Int.J.Curr.Microbiol.App.Sci (2017) *6*(9): 3133-3139

International Journal of Current Microbiology and Applied Sciences
ISSN: 2319-7706 **Volume 6 Number 9 (2017) pp. 3133-3139**
Journal homepage: http://www.ijcmas.com

Original Research Article https://doi.org/10.20546/ijcmas.2017.609.387

Genetic Divergence of Advanced Mutant Breeding Lines, In Sesame (*Sesamum indicum* L.) Assessed Through D^2 Statistics

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Keywords

Sesame, Advanced mutant breeding lines, D^2 analysis, Genetic diversity, Clusters.

Article Info

Accepted:
28 August 2017
Available Online:
10 September 2017

A B S T R A C T

Genetic divergence of 100 sesame (*Sesamum indicum* L.) advanced breeding lines was assessed using Mahalanobis's D^2 method and the lines were grouped into 12 clusters. Cluster-I was the biggest with 76 genotypes followed by cluster-III with 14 genotypes. Ten clusters (Cluster II, IV, V, VI, VII, VIII, IX, X, XI, XII) were solitary in nature. The intra cluster distance was maximum in cluster-III though it had only 14 entries, cluster-I was lowest despite 76 entries. Inter cluster distance was maximum between cluster-III and cluster-XII. The cluster means estimated for 11 traits revealed that the cluster-VI recorded lowest and cluster-IV registered highest mean values for most of the characters studied. Distance from ground to first capsule contributed maximum (54 %) to divergence followed by days to 50 per cent flowering (18 %), number of capsules per plant (7 %), days to maturity, indicated that distance of capsule bearing from ground alone trait could explain ≈ 55 per cent of variation. These traits can be utilized for future crop improvement program.

Introduction

Sesame (*Sesamum indicum* L.) is the oldest indigenous oil crops with longest history of its cultivation in India. India is still the world leader with maximum (25.8 %) production from the largest (29.8 %) area and highest export (40 %) of seeds of sesame. In India, sesame is being grown over an area of 16.67 lakh hectares with production of 6.57 lakh tonnes and productivity of 460 kg/ha (Anon., 2014). The lower productivity of this crop is due to cultivation of low yielding cultivars which are highly susceptible to diseases and pests and grown on marginal land with poor adoption of improved package of practices. Systematic breeding efforts are necessary to evolve high yielding sesame cultivars.

To achieve this, information about the nature and magnitude of genetic divergence in a given set of genotypes is essential for selection of diverse parents which upon hybridization lead to realization of a wide spectrum of gene recombinations for quantitatively inherited traits (Shekhawat *et al.*, 2013). In addition, transgressive segregations cannot be precluded. Germplasm, collections from different geographical regions are one set of genotypes subjected to divergence analysis, in addition hybridization and mutation breeding can also through segregants that are genetically diverse. Multivariate analysis by means of Mahalanobis's D^2 statistic is a powerful tool

in quantifying the degree of divergence at phenotypic level in most crops *vis a vis* sesame. Hence, the present investigation was undertaken to study the genetic diversity principally available in advanced mutant breeding lines along with a few collections, checks, parents, RILs that were maintained in the Department.

Materials and Methods

In the present study, 100 advanced breeding lines (67 advanced mutant lines, 12 RIL's, 5 checks, 4 collections, 7 varieties, 3 parents, 2 land races) were grown in a 10 x 10 Simple Lattice Design with two replications. Each breeding line was sown in three rows of 5m length with spacing of 30 cm between rows and 10 cm between plants during *kharif* 2015 at Agriculture College, Raichur (Karnataka). All the recommended practices were followed to raise a good crop. Five plants were chosen at random in each entry separately, in replications, and recorded observation for traits *viz*., days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of capsules/plant, distance from ground to first capsule (cm), capsule length (cm), number of seeds/capsule, capsule weight (g), test weight (g), and seed yield/plant (g). Although multivariate analysis was completed utilizing Mahalanobis (1936) D^2 statistics and genotypes were grouped into different clusters following Tocher's method as described by Rao (1952), INDOSTAT was the statistical package used to analyze the data. Contribution of each character towards genetic divergence was estimated from the number of times each character appeared in first rank.

