

Genetic Variability Parameters for Yield and Yield Contributing Traits Using D² Analysis of Sesame

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Abstract: Sixty genotypes of diverse origin have been evaluated for their genetic diversity for seed yield and yield contributing characters based on Mahalanobis D² statistics. Analysis of variance revealed significant differences between all the genotypes. The sixty genotypes have been divided into 8 clusters and cluster I was largest (48) followed by cluster II (6), cluster VI (3). The remaining clusters III, IV, V, VII and VIII were solitary. The average inter-cluster distance varied from 140.04 (between clusters I and III) to 1236.96 (between clusters III and VI). Maximum intra cluster distance was observed in cluster VI (152.00) followed by cluster II (108.56). Further, the character Number of capsules per plant has the highest contribution to total divergence (30.85) followed by the character number of capsules per axil (15.03). On the basis of inter cluster distance, clusters I, II, V, VI and VIII were found to be divergent and genotypes selected from these clusters can be used as parents in hybridization programme.

Keywords: D² statistics, genetic diversity, cluster distance.

INTRODUCTION

Sesame (*Sesamum indicum* L.) is one of the ancient cultivated oilseed crops in the world. It is commonly called as Til or Gingelly. Sesame belongs to the family Pedaliaceae and order Tubiflorae. Even though the genus *Sesamum* comprises of 36 species, *Sesamum indicum* is the most popular cultivated species. Sesame is a dual purpose crop as its seed as well as oil are edible. Seeds are popularly known as 'Seeds of immortality' and are rich in Calcium, Phosphorus, Magnesium and Potassium along with vitamins such as Niacin, Riboflavin and vitamin B6. The edible oil is rich in antioxidants like Sesamolol. India occupies second position in Sesamum production after Tanzania (FAOSTAT, 2016). Even though the crop originated in Africa, India remains to be the major Centre of diversity.

Owing to the number of advantages in consuming Sesame, attention has to be diverted towards genetic improvement of the crop and its increase in cultivation.

Genetic improvement in seed yield is not possible by phenotypic selection alone. Yield is polygenic in nature and has low heritability. Hence, selection of genotypes has to be done through a correlated response of several contributing factors affecting seed yield. Among the several methods of Multivariate analysis available, Mahalanobis D² analysis has been the perfect test for quantitative estimation of genetic diversity among genotypes and also to estimate the relative contribution of various attributes to total divergence. Genetic diversity studies also helps in recognising suitable genotypes to be used in a crossing programme for obtaining maximum heterosis. In this context, the present study aims to assess the genetic variability in sixty Indian Sesame genotypes using Mahalanobis D² statistics based on seed yield and its component characters and to identify promising parental lines which are diverse, to be used as parents in hybridization programme.

MATERIALS AND METHODS

The experimental material comprised of sixty genotypes of diverse origin collected from NBPGR, New Delhi and IOR, Hyderabad (Table 1) which was screened at Students' farm, Department of Agriculture, Loyola Academy during June to October 2021. The field layout was done in Randomized Complete Block Design with three replications. Each entry was represented in a row length of 5m with a spacing of 30 cm between the rows and 10 cm within the row between the plants. The seeds of each genotype were direct seeded at a depth of 2 cm. Two seeds were seeded per hill. All recommended package of practices were followed for raising the crop. A total of thirteen characters related to yield and yield contributing characters were studied.

Observations were recorded on five randomly selected plants per replication. Observations were recorded on thirteen quantitative traits i.e., Plant height (cm), number of branches per plant, seed yield per plant (g), 1000 seed weight (g), number of capsules per axil, capsule length (cm), number of capsules per plant, number of seeds per capsule, seed length (mm), seed width (mm), seed thickness (mm), and oil content.

Analysis of variance was computed for each character under study. The total variance was partitioned into Replications, Treatments and Error by adopting the analysis of variance technique for RBD as suggested by Panse and Sukhatme (1954). The expected Genetic gain, heritability and Genetic advance were calculated using the formula suggested by Johnson (1955).

