

GENETIC DIVERGENCE ANALYSIS OF SESAME GENOTYPES (*Sesamum indicum* L.)

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ABSTRACT

Divergence studies through Mahalanobis D² statistic on 50 sesame genotypes indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster distances. The 50 genotypes were grouped into 14 clusters based on the D² values. Among the fourteen clusters, cluster II was the largest comprising of fourteen genotypes followed by cluster V with ten genotypes, cluster III with nine genotypes, cluster I with seven genotypes. The genotypes JCS 3980, Swetha thil, GT 10, JCS 4039 and JCS 4053 from these clusters having high mean values and may be directly used for adaptation or may be used as parents in future hybridization programme. The highest inter cluster distance was found between clusters VII and XII, while lowest was between IV and VII. The maximum intra cluster distance was recorded for cluster V followed by cluster II. Among all the traits studied, maximum contribution towards genetic divergence was shown by days to 50 per cent flowering followed by days to maturity, oil content, seed yield per plant and number of seeds per capsule. Greater genetic divergence was found between clusters VII and XII indicating superior and novel recombinants and explore the fullest range of variability for the characters and to realize good recombinant can be realized by mating between the lines of these clusters in a definite fashion.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is known to be the most ancient oilseed crop dating back to 3050-3500 B.C. (Bedigian and Harlan, 1986) and commonly known as "Queen of oilseeds" due to its resistance to oxidation and rancidity, also it plays an important role as an industrial food crop because of its high nutritional value. The seeds of sesame contains 40 to 63 per cent oil, which contains significant amount of oleic and linoleic acids (Abate and Mekbib, 2015). It is basically considered a crop of tropical and sub-tropical regions, but it has also spread to the temperate parts of the world. It can set seed and yield well under fairly high temperature and it can grow in stored soil moisture without rainfall and irrigation. However, continuous flooding or severe drought adversely affect sesame plants and resulted in low yield (Mensah *et al.*, 2009).

The success of any crop improvement programme essentially depends on the nature and magnitude of genetic variability present in the crop. The knowledge of nature and magnitude of genetic variability is of immense value for planning efficient breeding programme to improve the yield potential of the genotypes. Improvement in yield is normally attained through exploitation of the genetically diverse parents in breeding programmes. For identifying such diverse parents Mahalanobis D² statistic (1936) has been used in several crops. This is a valuable tool to study genetic divergence at inter varietal and sub-species level in classifying the crop plants. For an efficient hybridization programme selection of

genetically diverse parents and superior genotypes is important, which ensures the better recombination of genes and exhibit transgressive segregants in selfing series. Hence, the present study was, thus, carried out to ascertain the nature and magnitude of genetic divergence among fifty sesame genotypes.

MATERIALS AND METHODS

A field experiment was conducted during Kharif, 2018 at Regional Agricultural Research Station, Jagtial in sesame utilizing 50 germplasm accessions representing different agroecological situations of India. The germplasm material was raised in randomized block design with three replications using two National Checks (TKG 22, GT 10) and one Zonal check (Rama), 4 Local checks (YLM 11, YLM 66, YLM 17, Madhavi). Each genotype was sown in three rows of two metres length, with inter-row spacing of 30 cm and intra row spacing of 10 cm. Sowing was done by dibbling the seed at 2-3 cm depth. All the standard package of practices were followed during crop growth period.

The traits *viz.*, plant height, number of branches per plant, number of capsules per plant, height of the plant from first capsule formation, capsule length, capsule width, number of seeds per capsule, seed yield per plant, 1000 seed weight, harvest index and oil content were recorded on five randomly selected plants. However, observations were made on whole plant basis for days to 50% flowering and days to maturity.

Differences between genotypes for different characters were tested for significance using analysis of variance. The data was subjected to the Mahalanobis D2 statistic (1936) to measure the genetic divergence and the genotypes were grouped into different clusters by Tocher's method as described by Rao (1952). Contribution of each character for genetic divergence was estimated from the number of times each character appeared in first rank.

RESULTS AND DISCUSSION

Analysis of variances for yield and yield components of sesame germplasm

The mean sum of squares for yield and yield attributing traits *i.e.*, days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, height of the plant from first capsule formation, capsule length, capsule width, number of seeds per capsule, 1000 seed weight and seed yield per plant, harvest index, and oil content are presented in Table 1. It was indicated that all the genotypes displayed considerable amount of differences in their mean performance with respect to all the traits studied, which indicates that the genotypes under study were genetically diverse. This result agreed with the observation of Saha *et al.* (2012).

