



Divergence Studies in Sesame (*Sesamum indicum* L.)

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ABSTRACT

Genetic divergence among 50 sesame genotypes based on 10 characters was studied using Mahalanobis' D^2 statistic and principal component analysis. Among the ten characters, number of seeds capsule⁻¹ contributed maximum towards genetic divergence (42.53%) followed by days to 50% flowering (40.90%) and number of capsules plant⁻¹ (10.04%). The PCA identified three principal components with eigen values more than one contributing 78.67% towards variability. The PCA enabled loading of similar type of variables on a common principal component. In both *Tocher's* and *Ward's minimum variance* methods the genotypes were grouped into eight clusters but vary in clustering pattern. Divergence studies indicated that genetic diversity is not always necessarily associated with the geographical diversity.

Key words : D^2 analysis, Sesame, Principal Component Analysis, *Tocher's* method, *Ward's minimum variance* method.

Sesame is an important oil seed crop grown in India and world since ancient times for its rich source of oil. It possesses an oil content of 40-54% and protein 25%. The presence of antioxidants viz., *sesamin* and *sesamol* in the oil, prevent the oxidative rancidity, thereby increase the shelf life. No other vegetable oil possess this unique phenomenon, hence sesame is being called as queen of oilseed crops. The diversity of parents is of prime importance, to get desirable recombinants in the progenies. Multivariate analysis based on Mahalanobis D^2 statistic is widely used for estimating the genetic diversity. Therefore, the present investigation is an attempt to study genetic divergence in 50 genotypes of sesame using D^2 analysis and principal component analysis.

MATERIAL AND METHODS

The present study was carried out with 50 sesame genotypes obtained from different research centres across the country in randomized block design with three replications at Agricultural Research Station, Yelamanchili, Visakhapatnam district during *rabi* 2014-2015. The plot size adapted is three rows each of four meter length in each replication with a spacing of 30 cm between the rows and 15 cm between the plants. The observations were recorded on five randomly selected plants from each genotype in three

replications for characters viz., plant height (cm), number of branches plant⁻¹, number of capsules plant⁻¹, capsule length (cm), number of seeds capsule⁻¹ and seed yield plant⁻¹ (g). Days to 50 per cent flowering, days to maturity, 1000 seed weight (g) and oil per cent were recorded on plot basis. The oil per cent was estimated by Nuclear Magnetic Resonance Spectrophotometer (NMR) at Main Agricultural Research Station (MARS), University of Agricultural Sciences (UAS), Raichur, Karnataka. The data was statistically analyzed using Mahalanobis' D^2 statistic as per Rao (1952), principal component analysis (PCA) as described by Jackson (1991) and cluster analysis as described by Anderberg (1993).

RESULTS AND DISCUSSION

The D^2 statistic showed that out of 10 characters, number of seeds capsule⁻¹ contributed maximum towards the genetic divergence (42.53%) followed by days to 50% flowering (40.90%) and number of capsules plant⁻¹ (10.04 %) indicating the possibility of genetic improvement of the characters. The other characters contributed less towards genetic diversity (Table 1). Parameshwarappa *et al.* (2012) and Spandana Bandila *et al.* (2011) also reported number of seeds per capsule contributed maximum towards genetic divergence.

Table 1. Contribution of different characters towards genetic divergence in 50 sesame genotypes.

S. No.	Character	Contribution towards divergence (%)	Times ranked first
1	Days to 50% flowering	40.90	501
2	Plant height (cm)	0.24	3
3	Number of branches / plant	0.24	3
4	Number of capsules / plant	10.04	123
5	Capsule length (cm)	1.06	13
6	Number of seeds per capsule	42.53	521
7	1000 seed weight (g)	3.67	45
8	Days to maturity	0.24	3
9	Seed yield / plant	0.57	7
10	Oil per cent	0.49	6

Table 2. Eigen values, proportion of the total variance represented by first three principal components, cumulative per cent variance and component loading of different characters in sesame (*Sesamum indicum* L.).

