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Genetic divergence study among the germplasm of sesame (*Sesamum indicum* L.)

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Abstract
Sixty sesame genotypes including three checks, AKT-64, AKT-101 and PKV-NT-11 for eleven characters evaluated at three locations during summer 2018-19 to assess the seasonal genetic diversity present in the sesame germplasm based on the Mahalanobis D^2 statistics for the identification of genetically diverse and agronomically superior genotypes which may be further used in the hybridization programme. The pooled analysis of variance showed highly significant differences for all characters showing the presence of genetic variability. Clustering pattern indicated that grouping was not according to their origin. The Maximum intra cluster distance was found in cluster I (35.76) followed by cluster XII (35.64). The extreme inter-cluster distance was recorded between cluster XV and cluster XVI (243.36) indicating the maximum divergence between the clusters. Cluster XVI exhibited high mean value for number of branches per plant, 1000-seed weight, oil content and seed yield per plant. Oil content (25.14%) showed maximum contribution.

Keywords: Sesame, germplasm, genetic divergence, D^2 statistics

Introduction

Sesame (*Sesamum indicum* L.) (2n = 26), also known as Til, it is one of the important oilseed crop of India and world. It is commonly known as "Queen of oilseeds". It plays an important role as an industrial food crop because of its high nutritional value. The seeds of sesame contain 40 to 56% oil, which contains significant amount of oleic and linoleic acids. Sesame is the most neglected oil seed crop grown on marginal lands under poor management practices resulting in low yields. Additionally, the poor yield is due to the unavailability of cultivars to suit the diverse agro-climatic conditions. Hence development of improved high yielding cultivars adapted to local conditions has become top priority. The objective of this research was identifying suitable diverse parents for hybridization using the Mahalanobis D^2 statistics is a unique tool to identifying the degree of genetic divergence in an experimental population and characters contributing to it.

Material and Methods

The experiment material comprises of sixty diverse germplasm lines of sesame including three checks evaluated during summer 2018-19 at experimental field of Department of Agricultural Botany, Dr. P.D.K.V. Akola, Head of Section of Agricultural Botany, College of Agriculture, Nagpur and Agriculture Technical School, Selsura, Dist. Wardha, Maharashtra. Randomised Block Design was adopted with three replications. Each genotype was raised in 3 rows of 3 metre long, adopting a spacing of 30 cm between rows and 10cm between plants. Recommended package of practices was followed to raise good and healthy crop stand.

Five competitive plants were randomly selected for recording the observations *viz.*, plant height, number of branches per plant, number of capsules per plant, capsule breadth, length of capsule, 1000-seed weight, number of seed per capsule, oil content and seed yield per plant. Days to 50% flowering and days to maturity were noted on plot basis.

The mean of five plants from three location was subjected to statistical analysis as the pooled data. Genetic diversity was studied by Mahalanobis (1936) [4] D^2 statistics and clustering of genotypes was done on the basis of D^2 values according to Tocher's method as described by Rao (1952) [9]. Statistical analysis was done by INDOSTAT program.

Result and Discussion

The season wise pooled analysis of variance showed the presence of significant variability among the genotypes for the seed yield per plant and other contributing characters under studied.

Based on Mahalanobis D^2 analysis all the genotypes grouped into seventeen clusters. The clustering was random and independent, cluster I was the biggest cluster comprising 42 sesame genotypes and other clusters were having solitary genotype (Table 1). Clustering of genotypes was not associated with the geographical spreading and was mainly grouped due to their phenotypically differences. Thus, showing evidence that geographical isolation is not the only factor causing genetic diversity in sesame. Similar result reported by Tanwar and Bisen (2018) [13] and Ramprasad *et al*. (2019) [8].

Intra cluster D^2 values (Table 2) ranged from 0 to 35.76. The Maximum intra cluster distance was found in cluster I (35.76) followed by cluster XII (35.64), representing that some quantity of diversity still existed among the genotypes of this cluster. Similar result reported by Tanwar and Bisen (2018) [13] and Sirisha *et al*. (2020) [10].

The inter cluster distance was higher than intra cluster distance, indicating the presence of wide genetic diversity among the genotypes under study. Maximum inter cluster distance was exhibited between cluster XV and XVI (243.36) followed by cluster XVI and XVII (174.50) and cluster V and XVI (169.78) (Table 2). Similar result previously reported by Parameshwarappa *et al*. (2010) [6]; Patil *et al*. (2017) [7] and Soundharya *et al*. (2017) [11]. Larger the distance between two clusters, broader the genetic diversity between the genotypes. Keeping this in sight, it is indicated that hybridization between the genotypes IS-562-A of cluster XV with GRT-8622 of cluster XVI; GRT-8622 of cluster XVI with IS-520 of cluster XVII and EC-370442 of cluster V with GRT-8622 of cluster XVI are predictable to yield highly heterotic hybrids. The genotypes of these clusters may be used as parentages in the crossing programme to create breeding material with high diversity and hybrids.

