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

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ABSTRACT

Sixty genotypes of sesame were evaluated for 10 quantitative characters to study genetic divergence by using Mahalanobis' D^2 statistic, cluster analysis and principal component analysis. Based on these clustering methods, 7 and 8 clusters were formed in D^2 statistic and cluster analysis, respectively. 1000- seed weight contributed maximum towards diversity in D^2 analysis. PCA identified 4 components with eigen value more than one which contributed 90.55 per cent of cumulative variance. Highest inter-cluster distance was observed between VI and VII followed by cluster IV and VI in D^2 statistic. Where as cluster IV and VI followed by IV and V showed maximum inter-cluster distance in hierarchical cluster analysis. For varietal improvement strains from these clusters were important on the basis of their genetic distance and highest cluster means. No relationship between geographic origin and genetic diversity was observed among all the divergence methods.

Key words : Cluster Analysis,Genetic Diversity, Principal Component Analysis, Sesame

. Genetic diversity between the parents plays an important role in producing heterotic effect and desirable segregants. This calls for identification of genetically divergent groups in the species, as crosses involving parents from widely divergent groups are very much likely to yield desirable genotypes. An attempt was therefore, made to quantify the genetic divergence and to determine the relationship, between genetic and geographical divergence in the present investigation through different methods of clustering *i.e.,* D^2 statistic, hierarchical cluster and principal component analyses (PCA) in sixty sesamum genotypes.

MATERIAL AND METHODS

Sixty genotypes were grown in randomized block design with three replications during *kharif* 2007 (Table 1). Each genotype consisted of 1 row of 2 m length with a spacing of 30 cm between rows and 10 cm between plants in each replication. Observations on days to 50% flowering, plant height (cm), days to maturity, number of primaries, number of secondaries, capsules per plant, seeds per capsule, 1000-seed weight, oil content and seed yield per plant were recorded on ten randomly selected plants in each genotype for each replication or plot basis. Recommended agronomic practices were followed to raise a good crop. The data were analysed using D^2 statistics (Mahalanobis, 1928), hierarchical cluster analysis (Anderberg, 1993) and principal component analysis (Jackson,1991).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the 60 sesame genotypes indicating substantial genetic variability for all the characters. On the basis of D^2 and cluster analysis 7 and 8 clusters were obtained respectively (Table 2). Out of 7 clusters obtained in D^2 analysis, cluster I was the biggest comprising 36 genotypes, followed by cluster II with 12 genotypes, cluster III with 8 genotypes and the remaining four clusters with one genotype each. The lack of correspondence between genetic diversity and geographical origin was observed in the present study as also reported by Nagarajan and Prasad (1980) and Sheriff and Shivshankar (1992). It could possibly be due to genetic drift, selection pressure and environment which might have resulted in greater diversity than geographic isolation.

The average intra-cluster D^2 values ranged from zero (IV, V, VI and VII) to 22.14 (cluster III). The maximum inter-cluster distance was observed between cluster VI and VII (159.727) followed by cluster IV and VI (145.453) suggesting that the genotypes from these two clusters could be used as donors in hybridization programme for obtaining a wide spectrum of variation among the segregants (Table 3). 1000-seed weight contributed maximum towards total divergence (48.02%) followed by plant height (12.82 %), number of secondaries (9.32 %) and capsules per plant (4.75%) (Table 5), as also reported by Swain and Dikshit (1997).

Table 1 List of genotypes and their source of origin in sesame (*Sesamum indicum* L.)