	PC ₁	PC ₂	PC ₃
Eigen Value (Root)	5.15	1.42	1.30
% Var. Exp.	51.53	14.19	12.95
Cum. Var. Exp.	51.53	65.72	78.67
Days to 50% flowering	0.37	0.16	0.35
Plant height (cm)	0.36	-0.17	-0.06
Number of branches/Plant	0.32	-0.18	0.22
Number of capsules/Plant	-0.39	-0.17	0.06
Capsule length (cm)	-0.11	-0.54	0.22
Number of seeds per capsule	0.17	-0.35	-0.66
1000 seed weight (g)	-0.13	-0.45	0.50
Days to maturity	-0.39	-0.28	-0.08
Seed yield per plant (g)	0.35	-0.45	-0.18
Oil per cent	0.38	-0.04	0.20

PC= Principal component

Based on the three principal components, a cumulative of 78.67% of variation formed the basis for the divergence into different clusters. The contribution by first PC was maximum and is loaded with contributing variables *viz.*, oil per cent (0.38), days to 50 % flowering (0.37), plant height (0.36), seed yield plant⁻¹ (0.35), number of branches plant⁻¹ (0.32) and number of seeds capsule⁻¹ (0.17) explained the maximum variance in first principal component and signifying their importance in yield improvement. The distribution of genotypes based on PCA values were shown in 3D plot (Fig. 3). The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and

confirm the results of principal component analysis. Main principal components are given in Table 2.

The results of multivariate analysis revealed the presence of considerable genetic variance among the 50 sesame genotypes and were grouped into eight clusters both in *Tocher's* and *Ward's minimum variance* methods.

In *Tocher's* method, the genotypes are grouped into eight clusters, where maximum genotypes were in cluster III (22) followed by clusters I (12), cluster II (nine) and cluster IV (three) while one genotype each were grouped in cluster V, cluster VI, cluster VII and cluster VIII (Table 3 and Fig. 1).

Table 3. Comparison between the Tocher's method and Ward's minimum variance methods for clustering of genotypes in sesame (*Sesamum indicum* L.).

<i>Tocher's method</i>			<i>Ward's minimum variance method</i>	
Cluster No.	No. of genotypes	Name of the genotypes	No. of genotypes	Name of the genotypes
I	12	DCB-1794, SKL-13, SKL-7, SKL-19, VZM-3, EC-355653, SI-75, SKL-2, VZM-11, SI-5354, DCB-1799, Vinayak	7	T.Brown, MT-10-23-3, Nirmala, VS-07023, RT-369, TKG-22, TKG-501
II	9	TMV-3, VZM-4, SKL-1, VSP-9, VZM-2, VSP-1, VSP-5, JCS-9707-2, VZM-7	3	JCS-302-11, MT-10-8, RT-366
III	22	T. Brown, MT-10-23-3, OSC-207, GT-10, RT-168, AT-282, JCS-120, AT-367, TKG-22, JCS-4082, PT-2, MT-11-8-2, MT-11-1-13, AT-249, PT-10, Nirmala, OSC-560, TKG-501, RT-369, VS-07023, OSC-79, VSP-15	10	AT-367, MT-11-1-13, AT-249, JCS-120, RT-168, GT-10, OSC-207, AT-282, MT-11-8-2, PT-2
IV	3	JCS-302-11, MT-10-8, RT-366	1	LT-210
V	1	VSP-16	2	PT-10, RT-371
VI	1	RT-371	4	TMV-3, VZM-4, Vinayak, SKL-1
VII	1	VSP-10	10	JCS-4082, OSC-560, OSC-79, VSP-5, VSP-15, JCS-9707-2, VZM-7, VSP-1, VSP-9, VZM-2
VIII	1	LT-210	13	SI-5354, DCB-1799, VZM-3, SKL-7, EC-355653, VZM-11, SKL-2, SI-75, DCB-1794, SKL-13, SKL-19, VSP-10, VSP-16

Table 4. Intra- and inter-cluster distance among eight clusters formed by *Tocher's* method in 50 sesame genotypes.