Genetic divergence was computed by using Mahalanobis generalized distance or D² statistics as proposed by Rao (1952). The characters were ranked on the basis of their contribution to D². Grouping of genotypes into different clusters was done according to Tochers' method. (Rao 1952).

RESULTS AND DISCUSSION

The Analysis of variance revealed highly significant differences among the genotypes for the characters studied (Table 2). According to ANOVA, the mean sum of squares for the genotypes was extremely significant (P 0.05 and P 0.01) for all characters i.e., Plant height (cm), number of branches per plant, seed yield per plant (g), 1000 seed weight (g), number of capsules per axil, capsule length (cm), number of capsules per plant, number of seeds per capsule, seed length (mm), seed width (mm), seed thickness

(mm), and oil content. The material under research showed no substantial changes in replication, proving that environmental error (genotype x environment) was less widespread. These findings demonstrated that substantial differences exist among genotypes for all parameters studied, which may provide breeders with a good chance to identify high-performing accessions with desired features to enhance crop breeding programmes.

Phenotypic coefficient of variation (PCV) was found to be slightly higher for all the characters compared to genotypic coefficient of variation (GCV) as indicated in Table 3. However the difference is negligible which suggests that selection of these characters based on phenotype would be good indication of genetic potential. Similar findings have been reported by Manjeet et al. (2019), Gokulakrishnan et al. (2018) and Kalaiyarasi et al. (2019).

The Clustering method proposed by Tocher Rao (1952) using the generalized Mahalanobis distances (D^2) divided the sixty genotypes into eight clusters in such a way that the genotypes within a cluster had a small or minimum D^2 value than those in between the clusters. The composition of clusters is presented in Table 4 and Fig 1. Cluster I had the maximum number of genotypes (46) followed by cluster II (6) and cluster VI (3). Minimum numbers of genotypes were observed in cluster III, IV, V, VII and VIII (1 each).

The maximum intra cluster distance was found in cluster VI (152.00) followed by cluster II (108.56) as indicated in Table 5. An intra-cluster distance of 152.00 revealed that the genotypes EC 301961, EC 346370, RT-351 were more divergent. Thus these genotypes can be used to produce superior hybrids and transgressive segregants. Genotypes of cluster I and III were the most genetically related, distance between them being $D^2=140.04$. The most genetically divergent genotypes were from clusters three and six, the distance being $D^2=1236.96$. Therefore, it is expected that crosses between genotypes of cluster three and six would result in high yielding segregants due to high inter-cluster distance. Similar findings were reported by B.Soundharya et al. (2017)

Further, the results of cluster means for characters under study revealed that the character capsules per plant showed highest cluster mean in cluster VI (Table 6). Maximum values for number of seeds per capsule were recorded in cluster V and maximum value for plant height was recorded in cluster IV indicating the desirability of genotypes from these clusters for improvement of these traits.

Relative contribution of various characters towards divergence has also been an important aspect to help the plant breeder in selecting parents for hybridization and also for effective selections in advanced generations. It was revealed that capsules per plant contributed to maximum diversity (30.85%) followed by number of capsules per axil (15.03%) and number of seeds per capsule (13.09%) (Table 7). Similar results were obtained by Manivannan and Nadarajan (1996). The contribution of other characters towards genetic divergence is relatively low. Contribution of characters to divergence depends on the number of characters studied and also the influence of environment on the characters studied.