S.no	Name of genotype	Pedigree	Source of origin
1	NRD-1110	Selection from local	Orissa
2	DCB-1799	Germplasm line	Jabalpur, Madhya Pradesh
3	So-12-2154	Crossed seed	Andhra Pradesh
4	EC-358022	Germplasm line	Peddapuram, Andhra Pradesh
5	BPT Local	Local variety	Andhra Pradesh
6	Nellore Brown Local	Local variety	Andhra Pradesh
7	Vinayak	Local variety	Orissa
8	SI-320	Pureline selection	Andhra Pradesh
9	EC-358039	Germplasm line	Andhra Pradesh
10	EC-355653	Germplasm line	Andhra Pradesh
11	Tanuku Brown	Pureline selection	Andhra Pradesh
12	Gowri	Pureline selection	Andhra Pradesh
13	Madhavi	Pureline selection	Andhra Pradesh
14	YLM-11	Vinayak X Kanak	Andhra Pradesh
15	YLM-17	Vinayak X Kanak	Andhra Pradesh
16	G2	Selection from local	Visakhapatnam, Andhra Pradesh
17	G4	Selection from local	Andhra Pradesh
18	G12	Selection from local	Andhra Pradesh
19	G18	Selection from local	Bobbili, Andhra Pradesh
20	G33	Selection from local	Srikakulam, Andhra Pradesh
21	G35	Selection from local	Srikakulam, Andhra Pradesh
22	SD-2132	Germplasm line	Madhya Pradesh
23	EC-357308	Germplasm line	Jabalpur, Madhya Pradesh
24	EC-358069	Germplasm line	Jabalpur, Madhya Pradesh
25	VB-7901	Germplasm line	Jabalpur, Madhya Pradesh
26	VRI-1	Germplasm line	Tamil Nadu
27	TMV-4	Germplasm line	Tamil Nadu
28	TMV-5	Germplasm line	Tamil Nadu
29	AKT-132	Germplasm line	Akola
30	Chandana	Pureline selection	Jagitial, Andhra Pradesh
31	JCS-9426	Pureline selection	Jagitial, Andhra Pradesh
32	E8	Germplasm line	Dharwad, Karnataka
33	RT-46	Germplasm line	Mandore, Rajasthan
34	SI-75	Pureline selection	Jabalpur, Madhya Pradesh
35	PS-201	Pureline selection	Jabalpur, Madhya Pradesh
36	SI-5354	Pureline selection	Jabalpur, Madhya Pradesh
37	DCR-1794	Pureline selection	Jabalpur, Madhya Pradesh
38	K-5170	Pureline selection	Jabalpur, Madhya Pradesh
39	Swetha Til	Germplasm line	Jagitial, Andhra Pradesh
40	YLM-66	YLM-17 X PS-201	Andhra Pradesh
41	VSP-7	Selection from local	Visakhapatnam, Andhra Pradesh
42	VSP-8	Selection from local	Visakhapatnam, Andhra Pradesh
43	VSP-9	Selection from local	Visakhapatnam, Andhra Pradesh
44	VSP-10	Selection from local	Visakhapatnam, Andhra Pradesh
45	VSP-11	Selection from local	Visakhapatnam, Andhra Pradesh
46	VSP-12	Selection from local	Visakhapatnam, Andhra Pradesh
47	VSP-13	Selection from local	Visakhapatnam, Andhra Pradesh
48	VSP-14	Selection from local	Visakhapatnam, Andhra Pradesh
49	VZM-7	Selection from local	Vizianagaram, Andhra Pradesh
50	VZM-8	Selection from local	Vizianagaram, Andhra Pradesh
51	VZM-10	Selection from local	Vizianagaram, Andhra Pradesh
52	VZM-11	Selection from local	Vizianagaram, Andhra Pradesh
53	VZM-12	Selection from local	Vizianagaram, Andhra Pradesh
54	VZM-21	Selection from local	Vizianagaram, Andhra Pradesh
55	VZM-22	Selection from local	Vizianagaram, Andhra Pradesh
56	VZM-23	Selection from local	Vizianagaram, Andhra Pradesh
57	VZM-25	Selection from local	Vizianagaram, Andhra Pradesh
58	VZM-26	Selection from local	Vizianagaram, Andhra Pradesh
59	VZM-28	Selection from local	Vizianagaram, Andhra Pradesh
60	SKL-Local	Selection from local	Srikakulam, Andhra Pradesh

Table 2. Clustering of 60 sesame (*Sesamum indicum* L.) genotypes by Tocher's and Ward's minimum variance method