Cluster No	I	II	III	IV	V	VI	VII	VIII
I	20.62	77.21	123.86	213.29	46.38	280.65	57.89	276.35
II		36.34	131.25	108.63	161.25	279.14	126.63	396.56
III			46.14	112.75	167.74	96.48	78.80	135.84
IV				22.31	311.77	215.16	196.27	358.51
V					0.00	348.65	37.57	257.98
VI						0.00	219.33	98.09
VII							0.00	171.47
VIII								0.00

Note: Bold and diagonal values indicate intra-cluster D^2 distance

Table 5. Intra- and inter-cluster Euclidian² values among eight clusters formed by Ward's minimum variance method.

Cluster No.	I	II	III	IV	V	VI	VII	VIII
I	75.67	169.41	164.32	562.12	230.02	506.13	199.12	450.30
II		66.93	458.33	1075.52	525.60	511.01	266.94	668.35
III			64.22	224.93	190.99	675.98	323.05	375.68
IV				0.00	330.21	1380.55	871.74	778.43
V					79.97	849.53	443.79	655.08
VI						61.92	194.59	233.65
VII							105.43	232.84
VIII								80.55

Note: Bold and diagonal values indicate intra-cluster distance

Table 6. Mean values of eight clusters estimated by *Tocher's* method from 50 genotypes of sesame.

Cluster No.	Days to 50% flowering	Plant height (cm)	No. of branches/ Plant	No. of capsules/ Plant	Capsule length (cm)	No. of Seeds / capsule	1000 seed weight (g)	Days to maturity	Seed yield per plant (g)	Oil percent
I	48.89	76.12	4.81	75.42	2.51	45.61	2.21	84.69	6.67	48.10
II	44.37	80.81	5.07	83.89	2.50	55.26	2.39	84.81	10.12	48.91
III	37.88	64.02	3.92	84.86	2.41	45.12	2.32	82.77	8.04	47.87
IV	35.67	58.38	4.00	77.33	2.32	57.11	2.14	82.78	8.58	46.80
V	48.67	84.33	6.00	80.00	2.37	36.67	1.78	82.67	4.41	49.00
VI	33.67	61.27	5.67	119.00	2.60	45.67	2.78	81.67	14.24	47.90
VII	41.67	80.33	4.33	74.00	2.37	38.67	2.00	82.67	4.78	48.00
VIII	37.67	56.20	3.67	100.00	2.60	35.00	2.18	82.00	6.67	46.80

Note: Bold figures are minimum and maximum values

Table 7. Mean values of eight clusters estimated by *Ward's minimum variance* method estimated from 50 genotypes of sesame.

Cluster No.	Days to 50% flowering	Plant height (cm)	No. of branches/ Plant	No. of capsules/ Plant	Capsule length (cm)	No. of Seeds / capsule	1000 seed weight (g)	Days to maturity	Seed yield per plant (g)	Oil percent
I	35.86	63.40	3.62	84.71	2.38	49.38	2.35	82.57	8.84	47.99
II	35.67	58.38	4.00	77.33	2.32	57.11	2.14	82.78	8.58	46.80
III	37.70	59.21	3.73	81.03	2.39	40.83	2.30	82.60	6.73	47.41
IV	37.67	56.20	3.67	100.00	2.60	35.00	2.18	82.00	6.67	46.80
V	35.83	65.50	5.67	118.50	2.62	47.33	2.66	81.83	14.07	48.40
VI	49.00	78.63	4.58	76.17	2.53	55.58	2.39	85.17	9.18	49.38
VII	41.97	79.03	5.00	87.30	2.46	51.63	2.35	84.10	9.66	48.64
VIII	48.31	77.18	4.87	75.54	2.49	43.92	2.15	84.49	6.21	48.05

Note: Bold figures are minimum and maximum values

In *Ward's minimum variance* method, maximum genotypes (13) were grouped in cluster VIII followed by cluster III and VII with 10 genotypes each. Seven genotypes were grouped in cluster I while, four, three, two and one genotypes were grouped in clusters VI, II, V, and IV, respectively (Table 3 and Fig. 2).

Based on D^2 values, intra-cluster distances ranged from zero (cluster V, cluster VI, cluster VII and cluster VIII) to 46.14 (cluster III), while, maximum inter-cluster distance was observed between clusters II and VIII followed by clusters IV and VIII. The minimum inter-cluster distance was observed between clusters V and VII as shown in Table 4.