Results and Discussions

Genetic diversity is the basic requirement for successful breeding program. Collection and evaluation of genotypes of any crop is a pre-requisite for whichever breeding program, which provides a greater scope for exploiting genetic diversity. The multivariate analysis (D^2) is a powerful tool to measure the genetic divergence within a set of genotypes (Murthy and Arunachalam, 1966) and generally used to quantify the divergence across land races, germplasm, segregants and even wild species. The present study was planned to examine the amount of genetic divergence in 100 advanced breeding lines of sesame in general and 67 stabilized advanced mutant lines in particular derived through induced mutagenesis.

The per cent contribution of different traits to the total divergence, when considered, the distance from ground to first capsule (54 %) had maximum contribution towards the total divergence followed by number of capsules/plant (18 %), days to maturity (7 %), number of seeds/ capsule (6 %), days to 50 per cent flowering (6 %), seed yield per plant (3 %) and capsule length (2 %). These observations were in accordance with observations of Narayanan and Murugan, (2013) for number of capsules/plant, days to 50 per cent flowering, seed yield/plant. Intriguingly, distance from ground to first capsule, number of capsules per plant, days to maturity, number of seeds per capsule and days to 50 per cent flowering could explain > 90 percent of variation in total variation. Other characters had very less contribution to total divergence. From the analysis it can be concluded that distance from ground to first capsule is a single character that can be considered for selection (Table 1). Incidentally genotypes that had shorter distance between ground and first capsules were high yielders. Further, most land races bear pods at a greater distance put forth more vegetative growth hence low yielders.

Using Tocher's procedure, 100 advanced breeding lines were grouped into 12 clusters

(Table 2), among these, cluster I was the largest and consists of 76 advanced breeding lines (54 mutants, 9 RIL's, 6 varieties, 3 collection, 2 checks and one each of parents and land races) followed by cluster-III with 14 advanced breeding lines (7 mutants, 3 checks and one each of land race, variety, collection and RIL). Rest all clusters (cluster II, IV, V, VI, VII, VIII, IX, X, XI, XII) had solitary entries. Similar results have been reported by Johnjoel *et al.,* (1998) and Gupta *et al.,* (2001).

Formation of more clusters in general and solitary clusters in particular is an indicative of existence of enormous amounts of diversity among the set of genotypes.

The genotypes that fall into solitary clusters more often have some unique characters which make them divergent. Additionally, the genotypes in a single cluster exhibit narrow range of genetic diversity among them, while between clusters indicate a wider range of variability depending on the intra and inter cluster distances. The pattern of group constellations proved that significant amounts of variability existed.

Maximum intra cluster distance was recorded for cluster-III (10.52) followed by cluster-I (9.92) revealing presence of divergent genotypes within different clusters (Table 3). Because of solitary cluster nature, the intra cluster distance for cluster II, IV, V, VI, VII, VIII, IX, X, XI and XII was zero. The inter cluster distance ranged from 8.32 cm to 30.93 cm. The highest inter cluster distance was recorded between cluster-III and XII. The maximum inter cluster distance suggest that the genotypes belonging to these clusters, if chosen for hybridization, are likely to throughout highly heterotic hybrids or broad spectrum of variability in subsequent generations or even a chance to recover transgressive segregants for specific characters concerned (Ghaderi *et al.,* 1984). Contrary, less heterotic and lower heritability cannot be precluded owing to higher sterility. More often these theoretical predictions are rarely experimented. Lowest cluster distance was measured from cluster-II and III; indicate the closer relationship among the genotypes between these clusters. The genetic divergence is computed based on the similarity for the traits between two genotypes.