Cluster Number	Clustering method	Number of genotypes	Genotypes
I	Tocher's method	36	NRD-1110, SI-5354, SI-75, K-5170, DCR-1794, VZM-7, VZM-8, VZM-10, VZM-11, VZM-12, VZM-21, VZM-22, VZM-25, VZM-26, VZM-28, YLM-17, YLM-66, G4, Nellore Brown Local, SI-320, VSP-7, VSP-8, VSP-9, VSP-10, VSP-11, VSP-12, VSP-13, G2, G18, G33, Chandana , RT-46 , VB-7901, EC-357308, SD-2132, EC-358022
	Ward's method	5	Swetha Til, TMV-4, Vinayak, E8, JCS-9426
II	Tocher's method	12	Swetha Til, TMV-4, Vinayak, PS-201, JCS-9426, TMV-5, BPT-Local, So-12-2154, EC -358069, SKL-Local, AKT-132, VRI-1
	Ward's method	10	BPT-Local, VB-7901, DCR-1794, VSP-9, VZM-22, VSP-13, PS-201, TMV-5, So-12-2154, SKL-Local
III	Tocher's method	8	Gowri, YLM-11, Madhavi, DCB-1799, G12, G35, Tanuku Brown, EC-358039
	Ward's method	7	G4, VZM-25, G18, EC-357038, EC-358069, YLM-17, VZM-10
IV	Tocher's method	1	VSP-14
	Ward's method	1	VZM-23
V	Tocher's method	1	EC-355653
	Ward's method	3	AKT-132, VRI-1, EC-355653
VI	Tocher's Method	1	E8
	Ward's method	6	Gowri, YLM-11, Madhavi, DCB-1794, EC-358039, Tanuku Brown
VII	Tocher's Method	1	VZM-23
	Ward's method	17	Nellore Brown Local, VSP-12, VZM-26, SD-2132, VSP-8, SI-75, YLM-66, G2, NRD-1110, SI-5354, Chandana, EC-358022, G12, G35, G33, K-5170, RT-46
VIII	Ward's method	11	VSP-10, VSP-11, VZM-11, VZM-12, VZM-8, VZM-21, VSP-7, VZM-7, VZM-28, VSP-14, SI-320

The relative importance of contribution of yield components towards divergence can be judged by comparing the group means of 10 characters (Table 4). The highest mean values for days to 50% flowering (44.33), days to maturity (85.33), number of primaries (4.13), number of secondaries (3.47), capsules per plant (51.53), seeds per capsule (122.33), oil content (51.00) and seed yield per plant (15.77) were depicted by cluster V (EC-355653). Cluster VI (E8) reported high mean value for 1000-seed weight (4.16). Cluster VII (VZM-23) noticed high mean value for plant height (110.00).

In the present study, the first four principal components with eigen values more than one contributed 90.55 per cent towards the total variability (Table 6). Principal components (5-10) had eigen value less than one which were considered as non-significant (Legendre and Legendre, 1984). It was therefore, inferred that the essential features of data set had been represented in first four principal components.

Table 3 Inter- and intra-(bold) cluster distance between 7 and 8 clusters formed by Mahalanobis' D^2 method and Ward's minimum variance method in 60 genotypes of sesame (*Sesamum indicum* L.*)*

		Cluster- I	Cluster- II	Cluster- III	Cluster- IV	Cluster- V	Cluster-VI	Cluster- VII	Cluster-VIII
Cluster- I	T	**14.3**	31.2	30.9	26.9	72.0	78.0	64.8	
	W	**43.0**	59.0	90.5	347.5	117.5	203.0	136.9	209.0
Cluster-II	T		**18.3**	48.0	70.7	54.0	34.3	98.6	
	W		**25.4**	50.9	279.6	131.3	126.3	54.8	108.6
Cluster-III	T			**22.1**	47.2	64.7	107.2	124.1	
	W			**30.5**	171.1	96.5	116.0	59.2	74.5
Cluster-IV	T				**0.0**	143.6	145.4	66.6	
	W				**0.0**	345.5	374.9	227.0	158.1
Cluster-V	T					**0.0**	79.8	135.0	
	W					**44.8**	137.1	175.3	205.5
Cluster-VI	T						**0.0**	159.7	
	W						**54.9**	88.8	109.7
Cluster-VII	T							**0.0**	
	W							**26.9**	46.1
Cluster-VIII	W								**33.5**

Bold and diagonal values represent intra-cluster distances T- Tocher's method W- Ward's method

Table 4 Mean values of seven clusters obtained from Tocher's method and eight clusters from Ward's minimum variance method estimated from 60 genotypes of sesame (*Sesamum indicum* L.*)*

