, 1000 seed weight and seed yield per plant. Cluster VI recorded highest mean value for number of branches per plant and capsule length whereas cluster III recorded highest mean value for. Days to 50% flowering and days to maturity.

The selection and choice of parent mainly depend upon contribution of character towards divergence (Loganathan *et al.,* 2001) and the contribution towards genetic divergence is represented in Table 4. It was observed that among all the traits, contribution of days 50% flowering was maximum (39.31%) followed by seed yield per plant (20.68%). Similar findings were observed by Tripathi *et al.* (2013). In addition, 1000 seed weight (15.63%), days to maturity (10.11%), number of capsules per plant (5.51%), number of seeds per capsule (3.90%) also contributed maximum towards the genetic divergence. Average intra and inter cluster distances among thirty genotypes revealed that the genetic diversity between the genotypes in cluster III showed a maximum intra cluster distance of 22.12 (Table 2) and it indicated that the genotypes within the cluster were more diverse while cluster II showed minimum intra cluster distance of 5.75.

It is well known that crosses between divergent parents usually produce greater heterotic effect than closely related ones. Considering the importance of character towards total divergence, the present study indicated that parental lines selected from cluster VIII (VRI 2) for plant height, number of branches, number of capsules per plant, capsule breadth, number of seeds per capsule, 1000 seed weight and seed yield per plant and from cluster VI (SVPR 1, TMV 3, VRI 1, VSO-07-23) for seed yield per plant could be used in crossing programme to achieve desire segregants.

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Table 1. List of survived genotypes selected for D^2 analysis

S. No.	Varieties / Cultures	Seed coat colour	Origin
1	TKG 306	White	Tikamgarh, M.P
2	MT 75	White	Kanpur, U.P
3	GT 1	White	Amreli, Gujarat
4	RT 346	White	Bikaner
5	YLM 66	Brown	Andhra Pradesh
6	THILATHARA	Blackish brown	Kayamkulam, Kerala
7	GT 2	White	Amreli, Gujarat
8	RT 46	White	Bikaner
9	GT 3	White seed	Amreli, Gujarat
10	JTS 8	White	Tikamgarh, M.P.
11	SAVITRI	Light brown seeds	Berhampore, West Bengal
12	GT 10	Black	Amreli, Gujarat
13	YLM 11	Brown	Andhra Pradesh
14	TKG 55	White	Tikamgarh, M.P
15	NIRMALA	White	Orissa
16	THILAK	Blackish brown	Kayamkulam, Kerala
17	JTS 8	Whit seed	Tikamgarh, M.P
18	TKG 22	White	Tikamgarh, M.P
19	VS-0-24	White	Tindivanam
20	RT 127	White	Mandore, Rajasthan
21	TMV 6	Brown	Tindivanam
22	SVPR 1	White	Srivilliputhur
23	PAIYUR 1	Black	Paiyur
24	TMV 3	Dark brown	Tindivanam
25	VRI (SV) 1	Brown	Virudhachalam
26	TMV 4	Brown	Tindivanam
27	TMV 5	Brown	Tindivanam
28	VS07-23	White	Tindivanam
29	VSO-15-1	White	Tindivanam
30	VRI (SV) 2	Reddish brown	Virudhachalam

Table 2. List of survived genotypes selected D^2 analysis

Clusters	Number of genotypes	Name of the genotypes
I	3	TKG 306, YLM 11, VSO 24
II	2	RT 46, GT 3
III	8	MT 75, GT 1, YLM 66, THILATHARA, GT 2, RT 346, JLT 7, TKG 55
IV	7	SAVITRI, GT 10, NIRMALA, THILAK, JTS 8, TKG 22, RT 127
V	3	TMV 6, PAIYUR 1, TMV 4
VI	4	SVPR 1, TMV 3, VRI 1, VSO-07-23
VII	2	TMV 5, VSO-15-1
VIII	1	VRI 2

Table 3. Intra and inter (diagonal) cluster average of D^2 and D (values in parentheses) and the extent of diversity among the clusters of sesame genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**449.69 (21.20)**	242.70 (15.57)	551.35 (23.48)	340.20 (18.44)	453.08 (21.28)	556.37 (23.58)	468.32 (21.64)	688.39 (26.23)
II		**33.09 (5.75)**	347.40 (18.63)	229.05 (15.13)	484.14 (22.00)	665.12 (25.79)	461.33 (21.47)	940.85 (30.67)
III			**489.34 (22.12)**	686.84 (26.208)	484.58 (22.01)	1173.47 (34.25)	451.14 (21.24)	1463.07 (38.25)
IV				**292.62 (17.10)**	697.09 (26.40)	490.27 (22.14)	688.23 (26.23)	643.15 (25.36)
V					**128.41 (11.33)**	758.98 (27.55)	130.21 (11.41)	881.82 (29.69)
VI						**232.36 (15.24)**	839.40 (28.97)	252.43 (15.88)
VII							**267.65 (16.36)**	1003.70 (31.68)
VIII								**0.00 (0.00)**

Table 4. Cluster means values of ten quantitative traits of sesame

Sl. No.	Cluster	Days to 50% flowering	Days to maturity	Plant height at maturity (cm)	Number of branches	Number of capsules per plant	Capsule length (mm)	Capsule breadth (mm)	Number of seeds per capsule	1000 seed weight (g)	Seed yield per plant (g)
1	I	46.66	87.77	76.38	5.18	53.55	24.44	5.55	51.77	2.66	3.37
2	II	48.00	88.16	59.41	2.36	25.50	27.50	5.33	49.00	1.90	1.81
3	III	52.91	90.95	62.00	3.59	47.87	24.33	5.33	50.79	2.17	2.22
4	IV	43.50	87.33	63.33	3.73	37.95	23.81	5.57	55.04	2.27	3.84
5	V	52.27	87.11	89.18	5.50	109.11	24.55	4.88	55.77	2.70	4.41
6	VI	41.04	78.66	79.58	6.44	82.83	28.25	5.08	55.08	2.81	7.18
7	VII	52.16	89.83	78.50	6.00	104.50	24.83	4.50	61.33	2.70	4.21
8	VIII	38.33	81.66	106.43	5.66	102.66	19.00	5.33	55.66	2.81	10.53
	General mean	46.85	86.43	76.85	4.80	70.49	24.58	5.19	54.30	2.50	4.69

Table 5. Contribution of different characters towards genetic divergence

S. No.	Characters	Contribution towards divergence (%)
1	Days to 50% flowering	39.31
2	Days to maturity	10.11
3	Plant height	2.29
4	Number of branches per plant	0.22
5	Number of capsules per plant	5.51
6	Capsule length (mm)	1.14
7	Capsule breadth (mm)	1.14
8	Number of seeds per capsule	3.90
9	1000 seed weight (g)	15.63
10	Seed yield per plant (g)	20.68