Table.1 Contribution of each trait towards divergence

Sl. No.	Source	Times Ranked 1st	Contribution %	Cumulative
1	Distance from ground to first capsule	2692	54	54
2	Number of capsules per plant	877	18	72
3	Days to maturity	366	7	79
4	Number of seeds per capsule	294	6	85
5	Days to 50 % flowering	272	6	91
6	Seed yield per plant	152	3	94
7	Capsule length	111	2	96
8	Number of branches per plant	68	1	97
9	Plant height	55	1	98
10	Test weight	42	1	99
11	Capsule weight	21	1	100

Table.2 Clustering pattern of one hundred advanced breeding lines of sesame

Cluster No.	Entries	Compo-sition	No. of Entries	Advanced mutant breeding lines + collections + landraces+RIL's + Parents + Checks				
I	76	Mutants generated through BARC/ BRNS Project	54	$10KRE_8$-1 $10KRE_8$-2 $10KRE_8$-3 30KRDS-1-3 30KRDS-1-4 30KRDS-1-8 30KRDS-1-9 30KRDS-1-10 30KRDS-1-11 30KRDS-1-14 30KRDS-1-15	30KRDS-1-16 30KRDS-1-17 30KRDS-1-18 30KRDS-1-19 30KRDS -1-20 30KRDS-1-21 30KRDS-1-22 30KRDS-1-23 30KRDS-1-24 30KRDS-1-25 30KRDS-1-26	30KRDS-1-27, 30KRDS-1-30 30KRDS-1-31 40KR E_8-1 $E_8$40KR-2 $E_8$40KR-3 60KRDS-1-1 60KRDS-1-2 $60KRE_8$-1-2 $60KRE_8$-1-3	$60KRE_8$-1-4 $60KRE_8$-1-5 $60KRE_8$-1-6 $60KRE_8$-1-9 $60KRE_8$-1-10 $E_8$50KR-2 $50KRE_8$-3 $R_6$2nd Block (2)-$P_3B_1P_2$ -(IP) $R_6$6th Block127-$8P_2B_1P_9$	R_6 135-(162) 4- $P_2B_1P_2$ $R_6$135-7-$P_2B_2P_9$ RCR-L0KR II13L6 to 8 locule -7 II13L6to8locule-2 $R_5$1st Block, $R_5$5th Block108 $R_5$5th Block112 IISL-2, IISL-3 LW, LR, L-2
		Varieties	6	TKG-22, OSC-79, OSC-560-1, OSC-560-2, SSD-22, SSD-7				
		Collections	3	Mall-2, Mall-3, N-8				
		Land race	1	Indi taluk-2				
		RIL's	9	32, 38, 82, 162, 173, 194, 198, 188, 182				
		Parent	1	TNL (Phyllody Resistant)				
		Checks	2	Swetha Til, DS-1				
II	1	RIL	1	73				
III	14	Mutants	7	30KRDS-1-1, $60KRE_8$-1-7, $50KRE_8$-1, 30KRDS-1-29, 30KRDS-1-12, LW-2, IISL-4				
		Variety	1	Hima				
		Collections	1	Mall-1				
		Land race	1	Indi taluk-1				
		RIL	1	196				
		Check	3	Rajeshwari, DSS-9-1, DSS-9-2				
IV	1	Mutant	1	$60KRE_8$-1-8				
V	1	Mutant	1	30KRDS-1-7				
VI	1	Parent	1	Kanakapura Local				
VII	1	Mutant	1	$60KRE_8$-1-1				
VIII	1	Mutant	1	30KRDS-1-28				
IX	1	Mutant	1	30KRDS-1-5				
X	1	Mutant	1	30KRDS-1-13				
XI	1	RIL	1	SC-50				
XII	1	Parent	1	RT-273 (Alternaria Resistant)				

Table.3 Average intra (diagonal) and inter cluster distance of one hundred advanced breeding lines of sesame