Cluster No	Clustering method	Days to 50% flowering	Plant height (cm)	Days to maturity	Number of primaries	Number of secondaries	Capsules per plant	Seeds per capsule	1000 seed weight (g)	Oil content (%)	Seed yield per plant
I	Tocher's	38.9	85.2	81.4	3.2	2.8	41.2	77.6	2.7	46.7	8.4
	Ward's	38.6	88.1	81.5	3.0	2.5	40.3	74.7	3.6	49.1	10.1
II	Tocher's	38.7	86.6	81.7	3.3	2.6	41.2	80.7	3.3	48.2	9.9
	Ward's	38.5	82.4	81.1	3.3	2.7	39.0	76.1	3.2	46.8	8.8
III	Tocher's	41.5	76.7	83.2	3.2	2.7	45.2	92.4	2.6	48.1	11.2
	Ward's	39.1	89.9	81.7	3.5	2.9	43.2	77.8	3.0	46.1	9.5
IV	Tocher's	37.0	84.3	79.0	2.4	2.4	35.1	65.0	2.2	47.3	6.4
	Ward's	37.6	110.0	79.3	3.7	3.1	35.8	68.6	2.4	47.6	6.6
V	Tocher's	44.3	91.3	85.3	4.1	3.4	51.5	122.3	3.3	51.0	15.7
	Ward's	40.6	91.5	82.6	3.5	3.1	50.6	109.8	3.3	49.8	13.6
VI	Tocher's	42.7	78.0	84.3	3.3	2.8	46.4	98.2	2.6	48.3	12.2
	Ward's	37.6	86.0	79.3	3.0	3.1	40.3	70.3	4.1	47.0	10.0
VII	Tocher's	39.0	81.7	81.7	3.1	2.7	40.1	75.6	2.7	47.3	8.1
	Ward's	37.6	110.0	79.3	3.7	3.1	35.8	68.6	2.4	47.6	6.6
VIII	Ward's	38.4	86.9	80.6	3.1	2.8	41.6	79.6	2.4	46.2	7.9

Table 5 Relative contribution of different characters towards genetic diversity (D^2) in sesame (*Sesamum indicum* L.)

Source	Number of times ranked first	Contribution % towards divergence
Days to 50% flowering	5	0.28
Plant height	341	19.27
Days to maturity	2	0.11
Number of primaries	65	3.67
Number of secondaries	165	9.32
Capsules plant^{-1}	84	4.75
Seeds capsule^{-1}	10	0.57
1000 seed weight	850	48.02
Oil content (%)	21	1.19
Seed yield plant^{-1}	227	12.82

Table 6 Eigen values, proportion of the total variance represented by first four principal components, cumulative per cent variance and component loading of different characters in sesame (*Sesamum indicum* L.)

	PC1	PC2	PC3	PC4
Eigen value (Root)	362.529	204.232	165.648	70.421
% variance explained	40.889	23.035	18.683	7.943
Cum. variance explained	40.889	63.924	82.607	90.549
Days to 50% flowering	0.001	0.174	0.077	0.008
Plant height	0.063	-0.534	0.713	-0.357
Days to maturity	0.021	0.041	-0.012	-0.057
Number of primaries	0.054	-0.080	0.279	0.142
Number of secondaries	-0.024	-0.016	0.364	0.892
Capsules plant^{-1}	0.081	0.380	0.326	-0.147
Seeds capsule^{-1}	0.027	0.393	0.120	-0.122
1000 seed weight	0.962	-0.146	-0.153	0.068
Oil content (%)	0.142	0.155	-0.035	0.049
Seed yield plant^{-1}	0.197	0.576	0.361	-0.100

PC= Principal component

The first principal component (PC_1) contributed maximum towards variability (40.88%) with a positive significant loading of 1000-seed weight (0.96) followed by seed yield per plant (0.20), oil content (0.14), capsules per plant (0.08) and plant height (0.06). The second principal component (PC_2) accounted 23.03 per cent of total variance and it reflected significant positive loading of seed yield per plant (0.58), seeds per capsule (0.39), capsules per plant (0.38), days to 50% flowering (0.17), oil content (0.15) and days to maturity (0.04). The third principal component (PC_3) was characterized conspicuously by high loading of plant height (0.713), number of secondaries (0.36) and capsules per plant (0.33). Based on these first three principal components mean genotype scores were computed. Principal factor scores for all the 60 genotypes were estimated for all three principal components and utilized to construct precise 3D plot (Fig 2). All the genotypes were plotted for PC_1, PC_2, and PC_3 which cumulatively explained 82.61 per cent variability which accounted for all the characters.

Fig 1 Diagram illustrating the cluster pattern by Ward's minimum variance method for the genotypes of sesame (*Sesamum indicum* L.)