Genetic divergence through D2 analysis

In the present study genetic divergence was assessed by using Mahalanobis D2 statistic which is found to be useful tool in quantifying the degree of divergence between biological populations at genotypic level. This can narrow the problem of selection of parents for hybridization programme, if one can identify the characters responsible for discrimination between populations.

Wilk's 'V' criterion test

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the Wilk's V criterion. The Wilk's criterion thus obtained was used in calculations of 'V' statistic. The statistic 3054.35 was highly significant (more than the tabulated \pm value) revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested sesame germplasm was considered to be relevant. These results were found to be similar with the findings of Tripathi *et al.* (2013).

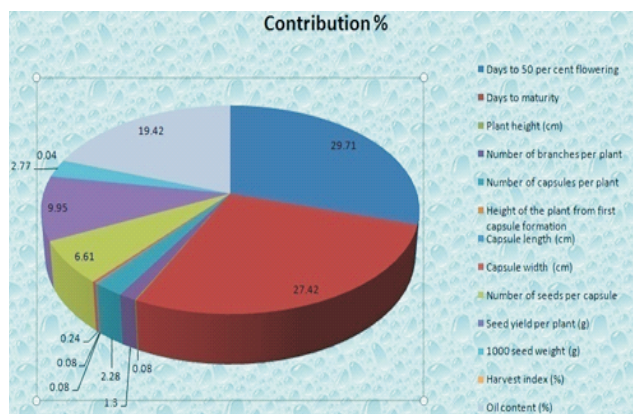


Figure 1: Relative contribution (%) of yield and yield attributing traits in sesame genotypes towards divergence

Relative contribution of different traits towards divergence

The per cent contribution towards genetic divergence by all the yield and yield contributing traits is presented in Table 2 and Fig 1. The maximum contribution towards genetic divergence was by days to 50% flowering (29.71 per cent), followed by days to maturity (27.42 per cent), oil content (19.42 per cent), seed yield per plant (9.95 per cent), number of seeds per capsule (6.61 per cent), 1000 seed weight (2.77 per cent), number of capsules per plant (2.28 per cent), number of branches per plant (1.30 per cent), capsule width (0.24 per cent), capsule length (0.08 per cent), plant height (0.08 per cent), height of the plant from first capsule formation (0.08 per cent) and harvest index (0.04 per cent). These results were in accordance with the reports of Ajay Tanwar and Rajani Bisen (2018) and Gogoi *et al.* (2018).

Clustering pattern

Based on the D2 values, the distribution patterns of breeding lines done into fourteen clusters are presented in Table 3, such that the genotypes belonging to same cluster had an average smaller D2 values than those belonging to different clusters. The diagrammatic representation of fourteen clusters consisting of different advanced breeding lines is shown in Fig. 2. Among the fourteen clusters, cluster II was the largest comprising of 14 genotypes followed by cluster V with 10 genotypes, cluster III with 9 genotypes, cluster I with 7 genotypes. Remaining clusters IV, VI, VII, VIII, IX, X, XI, XII, XIII, XIV were solitary indicating high degree of heterogeneity among the genotypes. Solitary clusters may be of distinct recombinant or rare segregants. More number of cluster

Table 1: Analysis of variance for yield and yield attributing traits in sesame

Source of Variation	df	Mean Sum of Squares												
		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Height of the plant from first capsule formation (cm)	Capsule length (cm)	Capsule width (cm)	Number of seeds per capsules	Seed yield per Plant (g)	1000 seed weight (g)	Harvest index (%)	Oil content (%)
Replications	2	0.01	0.05	0	0.02	4.53	7.32	0	0	4.94	0.05	0.04	0.02	0.4
Genotypes	49	140.58**	74.84**	185.84**	0.31**	252.95**	75.75**	0.03**	0.002**	172.73**	7.23**	0.89**	7.04**	16.93**
Error	98	1.04	0.63	43.18	0.02	8.13	6.73	0.01	0	2.74	0.16	0.03	2.5	0.24
Total	149	46.92	25.03	89.51	0.12	88.59	29.44	0.02	0	58.67	2.48	0.31	3.96	5.73

*- Significance at 5% level of probability (1.43); **- Significance at 1% level of probability (1.65)

Table 2: Relative contribution (%) of yield and yield attributing traits towards divergence

Character	Times ranked 1st	Contribution %
Days to 50% flowering	364	29.71
Days to maturity	336	27.42
Plant height (cm)	1	0.08
Number of branches per plant	16	1.3
Number of capsules per plant	28	2.28
Height of the plant from first capsule formation (cm)	1	0.08
Capsule length (cm)	1	0.08
Capsule width (cm)	3	0.24
Number of seeds per capsule	81	6.61
Seed yield per plant (g)	122	9.95
Test weight (g)	34	2.77
Harvest index (%)	1	0.04
Oil content (%)	238	19.42

geographical regions into various clusters was at random indicating that there is no parallelism between geographical diversity and genetic diversity. Therefore, the choice of suitable diverse parents selected on the basis of genetic diversity analysis would be more rewarding than the choice made on the basis of geographic diversity.