The cluster means (Table 3) shown that considerable differences existed for all the characters under study. The data showed that the cluster mean for days to 50% flowering was highest in cluster XIV (43.00) and the lowest in cluster XI (35.00). Days to maturity was highest in the cluster X (104.67) and lowest means in cluster XIII (90.00). Cluster VII recorded highest mean for plant height (136.87), whereas lowest in the cluster XI (101.93). Cluster XVI (3.20) recorded the highest number of branches per plant and the lowest in cluster XV (1.53). The number of capsules per plant was maximum in cluster XII (66.07) and lowest in cluster XV

(23.87). The highest mean for capsule breadth was in the cluster VI, XIII, and XIV (6.40 mm) while lowest for XVI (5.47). Cluster VI (2.67) exhibited highest length of capsule whereas in cluster XV (2.22) it was lowest. Maximum 1000-seed weight was recorded in cluster II (3.53), cluster XVI (3.53) and lowest in cluster VII (3.35). The maximum mean recorded in cluster XV (78.00) and minimum in cluster VII (62.27) for number of seeds per capsule. Highest mean recorded in cluster XVI (53.02) and cluster II (39.83) lowest for oil content. Cluster XVI (14.71) expressed the highest seed yield per plant and the lowest in cluster IV (5.82). The results show that selection of genotype with high cluster mean values for particular attribute might be used in the hybridization programme for enhancement of that character. Similar result of range for cluster mean has been reported by Parameshwarappa *et al*. (2010) [6] for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, 1000 seed weight and seed yield per plant and Patil *et al*. (2017) [7] for days to 50% flowering, days to maturity, plant height, number of branches per plant, number of capsules per plant, capsule length, number of seeds per capsule, capsule weight, test weight, and seed yield per plant.

The number of times that each of eleven characters appeared in first rank and its corresponding per cent contribution towards genetic divergence (Table 4). The results exhibited that oil content (25.14%) was highest contribution towards genetic divergence by taking 445 times ranking first, followed by number of capsules per plant (21.98%) by 389 times, plant height (12.60%) by 223 times, seed yield per plant (10.17%) by 180 times, number of seeds per capsule (7.63%) by 135 times, 1000-seed weight (6.33%) by 112 times, days to maturity (5.20%) by 92 times, days to 50% flowering (4.52%) by 80 times, number of branches per plant (4.41%) by 78 times, capsule of length (1.86%) by 33 times, capsule breadth (0.17%) by 3 times rank first to the genetic divergence in declining order. This result accordance with Tanwar and Bisen (2018) [13] for oil content; Chandra mohan (2014) [2] for number of capsules per plant; Kadir *et al*. (2001) [3] for plant height; Arpitha *et al*. for seed yield per plant; Navale *et al*. (2001) [5] for number of seed per capsule and Swapna *et al*. (2009) [12] for 1000-seed weight.

Out of eleven characters studied, six characters namely, oil content, number of capsules per plant, plant height, seed yield per plant, number of seed per capsule and 1000-seed weight together contributed 83.85% towards total divergence. Consequently, these characters should be given importance during cross breeding and selection of segregating populations for getting higher yield.

Table 1: Season wise (summer 2018-19) clustering pattern across the location (Akola, Nagpur and Selsura) among 60 germplasm lines of sesame by Tocher's method

Cluster number	Number of germplasm	Name of germplasm included in cluster
Cluster I	42	IC-203955, IC-204045, SI-2039-A, IC-203884, EC-370402, EC-370372, Tireendre Local, NIC-17868, EC- 370371, IS-93-B, DS-46-3, IC-203892, IC- 204062, IS-157-A, SI-3278, NIC-54-164-B, EC- 370430, EC- 370362, EC-370382, EC-370373, IC-204056, ES-46-A, SI-3299-A, IC-204059, IC- 203888, EC-370455, IC-203887, EC-370343, IC-204060, IC-203959, IC-203883, IC-204049, IS-24-A, SI-1782-A, GRT-839-A, EC-370354, JLS-709-1, IC-204037, NIC-8600-A, IC-204047, IC-203889, IC-203931
Cluster II	1	TKG-15-2-2
Cluster III	1	IC-204054
Cluster IV	1	IC-203886
Cluster V	1	EC-370442