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Table 1: List of Genotypes

Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype	Sr. No.	Genotype
1	EC 304231	16	CUMS-17	31	IC 204785	46	GT-10
2	AKT-101	17	ES-21086-2	32	IC 511141	47	JLT-408
3	AGRA BALIK	18	CHAGATAM LOCAL	33	EC 346665	48	DORG-3052
4	EVC-122	19	ANAMIDI 74	34	EC 346829	49	DORG-60KRDS
5	CT-50	20	B-67	35	EC 346370	50	DORG-B7-11
6	TMV-4	21	RT-125	36	IC 500448	51	DORG-135-011
7	TMV-6	22	JLT-7	37	IC 500463	52	DORG-37-11
8	RT-372	23	VINAYAK	38	IC 500393	53	TKG-22

9	YLM-66	24	CT-44	39	VRI-1	54	DORG-BLSG-9
10	PHULE TIL-1	25	T-78	40	MADHAVI	55	IC 204550
11	EC-208652	26	TMV-7	41	CHANDANA	56	EC 370712
12	CT-51	27	VRI-2	42	YLM-17	57	IC 204248
13	EC 301961	28	IC 127622	43	YLM-4	58	IC 500506
14	CT-35	29	YLM-11	44	SWETHA	59	IC 132828
15	RT-351	30	IC 511151	45	KIS-304	60	IC 129908

Table2: Analysis of Variance

S.No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	59	118
1	Days to 50% Flowering	1.3720	14.668**	0.497
2	Plant Height	70.4260	952.922**	50.083
3	No. of branches	0.2750	4.634**	0.097
4	1000 seed weight	0.0210	0.515**	0.054
5	No. of capsules/axil	0.0010	1.241**	0.004
6	Capsule length	0.0410	0.311**	0.015
7	Capsules per plant	11.10	1697.749**	7.372
8	No. of seeds per capsule	4.6280	751.753**	14.106
9	seed length	0.0040	0.143**	0.044
10	seed width	0.0060	0.115**	0.011
11	seed thickness	0.0020	0.051**	0.003
12	oil content	0.1360	70.799**	1.575
13	Seed Yield per plant	0.830	3.463**	0.318

Table 3: ECV, PCV, GCV, Heritability and Genetic advance

Sl. No	Character	Var Environ mental	ECV	Var Genoty pic	GCV	Var Phenoty pic	PCV	h2 (Broad Sense)	Genetic Advance 5%	Gen. Adv as % of Mean 5%
1	Days to 50% Flowering	0.497	1.738	4.724	5.361	5.22	5.636	90.489	4.259	10.506
2	Plant Height	50.083	7.14	300.946	17.503	351.029	18.904	85.733	33.089	33.386
3	No. of branches	0.097	9.725	1.512	38.474	1.609	39.684	93.994	2.456	76.839
4	1000 seed weight	0.054	8.038	0.154	13.527	0.208	15.735	73.906	0.694	23.956
5	No. of capsules/axil	0.004	5.357	0.412	54.112	0.416	54.377	99.029	1.316	110.929
6	Capsule length	0.015	5.001	0.099	12.883	0.114	13.82	86.905	0.604	24.741
7	Capsules per plant	7.372	5.563	563.459	48.636	570.831	48.953	98.709	48.582	99.541
8	No. of seeds per capsule	14.106	5.067	245.882	21.156	259.988	21.754	94.574	31.414	42.383
9	seed length	0.044	6.555	0.033	5.704	0.077	8.689	43.091	0.246	7.713
10	seed width	0.011	5.755	0.035	10.003	0.046	11.541	75.131	0.332	17.861
11	seed thickness	0.003	5.847	0.016	13.796	0.019	14.984	84.772	0.239	26.167
12	oil content	1.575	5.267	23.075	20.161	24.65	20.837	93.611	9.574	40.182
13	Seed Yield per plant	0.318	8.136	1.048	14.783	1.366	16.874	76.753	1.848	26.679