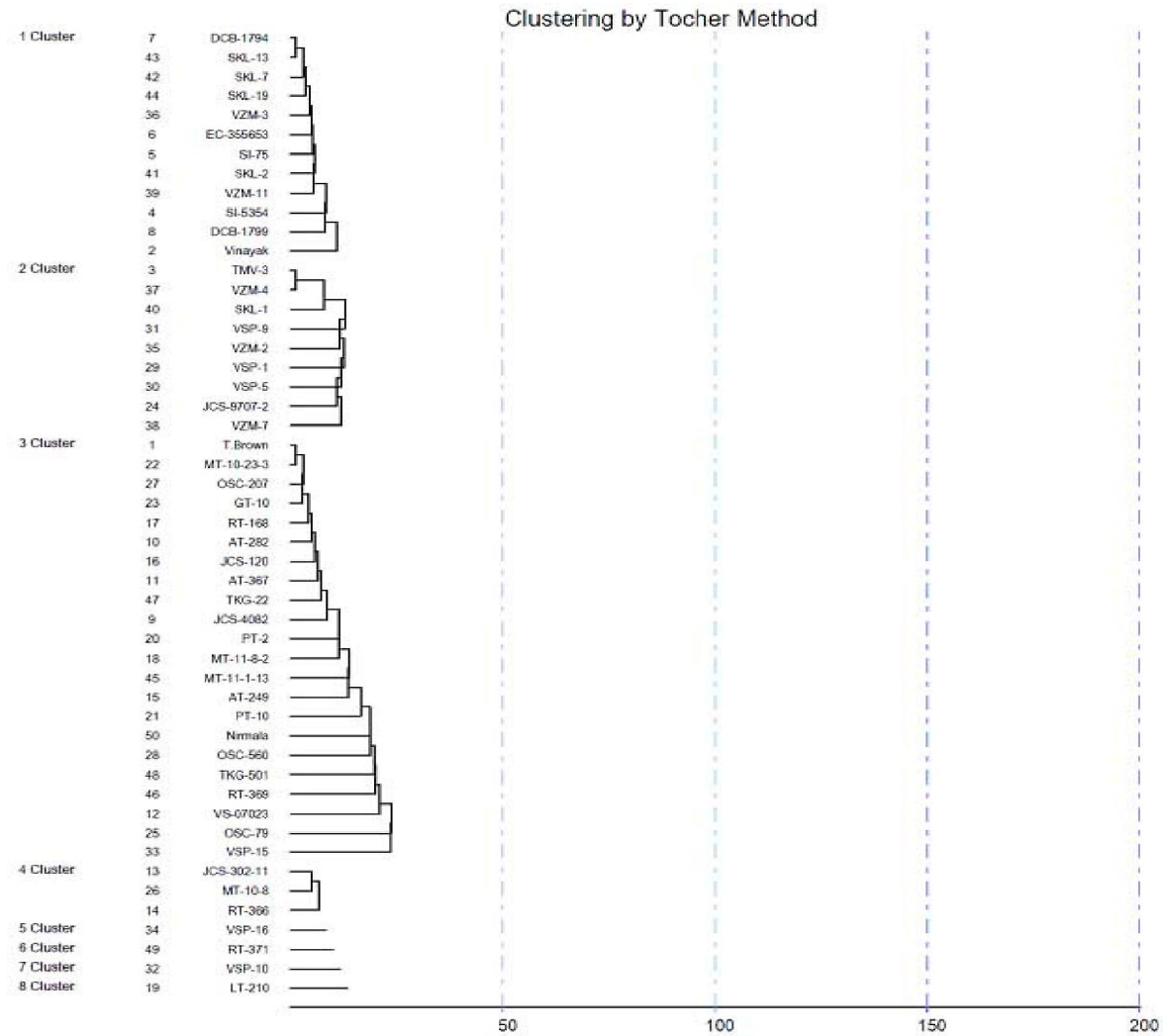
On the basis of Euclidian² values, intra-cluster distances ranged from 0.00 (cluster IV) to 105.43 (cluster VII). Where as the maximum inter-

cluster distance was observed between clusters IV and VI followed by clusters II and IV while, the minimum inter-cluster distance was observed between clusters I and III as shown in Table 5.