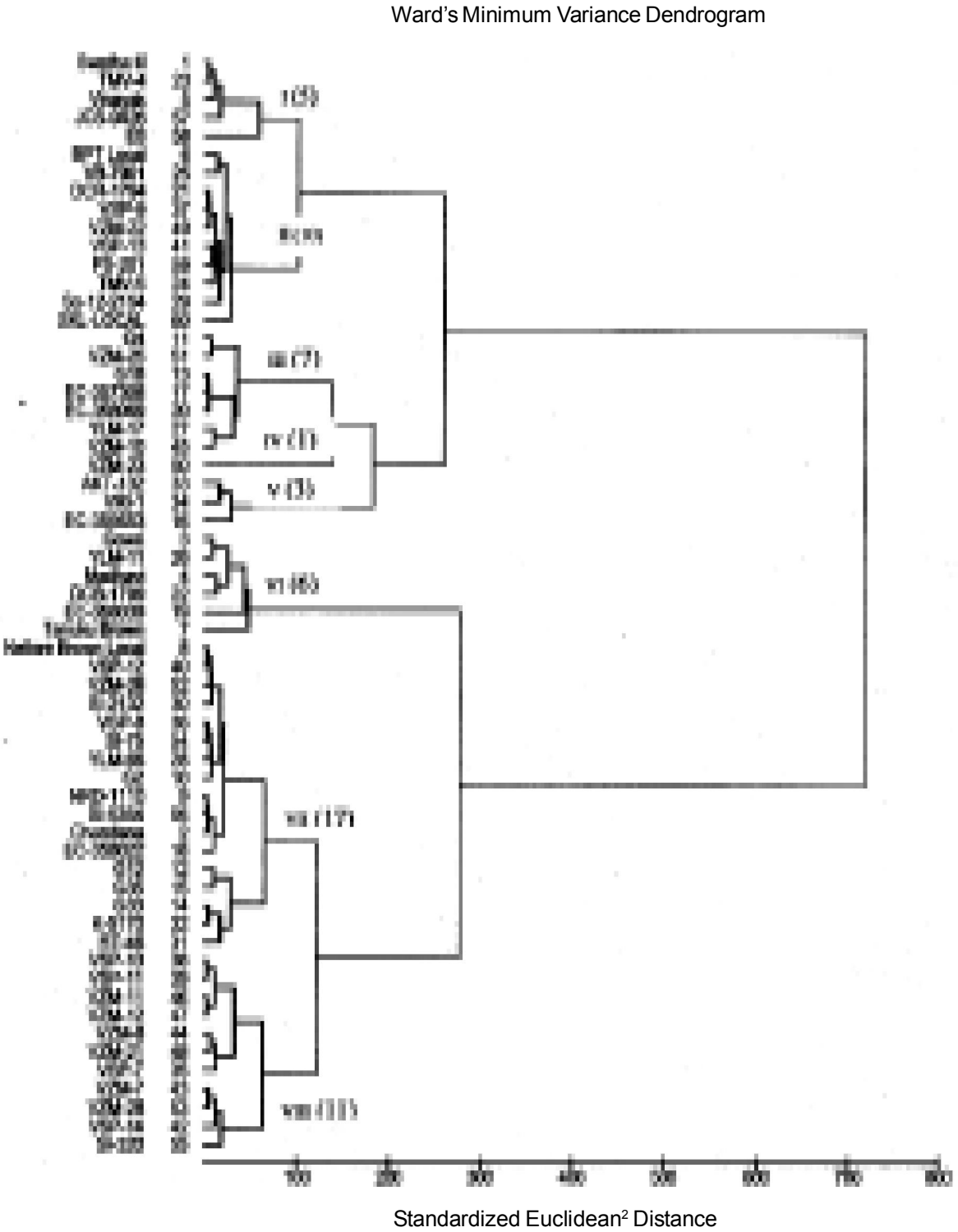
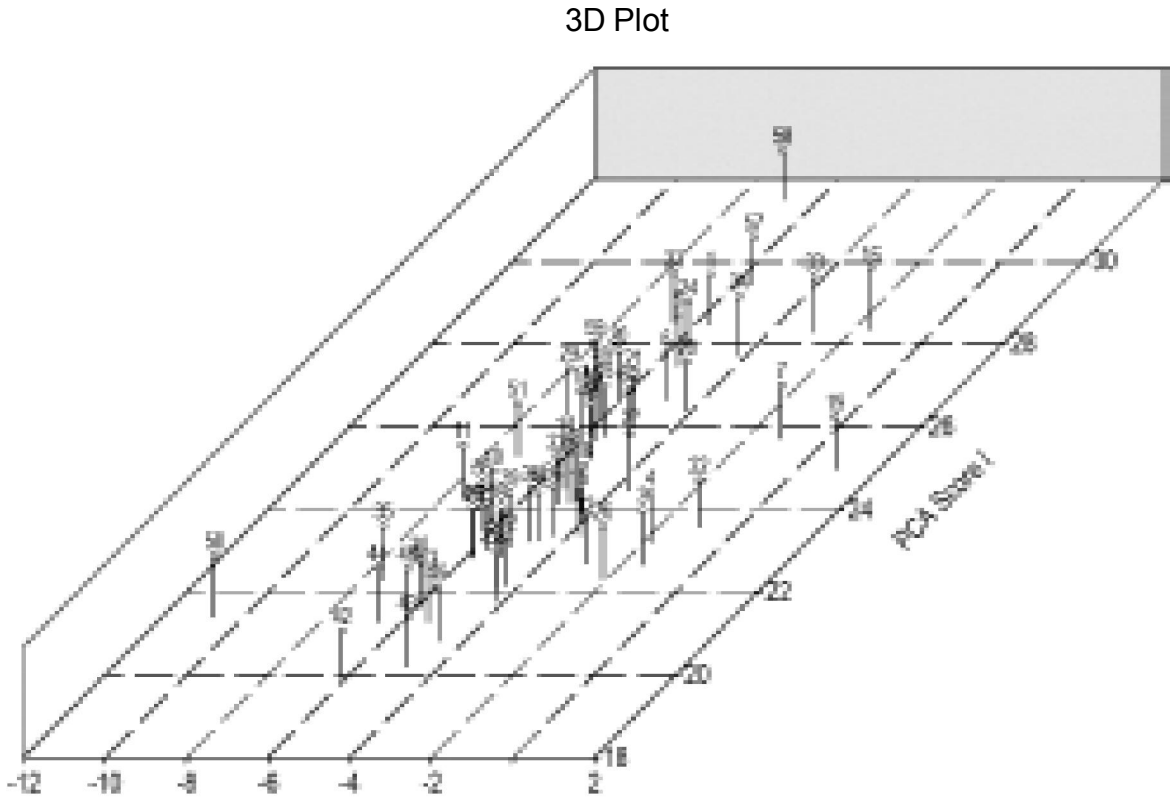