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**9.92**	12.42	15.53	12.51	12.10	12.80	13.65	12.54	13.83	14.47	13.35	20.56
II		**0**	8.32	12.77	14.40	13.75	20.26	14.70	9.63	17.68	14.69	29.17
III			**10.52**	17.51	17.27	14.73	23.38	18.92	14.28	21.48	15.83	30.93
IV				**0**	14.44	19.48	16.40	8.49	10.62	9.37	18.07	24.87
V					**0**	15.58	12.78	15.72	18.69	14.18	20.34	19.27
VI						**0**	16.02	19.25	18.25	22.14	11.69	21.78
VII							**0**	16.90	21.19	16.8	19.95	12.48
VIII								**0**	9.68	7.42	16.78	23.62
IX									**0**	13.95	14.65	29.87
X										**0**	20.97	22.64
XI											**0**	24.47
XII												**0**

Table.4 Cluster wise means of 100 advanced breeding lines of sesame for morphological, yield and yield attributing traits

Cluster No	Days to 50% flowering	Days to maturity	Plant height	Number of branches/ plant	Number of capsules/ plant	Distance from ground to first capsule	Capsule length	Number of seeds/ capsule	Capsule weight	Test weight	Seed yield/plant	Overall Score	Rank
I	41.67 ± 2.40 (7)	88.40 ± 2.83 (6)	81.59 ± 13.93 (5)	3.16 ± 0.37 (6)	27.56 ± 5.42 (6)	40.20 ± 8.24 (5)	2.50 ± 0.17 (5)	66.80 ± 7.49 (5)	0.28 ± 0.04 (6)	2.80 ± 0.40 (6)	0.93 ± 0.36 (6)	68	6
II	41.00 ± 0 (5)	91.00 ± 0 (8)	94.00 ± 0 (11)	3.55 ± 0 (7)	29.20 ± 0 (5)	55.50 ± 0 (10)	2.54 ± 0 (4)	6868.25 ± 0 (4)	0.29 ± 0 (5)	3.09 ± 0 (5)	1.13 ± 0 (5)	86	7
III	41.75 ± 1.79 (8)	88.11 ± 3.84 (5)	100.54± 14.62 (12)	2.76 ± 1 (4)	24.38 ± 8.35 (9)	58.38 ± 8.42 (11)	2.36 ± 0.32 (7)	62.25 ± 12.18 (8)	0.25 ± 0.05 (9)	2.68 ± 0.63 (7)	0.76 ± 0.55 (7)	66	5
IV	42.00 ± 0 (9)	93.50 ± 0 (10)	91.80± 0(10)	4.65 ± 0 (10)	40.75 ± 0 (1)	43.00 ± 0 (8)	2.69 ± 0 (3)	92.00 ± 0 (1)	0.39 ± 0 (1)	3.95 ± 0 (1)	1.99 ± 0 (4)	109	11
V	50.50 ± 0 (12)	95.50 ± 0 (12)	90.75 ± 0 (9)	3.10 ± 0 (5)	22.50 ± 0 (10)	41.10 ± 0 (6)	2.19 ± 0 (8)	58.40 ± 0 (9)	0.27 ± 0 (7)	2.58 ± 0 (9)	0.61 ± 0 (10)	64	4
VI	37.50 ± 0 (2)	85.00 ± 0 (2)	56.85 ± 0 (2)	2.40 ± 0 (1)	13.5 ± 0 (12)	42.00 ± 0 (7)	1.95 ± 0 (9)	50.20 ± 0 (11)	0.17 ± 0 (10)	1.95 ± 0 (11)	0.27 ± 0 (11)	23	1
VII	40.50 ± 0 (4)	95.00 ± 0 (11)	56.75 ± 0 (1)	4.00 ± 0 (8)	24.50 ± 0 (8)	24.35 ± 0 (2)	2.38 ± 0 (6)	62.50 ± 0 (7)	0.26 ± 0 (8)	2.56 ± 0 (10)	0.68 ± 0 (9)	51	3
VIII	41.50 ± 0 (6)	88.50 ± 0 (7)	77.25 ± 0 (4)	4.45 ± 0 (9)	39.50 ± 0 (2)	37.35 ± 0 (4)	3.05 ± 0 (2)	89.00 ± 0 (2)	0.37 ± 0 (2)	3.75 ± 0 (3)	2.34 ± 0 (1)	91	9
IX	38.50 ± 0 (3)	88.00 ± 0 (4)	87.35 ± 0 (6)	4.90 ± 0 (11)	38.00 ± 0 (3)	47.90 ± 0 (9)	3.25 ± 0 (1)	87.50 ± 0 (3)	0.32 ± 0 (4)	3.65 ± 0 (4)	2.03 ± 0 (3)	88	8
X	48.50 ± 0 (11)	92.00 ± 0 (9)	91.7 ± 0 (8)	4.65 ± 0 (10)	37.00 ± 0 (4)	34.50 ± 0 (3)	3.05 ± 0 (2)	92.00 ± 0 (1)	0.34 ± 0 (3)	3.80 ± 0 (2)	2.09 ± 0 (2)	100	10
XI	35.00 ± 0 (1)	75.50 ± 0 (1)	90.15 ± 0 (7)	2.70 ± 0 (3)	26.75 ± 0 (7)	42.00 ± 0 (7)	2.54 ± 0 (4)	64.00 ± 0 (6)	0.26 ± 0 (8)	2.63 ± 0 (8)	0.70 ± 0 (8)	51	3
XII	44.50 ± 0 (10)	86.00 ± 0 (3)	66.75 ± 0 (3)	2.50 ± 0 (2)	18.25 ± 0 (11)	12.50 ± 0 (1)	1.94 ± 0 (10)	54.10 ± 0 (10)	0.27 ± 0 (7)	1.93 ± 0 (12)	0.25 ± 0 (11)	30	2