Table4: Cluster analysis

Cluster Group	No. of Genotypes	List of Genotypes
1 Cluster	46	ES-21086-2, DORG-BLSG-9, IC 511141, IC 204785, AGRA BALIK, TMV-6, YLM-4, YLM-66, IC 132828, EC 346665, TKG-22, CHAGATAM LOCAL, YLM-17, TMV-4, PHULE TIL-1, TMV-7, VINAYAK, VRI-2, B-67, KIS-304, EC 370712, EC 304231, DORG-60KRDS, IC 127622, CUMS-17, CHANDANA, CT-44, IC 500506, AKT-101, EVC-122, DORG-3052, YLM-11, IC 500463, MADHAVI, ANAMIDI 74, IC 204550, CT-35, JLT-7, GT-10, IC 204248, RT-372, CT-50, DORG-B7-11, DORG-135-011, JLT-408, T-78
2 Cluster	6	IC 500448, SWETHA, VRI-1, EC-208652, IC 511151, IC 500393
3 Cluster	1	IC 129908
4 Cluster	1	DORG-37-11
5 Cluster	1	EC 346829
6 Cluster	3	EC 301961, EC 346370, RT-351
7 Cluster	1	CT-51
8 Cluster	1	RT-125

Table 5: Inter and Intra-cluster distances

Cluster Distances								
	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	73.28	165.27	140.04	140.28	179.48	968.89	204.99	851.20
Cluster 2	165.27	108.56	308.13	244.81	287.09	732.74	267.97	975.53
Cluster 3	140.04	308.13	0.00	232.23	373.83	1236.96	331.78	988.89
Cluster 4	140.28	244.81	232.23	0.00	292.34	1140.00	296.89	951.05
Cluster 5	179.48	287.09	373.83	292.34	0.00	1142.04	305.72	1004.14
Cluster 6	968.89	732.74	1236.96	1140.00	1142.04	152.00	452.41	491.31
Cluster 7	204.99	267.97	331.78	296.89	305.72	452.41	0.00	274.30
Cluster 8	851.20	975.53	988.89	951.05	1004.14	491.31	274.30	0.00

Table 6: Cluster Means: Tocher method

	Days to 50% Flowering	Plant Height	No. of branches	1000 seed weight	No. of capsules axil	Capsule leng	Capsules per plant	No. of seeds per capsule	seed length	seed width	seed thickness	oil content	Seed Yield p plant
Cluster 1	40.53	98.97	3.01	2.91	1.00	2.46	42.14	73.68	3.19	1.88	0.92	24.41	6.92
Cluster 2	41.56	104.73	4.23	2.55	1.00	2.24	79.40	73.58	3.13	1.80	0.83	20.71	7.12
Cluster 3	39.33	67.53	0.20	2.35	1.00	2.18	26.00	29.33	3.14	1.83	0.86	25.44	5.83
Cluster 4	43.67	109.33	2.53	3.12	1.00	2.79	33.73	98.13	3.32	1.89	0.81	6.12	4.84
Cluster 5	37.67	91.20	3.27	3.37	1.00	3.15	49.80	109.53	3.40	2.40	1.52	29.97	7.64
Cluster 6	40.33	104.56	5.71	3.17	3.33	2.23	110.82	69.00	3.11	1.61	0.81	23.44	7.04
Cluster 7	39.33	100.73	2.80	3.21	2.33	2.76	48.34	84.47	3.49	2.01	0.89	25.73	7.46

Cluster 8	37.67	83.27	2.20	3.18	3.87	2.40	23.07	87.87	3.35	1.66	0.90	24.76	7.79
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Table7: Percent contribution of each character towards diversity

Sl.no	Source	Contribution %	Times ranked 1st
1	Days to 50% Flowering	5.88	104
2	Plant Height	1.92	34
3	No. of branches	7.01	124
4	1000 seed weight	0.85	15
5	No. of capsules/axil	15.03	266
6	Capsule length	5.65	100
7	Capsules per plant	30.85	546
8	No. of seeds per capsule	13.79	244
9	seed length	0.45	8
10	seed width	0.51	9
11	seed thickness	4.24	75
12	oil content	11.07	196
13	Seed Yield per plant	2.77	49

Fig1: Intra and Inter cluster distance in Sesame