Average intra and inter cluster distance

The average D2 values of intra and inter cluster distances are presented in Table 4 and Fig. 3 and 4. The maximum intra cluster distance was recorded for cluster V (53.82) followed by cluster II (52.54). Because of solitary nature clusters IV, VI, VII, VIII, IX, X XI, XII, XIII, and XIV recorded zero. These findings were in conformity with Venkatesh *et al.* (2011) and Ahadu Menzir (2012). The inter cluster distance ranged from 24.55 and 347.02. The highest distance was between clusters VII and XII while the lowest was between IV and VII.

The inter cluster distances were higher than intra cluster distances indicating the presence of wider genetic diversity between clusters than within clusters. The highest intra cluster distance for cluster V depicts that it has maximum divergence among the genotypes present in that cluster. Promising genotypes included in cluster V that had maximum intra cluster distance are JCS3890, JCS3885, JCS3880, JCS3878, JCS2698, JCS3887, JCS3889, JCS3893, JCS3880, JCS2420 which are highly divergent among themselves. This could be made use in the yield improvement through recombination breeding. While, the maximum inter-cluster distances suggest that the genotypes belonging to these clusters if chosen for hybridization are likely to produce maximum amount of heterosis. The greater the distance between clusters wider is the diversity between genotypes.

It is assumed that maximum amount of heterosis will be manifested in cross combinations involving the parents belonging to most divergent clusters. Keeping this in view, the JCS 3980 of cluster VII and Swetha thil of cluster XII, cluster I (GT 10) and cluster XIV (JCS 4053) has wider diversity. Therefore the genotypes of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

Cluster mean

The cluster means with respect to thirteen yield and yield contributing traits across fourteen clusters are presented in Table 5. In case of days to 50% flowering, cluster means ranged between 43.58 (cluster I) and 62 days (cluster XII). Genotypes of cluster I showed characteristic early flowering habit with 43.58 number of days to flowering while, genotypes of cluster XII had late flowering habit with 62 days.

For days to maturity, cluster mean ranged between 86.48 and 99.67 days. Genotypes under cluster I was of early maturity type with number of days to mature being 86.48 days. While, that under cluster VII were of late maturity types (99.67 days).

With regard to plant height, the genotypes of cluster XII exhibited the highest mean plant height (105.75 cm). Cluster I comprised of genotypes with a lowest mean plant height (82.48 cm). The mean values of remaining clusters were intermediate.

For number of branches per plant, cluster mean ranged

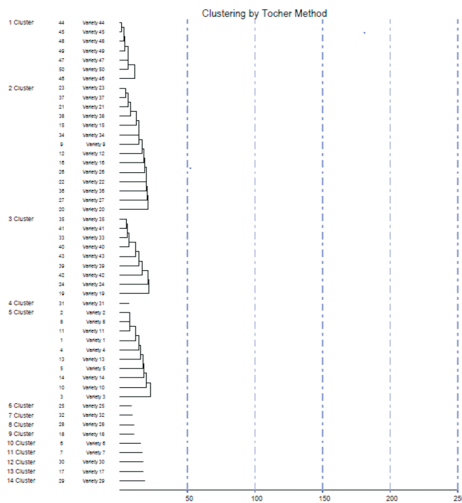


Figure 2: Clustering pattern of sesame genotypes based on Tocher's method

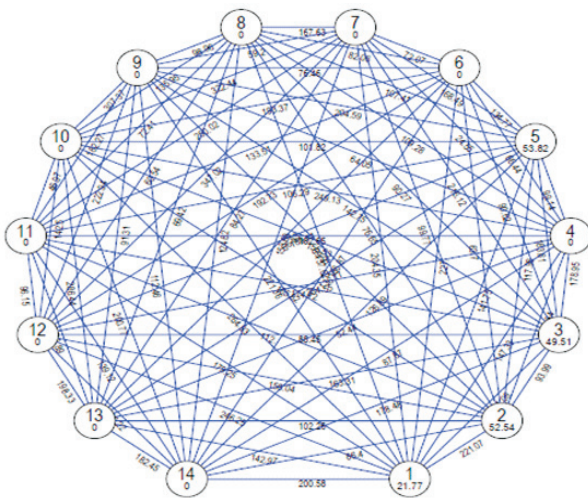


Figure 3 : Mahalanobis Euclidean Distance among 50 genotypes of sesame

formation is an indication of higher divergence. The pattern of distribution of genotypes from different eco-