In general higher the divergence between the genotypes, higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between the genotypes belonging to distant clusters for getting heterosis which may give rise to wide range of segregants.

In *Tocher's* method, low cluster means were observed in cluster VI for days to 50 % flowering (33.67) and days to maturity (81.67) which may be useful in evolving early types (Table 6). High cluster means were observed in cluster V for plant height, number of branches plant⁻¹ and oil per cent. High mean values were also observed in cluster VI for number of capsules plant⁻¹, 1000 seed

Fig. 1. Diagram illustrating the cluster pattern by Tocher's method for the genotypes of sesame.



weight and seed yield plant⁻¹ and high mean value for number of seeds capsule⁻¹ in cluster IV may be useful for evolving high yielding types. Low mean values for days to 50% flowering and days to maturity with high mean values for other characters is important to select the genotypes from the clusters. In view of the maximum inter cluster distances and also mean values it is suggested to cross the genotypes VSP-1 and VZM-7 from cluster II with LT-210 from cluster-VIII followed by RT-366 from cluster IV and LT-210 from cluster-VIII, which may give rise to high heterosis.

The cluster mean values for all the 10 characters based on *Ward's minimum variance* method are presented in Table 7. Cluster V recorded high mean values for number of branches plant⁻¹, number of capsules plant⁻¹, capsule length, 1000 seed weight and seed yield plant⁻¹ coupled

with low mean value for days to maturity. Low mean values for cluster II for days to 50 per cent flowering (35.67); cluster V for days to maturity (81.83) and high mean value for plant height were observed in cluster VII. In cluster II high mean value was observed for number of seeds capsule⁻¹, while in cluster VI high mean values were recorded for days to 50% flowering, days to maturity and oil per cent. Considering the intercluster distances and cluster mean values, the crosses between LT-210 (cluster IV) and SKL-1 (cluster VI) may give rise to high heterosis.

Narayanan and Murugan (2013) also studied divergence in sesame genotypes and found eight clusters based on seven characters. Similar results were also found by Shekhawat *et al.* (2013), Chandra Mohan (2014) and Anjay Tripathi *et al.* (2014).

Fig. 2. Diagram illustrating the cluster pattern by *Ward's minimum variance* method for the genotypes of sesame.