Cluster VI	1	EC-370450
Cluster VII	1	IC-203920
Cluster VIII	1	EC-370374
Cluster IX	1	IC-203954
Cluster X	1	EC-370345
Cluster XI	1	IC-204063
Cluster XII	3	NIC-9852-A, PKV-NT-11, IC-204058
Cluster XIII	1	AKT-64
Cluster XIV	1	AKT-101
Cluster XV	1	IS-562-A
Cluster XVI	1	GRT-8622
Cluster XVII	1	IS-520

Table 2: Season wise (summer 2018-19) intra (diagonal) and inter cluster D^2 values over the location (Akola, Nagpur and Selsura) among 60 germplasm lines of sesame

Clusters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX	Cluster X	Cluster XI	Cluster XII	Cluster XIII	Cluster XIV	Cluster XV	Cluster XVI	Cluster XVII
Cluster I	35.76	56.10	52.27	49.98	47.89	48.02	47.75	55.65	51.98	49.56	52.13	71.74	56.55	76.21	83.54	118.16	82.08
Cluster II		0.00	85.56	109.83	82.81	91.97	77.62	27.77	45.16	56.40	30.80	54.46	68.06	101.20	88.92	126.56	85.93
Cluster III			0.00	96.24	30.58	64.00	49.00	108.37	84.09	85.19	86.68	101.81	93.90	100.20	65.12	153.51	97.42
Cluster IV				0.00	66.91	24.11	59.29	73.79	55.80	59.91	62.57	67.40	42.51	62.09	140.19	75.86	96.24
Cluster V					0.00	55.50	75.17	109.20	87.98	87.05	69.56	98.21	77.79	91.20	58.98	169.78	53.44
Cluster VI						0.00	42.12	75.69	50.98	53.58	58.37	58.06	37.45	79.57	101.81	92.74	118.16
Cluster VII							0.00	39.69	67.57	17.22	78.32	57.30	71.40	102.62	111.09	128.14	113.00
Cluster VIII								0.00	46.51	22.28	39.06	40.20	61.15	103.02	132.48	113.00	93.51
Cluster IX									0.00	70.39	24.70	37.70	60.06	82.08	114.28	55.95	78.32
Cluster X										0.00	77.62	49.00	67.73	100.80	119.90	130.19	119.03
Cluster XI											0.00	47.89	54.17	103.84	102.21	84.46	58.52
Cluster XII												35.64	72.93	100.20	155.00	71.06	91.58
Cluster XIII													0.00	28.84	80.46	105.06	129.05
Cluster XIV														0.00	118.37	108.99	133.86
Cluster XV															0.00	243.36	149.08
Cluster XVI																0.00	174.50
Cluster XVII																	0.00

Table 3: Season wise (summer 2018-19) cluster mean over the location (Akola, Nagpur and Selsura) for yield and yield contributing traits among 60 germplasm lines of sesame

Cluster Number	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of branches Plant⁻¹	No. of capsule Plant⁻¹	Capsule breadth (mm)	Length of capsule (cm)	1000 Seed weight (gm)	No. of seed capsule⁻¹	Oil content%	Seed yield Plant⁻¹ (gm)
Cluster I	37.63	101.41	110.31	2.00	39.28	6.00	2.37	3.45	65.08	45.77	7.94
Cluster II	38.33	102.67	111.27	2.20	53.07	6.07	2.34	3.53	68.93	39.83	11.09
Cluster III	37.33	101.00	123.87	2.80	31.67	5.93	2.27	3.40	66.67	44.92	6.48
Cluster IV	37.33	97.33	109.67	1.87	45.40	6.07	2.41	3.44	64.80	52.71	9.12
Cluster V	37.00	98.67	114.47	2.20	34.53	5.87	2.33	3.48	70.93	47.03	5.82
Cluster VI	35.33	95.67	124.47	2.13	43.47	6.40	2.67	3.43	71.73	49.70	9.66
Cluster VII	37.00	101.67	136.87	2.17	46.40	6.07	2.36	3.35	62.27	46.04	9.27
Cluster VIII	37.67	102.00	119.33	1.93	59.80	6.33	2.31	3.44	62.80	42.77	11.90
Cluster IX	38.33	104.33	105.33	2.53	57.13	6.00	2.49	3.39	71.20	46.93	12.44
Cluster X	38.33	104.67	134.87	1.67	48.93	6.33	2.37	3.47	63.73	45.40	9.94
Cluster XI	35.00	97.67	101.93	2.47	57.80	5.93	2.31	3.46	69.47	44.85	11.67
Cluster XII	38.67	102.56	129.69	2.62	66.07	6.27	2.42	3.48	70.00	47.39	13.53
Cluster XIII	37.67	90.00	108.4	1.73	42.73	6.40	2.39	3.43	70.13	46.10	9.85
Cluster XIV	43.00	94.00	104.07	2.00	38.67	6.40	2.28	3.45	66.53	47.77	8.72
Cluster XV	36.00	97.67	106.6	1.53	23.87	5.80	2.22	3.36	78.00	41.35	5.95
Cluster XVI	39.67	101.67	112.33	3.20	62.60	5.47	2.25	3.53	64.67	53.02	14.71
Cluster XVII	38.33	103.00	102.67	2.60	59.20	6.20	2.25	3.43	67.20	46.57	8.82