Table 3. Clustering pattern of sesame genotypes based on D2 values

Cluster	No. of Genotypes	Genotypes
Cluster I	7	TKG 22, GT 10, YLM 66, YLM 17, YLM 11, Madhavi and Rama
Cluster II	14	JCS 3739, JCS 4036, JCS 3915, JCS 3970, JCS 2477, JCS 3985, JCS 3899, JCS 3910, JCS 3594, JCS 3894, JCS 4050, JCS 4060, JCS 4052 and JCS 3180
Cluster III	9	JCS 4005, JCS 4001, JCS 3981, JCS 3990, JCS 3987, JCS 4049, JCS 3993, JCS 3884 and JCS 3755
Cluster IV	1	JCS 3965
Cluster V	10	JCS 3890, JCS 3885, JCS 3880, JCS 3878, JCS 2698, JCS 3887, JCS 3889, JCS 3893, JCS 3880 and JCS 2420
Cluster VI	1	JCS 3886
Cluster VII	1	JCS 3980
Cluster VIII	1	JCS 4039
Cluster IX	1	JCS 3751
Cluster X	1	JCS 2489
Cluster XI	1	JCS 3881
Cluster XII	1	Swetha thil
Cluster XIII	1	JCS 3604
Cluster XIV	1	JCS 4053

Table 4: Average intra (diagonal) and inter cluster distances of sesame genotypes

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	21.77	221.07	311.08	147.33	141.75	227	204.35	137.62	221.36	264.93	179.25	246.25	142.97	200.58
II		52.54	93.99	69.64	117.98	63.7	99.77	76.65	69.95	165.82	112	158.04	102.26	86.4
III			49.51	178.95	183.61	90.62	216.12	90.27	142.75	155.53	114.72	88.45	163.31	178.48
IV				0	99.14	66.44	24.55	109.28	64.05	249.13	182.65	254.55	52.44	87.87
V					53.82	134.77	168.49	107.41	204.59	101.82	106.29	189.71	136.77	126.89
VI						0	72.07	82.06	76.46	193.37	133.51	192.73	56.83	186.87
VII							0	167.63	59.2	322.44	250.02	347.02	84.27	153.68
VIII								0	98.96	135.95	72.41	60.54	69.42	124.62
IX									0	307.37	182.27	222.94	91.31	112.46
X										0	46.97	142.5	286.44	200.77
XI											0	96.15	206.89	139.12
XII												0	198.33	186.22
XIII													0	182.45
XIV														0

Table 5: Cluster means for yield and yield attributing traits using Tocher's method

	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Height of the plant from first capsule formation (cm)	Capsule Length (cm)	Capsule width (cm)	Number of seeds per capsule	Seed yield per plant (g)	1000 seed weight (g)	Harvest index (%)	Oil content (%)
Cluster I	43.58	86.48	82.48	2.5	36.52	40.36	2.31	0.58	73.52	5.41	3.81	15.37	44.78
Cluster II	55.31	97.38	94.6	2.53	30	48.99	2.23	0.53	57.57	3.97	2.97	14.09	42.05
Cluster III	60.41	98.63	94.69	2.32	21.71	51.41	2.19	0.54	57.77	2.32	2.43	12.51	45.87
Cluster IV	46	98	103.2	2.3	38.4	50.57	2.23	0.55	60.93	5.1	3.33	15.31	40.78
Cluster V	46.9	90.8	94.22	2.42	25.4	46.85	2.09	0.53	54.28	3.23	3.18	13.38	42.24
Cluster VI	52.67	99.33	94.8	2.5	39.6	47.57	2.26	0.54	50	6	2.57	16.02	45.39
Cluster VII	46	99.67	95.47	2.7	42.43	50.47	2.47	0.55	61.8	6.2	2.53	16.19	40.95
Cluster VIII	56.33	93.33	97.73	3.13	33.27	53.73	2.21	0.55	61.47	3.5	3.8	13.74	45.94
Cluster IX	56	99	95.13	2.7	39.23	54.97	2.35	0.5	66.87	6.07	2.9	16.07	42.25
Cluster X	58	87	96.07	2.67	18.3	45.97	2.11	0.56	47.07	2.07	2.37	12	43.43
Cluster XI	60.33	87.33	90.93	2.1	31.17	43.17	2.15	0.55	54.17	4.17	2.9	14.54	44.04
Cluster XII	62	93	105.75	2.5	11.2	55.77	2.21	0.57	65.23	1.3	3.47	11.45	47.54
Cluster XIII	45.67	99	93.63	2.93	35.83	48.2	2.27	0.52	60.3	5.63	3.77	15.67	46.14
Cluster XIV	55	94.33	94.9	2.13	22.03	47.63	2.25	0.57	68.17	2.3	3.83	12.37	37.6