Values in parentheses indicate trait specific ranking of Clusters based on cluster means

Cluster mean analysis indicated that cluster IV was solitary and showed high mean values for number of capsules/plant, number of seeds/capsule and test weight. Cluster-VI was solitary and showed lower mean values for number of branches/plant, number of capsules/plant, number of seeds/capsule and capsule weight. Cluster -X was solitary and had an entry that was earliest to reach 50 per cent flowering and even to maturity. Cluster-XII was also solitary and showed low mean values for distance from ground to first capsule, capsule length, test weight and seed yield/plant. Solanki and Gupta (2001), Kumaresan and Nadarajan (2003) and Jadhav and Mohrir (2013) also reported the presence of solitary clusters. Based on the overall score across the eleven traits, the clusters were ranked. The cluster-VI with a single genotype ranked first and this genotype appears to be most potential one (Table 4). In addition the cluster- IV (1 genotype), VII (1 genotype) and V (1 genotype), which ranked 2^{nd}, 3^{rd}, and 4^{th} respectively were also promising and these genotypes can be considered and selected for further work. In breeding programs, parents having high yield potential with wide genetic diversity are likely to yield superior transgressive segregants within a short period (Maurya and Singh, 1977). In the present study, two clusters *viz*., cluster-III and XII recorded highest inter cluster distance; hence crosses may be made between these two clusters in order to obtain transgressive segregants in desired direction. Exploitation of heterosis through hybrids production in sesame is still in infancy. High heterotic combinations can be realized through a systematic combinations of the genotypes from different clusters would be the next focus in research.

Acknowledgements

Corresponding author wish to acknowledge BARC/BRNS for a project; completed during 2010 and PC Unit, Jabalpur and GOK for financial support.

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How to cite this article:

Mahalaxmi K. Patil, R. Lokesha and Diwan, J.R. 2017. Genetic Divergence of Advanced Mutant Breeding Lines, In Sesame (*Sesamum indicum* L.) Assessed Through D^2 Statistics. *Int.J.Curr.Microbiol.App.Sci.* 6(9): 3133-3139. doi: https://doi.org/10.20546/ijcmas.2017.609.387