Fig 2. Three- dimensional graph showing relative position of sesame (*Sesamum indicum* L.) genotypes based on PCA score, (Number of genotypes correspond to Table 1)



The principal component scores of genotypes were used as input for clustering procedures in order to group the genotypes into various clusters and to confirm the results of principal component analysis. Hierarchical clustering (Ward's minimum variance) method was followed to create dendrogram based on Euclidean distance (dissimilarity coefficients) (Table 2 and Fig. 1). The 60 genotypes were grouped into 8 clusters. Distribution of various genotypes into clusters was random indicating that the geographical diversity and genetic diversity were not related.

The biggest cluster was VII (17 genotypes) followed by cluster VIII (11 genotypes). Based on cluster analysis, the intra-cluster values were ranged from zero (cluster IV) to 54.985 (cluster VI). The maximum inter-cluster distance was observed between cluster IV and VI (374.994), followed by cluster I and IV (347.574) and cluster IV and V (345.559) as shown in Table 3. Cluster V (AKT-132, VRI-1 and EC-355653) was characterized by high mean value for number of secondaries (3.53), capsules per plant (50.6), seeds per capsule (109.89), oil content (49.89) and seed yield per plant (13.69) and cluster VI (Gowri,YLM-11, Madhavi, DCB-1794, EC - 358039 and Tanuku Brown) registered high mean value for days to 50% flowering (42.72) and days to maturity (84.39) as shown in Table 4. Based on cluster analysis, crosses may be effective between the genotypes of cluster V and cluster VI to obtain better and desirable segregants.

The results of hierarchical cluster analysis and principal component analysis confirmed the findings of each other. The plot of PC_1, PC_2, PC_3 and PC_4 accounted for 90.55 per cent of variation. Genotypes belonging to a common cluster have fallen nearer to each other and *vice-versa* confirming the results of cluster analysis.

All the three methods of grouping revealed a single concept of non-correspondence of genetic divergence and geographic diversity. In a broad sense all the three methods of classifying genotypes into different groups are equally useful but hierarchical cluster analysis gave an additional advantage of identifying sub-clusters of the major groups at different levels so that each small group can be critically analyzed.

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