Table 4: Season wise (summer 2018-19) relative contribution of different characters toward genetic diversity over the location (Akola, Nagpur and Selsura) in 60 germplasm lines of sesame

Sr.no.	Characters	Times ranked 1st	Contribution (%)
1	Days to 50% flowering	80	4.52
2	Days to maturity	92	5.20
3	Plant height (cm)	223	12.60
4	Number of branches plant^{-1}	78	4.41
5	Number of capsules plant^{-1}	389	21.98
6	Capsule breadth (mm)	3	0.17
7	Length of capsule (cm)	33	1.86
8	1000 Seed weight (g)	112	6.33
9	Number of seed capsule^{-1}	135	7.63
10	Oil content (%)	445	25.14
11	Seed yield plant^{-1} (g)	180	10.17

References

1. Arpitha GD, Manonmani S, Viswanathan PL, Raveendran M. Genetic diversity study in germplasm lines of sesamum (*Sesamum indicum* L.). Electronic Journal of Plant Breeding. 2019;10(2):772-777.
2. Chandra Mohan Y. Variability and genetic divergence in sesame (*Sesamum indicum* L.). International Journal of Applied Biology and Pharmaceutical Technology. 2014;5(3):222-225.
3. Kadir MM, Ali MM, Islam MN, Golam Masum Akond ASM. Genetic diversity in sesame. Bangladesh Journal of Agricultural Research. 2001;26(1):131-135.
4. Mahalanobis PC. On the generalized distance in statistics. Proceedings of National Institute of Sciences. India. 1936;2:49-55.
5. Navale PA, Nimbalkar CA, Gandhi HT. Genetic divergence in sesame (*Sesamum indicum* L.). Journal of Maharashtra Agricultural University. 2001;26(2):144-146.
6. Parameshwarappa SG, Palakshappa MG, Salimath PM, Parameswarappa KO. Analysis of genetic divergence in sesame (*Sesamum indicum* L.). Karnataka Journal of Agricultural Sciences. 2010;23(2):227-230.
7. Patil MK, Lokesha R, Diwan JR. Genetic divergence of advanced mutant breeding lines, in sesame (*Sesamum indicum* L.); c2017.
8. Ramprasad E, Senthilvel S, Lal Jatothu J, Yamini KN, Singh Dangi K. Analysis of genetic diversity in sesame (*Sesamum indicum* L.) advanced breeding lines and varieties collected from major breeding centers in India. Electronic Journal of Plant Breeding. 2019;10(3):1269-1274.
9. Rao CR. Advanced Statistical Methods in Biometric Research. John Wiley Sons, New York; c1952. p. 390.
10. Sirisha ABM, Banu SKH, Saritha R. Genetic divergence studies using Mahalanobis D square analysis in sesame (*Sesamum indicum* L.) germplasm. International Journal of Current Microbiology and Applied Sciences. 2020;9(8):2224-2229.
11. Soundharya B, Hemalatha V, Shobha Rani T, Edukondalu B. Genetic divergence studies in sesame (*Sesamum indicum* L.) genotypes. International Journal of Current Microbiology and Applied Sciences. 2017;6(9):2615-2619.
12. Swapna J, Kumar PVR, Panduranga Rao C, Srinivasa Rao V. Genetic divergence in Sesame (*Sesamum indicum* L.). The Andhra Agricultural Journal. 2009;56(4):421-428.
13. Tanwar A, Rajani Bisen. Genetic divergence in light brown sesame germplasm. International Journal of Current Microbiology and Applied Sciences. 2018;6:1119-1124.