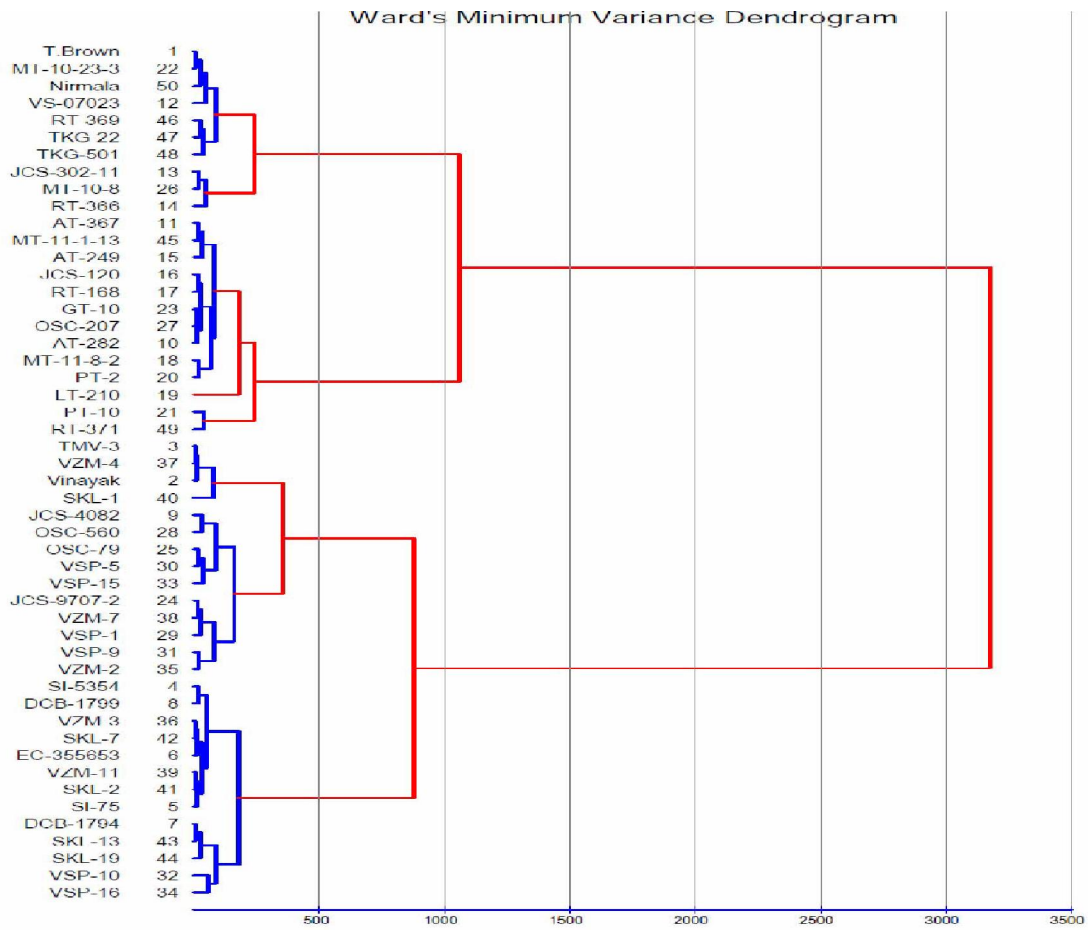
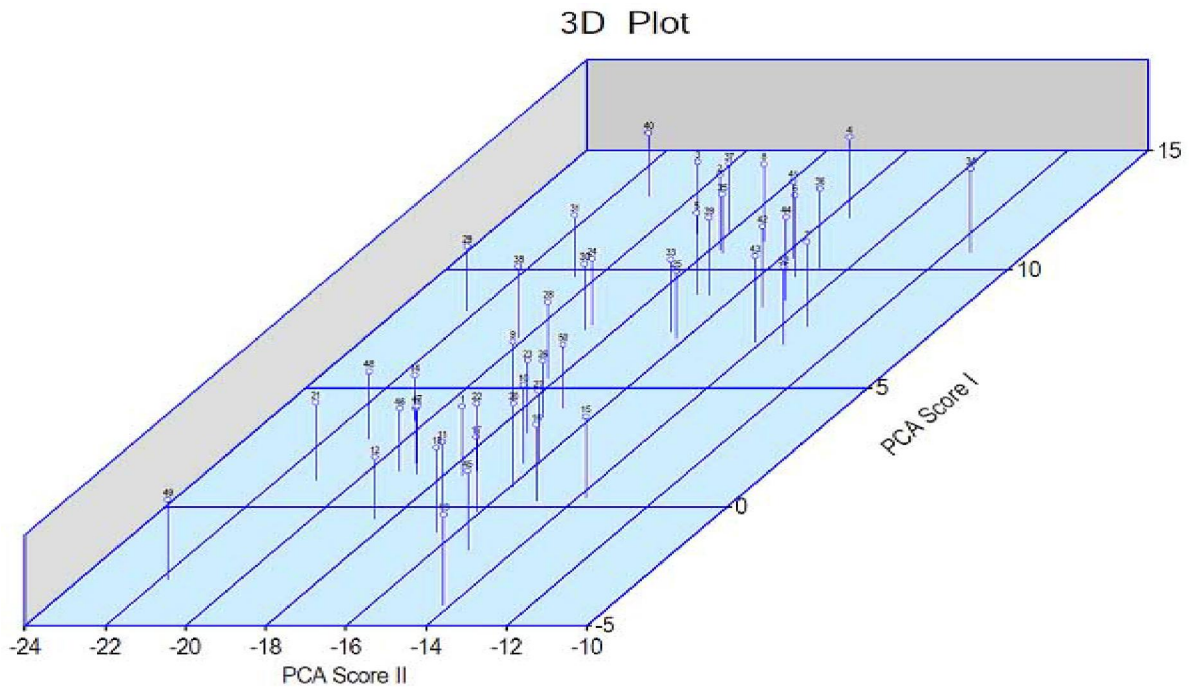


Fig. 3. Three dimensional graph showing relative position of 50 sesame genotypes based of PCA scores.



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