between 2.10 and 3.13 sesame genotypes under cluster XI (2.10) followed by cluster XIV (2.13) had less number of branches per plant and those in cluster VIII (3.13) had more number of branches per plant.

In case of number of capsules per plant, cluster means ranged between 11.20 (cluster XII) and 42.43 (cluster VII). Genotypes under cluster XII (11.20) had less number of capsules per

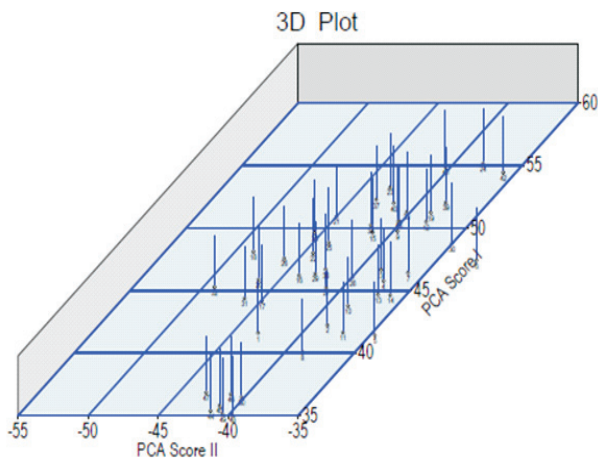
plant and those in cluster VII (42.43) had more number of capsules per plant.

For the trait height of the plant from first capsule formation, the genotypes of cluster I exhibited lowest mean (40.36 cm) while genotypes of cluster XII exhibited highest mean (55.77 cm). Remaining clusters showed intermediate values.

With regard to the capsule length, the cluster means ranged

Table 6: Promising genotypes having outstanding mean values for yield and its component traits.

Cluster	Character	Genotype
VII	Days to maturity, number of capsules per plant, capsule length, seed yield per plant and harvest index	JCS 3980
XII	Days to 50% flowering, plant height, height of the plant from first capsule formation and oil content	Swetha thil
I	Capsule width and number of seeds per capsule	GT-10
VIII	Number of branches per plant	JCS 4039
XIV	1000 seed weight	JCS 4053

**Figure 4: Statistical distances among 50 genotypes of sesame (3Dplot)**

between 2.09 and 2.47. Genotypes under cluster V (2.09 cm) showed lowest mean while genotypes of cluster VII (2.47 cm) had capsules with maximum length.

For the trait capsule width, cluster XIII had the lowest mean value (0.52 cm) and cluster I had highest capsule width (0.58 cm).

In case of number of seeds per capsule, the cluster means ranged between 47.07 and 73.52. Genotypes under cluster X (47.07) recorded lowest mean while genotypes of cluster I (73.52) showed highest mean value.

Cluster mean for seed yield varied from as low as 1.30 g to as high as 6.20 g. Genotypes in cluster XII (1.30 g) showed lowest and those in cluster VII (6.20 g) has highest seed yield per plant.

With respect to 1000 seed weight, cluster XIV had the highest mean value (3.83 g) followed by cluster I (3.81 g) and cluster IX had lowest 1000 seed weight (2.37 g).

In case of harvest index, the cluster means ranged between 11.45 and 16.19 %. Genotypes under cluster XII (11.45 %) recorded lowest mean, while cluster VII (16.19 %) showed highest mean value. With respect to oil content, cluster XIV (37.60 %) exhibited lowest mean value, while cluster XII (47.54 %) showed highest mean.

The results indicated that selection of genotypes having high values for particular trait could be made and used in the

hybridization programme for improvement of that character. The genotypes JCS 3980, Swetha thil, GT 10, JCS 4039 and JCS 4053 from these clusters having high mean values for the characters listed in Table 6 may be directly used for adaptation or may be used as parents in future hybridization programmes.

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