

GENETIC DIVERGENCE ANALYSIS IN SESAME [*Sesamum indicum* L.]

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ABSTRACT

*The present study was conducted at the Sagdividi Farm, Department of Seed Science and Technology, College of Agriculture, Junagadh Agricultural University, Junagadh during summer-2015 to assess the genetic diversity among 40 genotypes of sesame (*Sesamum indicum* L.). The genetic diversity analysis revealed the formation of three clusters indicated the existence of genetic diversity among the genotypes. The cluster I contained 36 and cluster II contained three genotypes from same origins, while cluster III possessed only one genotype. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that height to first capsule followed by number of capsules per leaf axil, length of capsule, seed yield per plant and number of seeds per capsule contributed maximum towards total genetic divergence. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster I with the genotypes of cluster II and cluster III, which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in sesame.*

KEY WORDS: Genetic divergence, D^2 statistic, *Sesamum indicum* L.

INTRODUCTION

Sesame (*Sesamum indicum* L., $2n = 26$) is a very ancient oilseed crop grown next to groundnut, rapeseed and mustard in India. It belongs to the order *Tubiflorae*, family *Pedaliaceae*. It is basically considered a crop of tropical and sub-tropical regions, but it has also spread to the temperate parts of the world. Africa has been considered to be the primary centre of origin of sesame and it spread early through West Asia to India, China and Japan, which themselves became secondary distribution centers (Weiss, 1983). Sesame is a self pollinated crop

with an average cross pollination to the extent of 4 to 5 per cent. However, the amount of out crossing ranges from 0 to 50 per cent depending upon the pressure of pollinating agents, whereas wind plays no part in natural cross pollination. Sesame is one of the oldest oilseed crops from which oil was extracted by the ancient Hindus, which was used for certain ritual purposes (Weiss, 1983).

At present, Myanmar is the largest producer of sesame seed in the world followed by India, China, Turkey and Pakistan in Asia; Egypt and Sudan in Africa; Greece in

Europe; Venezuela, Argentina and Columbia in South America; Nicaragua and El-Salvador in Central America; and Mexico and the U.S.A. in North America. India is still the world leader with maximum (25.80 %) production from the largest (29.30 %) area and highest (40.00 %) export of sesame in the world. In India, during 2013-14, sesame is cultivated in an area of 16.67 lakh ha with a production of 6.75 lakh tones annually and productivity of 405 kg/ha (Anonymous, 2014). Being the fourth important oilseed crop in Indian agriculture after groundnut, rapeseed and mustard, it is widely cultivated in the states of Uttar Pradesh, Rajasthan, Orissa, Gujarat, Andhra Pradesh, Tamil Nadu, Karnataka, West Bengal, Bihar and Assam. In Gujarat, during 2013-14, sesame is cultivated in an area of 2.36 lakh ha with a production of 1.24 lakh tones and productivity of 525 kg/ha (Anonymous, 2014). This crop is generally cultivated as sole or mixed crop during *kharif*, semi-*rabi* and summer season. The productivity of sesame is very low as compared to other oilseeds hence, it is necessary to raise the productivity and thereby total oilseeds production in order to meet edible oil requirements of the country.

The genetic diversity is a crucial factor in determining the success of hybridization programme and its importance in crop improvement has long been recognized by breeder. The more diverse parents within overall limits of fitness, the greater are the chances of heterotic F_1 's and broad spectrum of variability in segregating generation (Arunachalam, 1981; Falconer, 1989). Yield and yield contributing characters are controlled by polygenes and highly influenced by environment; the exploration of genetic variability in available germplasms is prerequisite.

Therefore, evaluation of germplasm to local conditions is very important. Genetic diversity is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding (Mukhtar *et al.*, 2002). Genetic diversity is very important factor for any hybridization programme aiming at genetic improvement of yield especially in self pollinated crops (Joshi and Dhawan, 1966). Different methods have been used to assess genetic diversity, of which Mahalanobis (1936) D^2 statistic is the most efficient tool for estimating genetic divergence.

MATERIALS AND METHODS

The study was conducted at the Sagdividi Farm, Department of Seed Science and Technology, College of Agriculture, Junagadh Agricultural University, Junagadh during summer-2015 to assess the genetic diversity among 40 genotypes of sesame (*Sesamum indicum* L.). The germplasm were selected from the gene pool maintained at Agricultural Research Station, Junagadh Agricultural University, Amreli, Gujarat. Forty genotypes of sesame were sown in a Randomized Block Design (RBD) with three replications. Each genotype was accommodated in a single row of 4.0 m length with a spacing of 45 cm between rows and 15 cm between plants within the row. The experiment was surrounded by two guard rows to avoid damage and border effects. Recommended agronomic practices were followed to raise a good crop. Observations were recorded from five randomly selected plants from each genotype on different characters viz., plant height (cm), number of branches per plant, number of capsules per plant, height to first capsule (cm), length of capsule (cm), width of

capsule (mm), number of capsules per leaf axil, number of seeds per capsule, 1000 seed weight (g), seed yield per plant (g) and harvest index (%). Days to flowering and days to maturity was measured on plot basis. The data were analysed as per the multivariate analysis of genetic divergence using Mahalanobis (1936) D^2 statistic. The genotypes were grouped into different clusters following the Tocher's method (Rao, 1952).

RESULTS AND DISCUSSION

The analysis of variance showed significant difference among the genotypes for the characters studied. On the basis of D^2 values, 40 genotypes were grouped into 3 clusters (Table 1). This indicated the existence of genetic diversity among the genotypes. The cluster I contained 36 and cluster II contained three genotypes from same origins, while cluster III possessed only one genotype. In general, intra-cluster distance values were lower than the inter-cluster distances. Thus, the genotypes included within a cluster tended to diverse less from each other. The lowest intra-cluster distance was in cluster I ($D = 9.69$), whereas the highest intra-cluster distance was in cluster II ($D=10.45$) (Table 2). The maximum inter-cluster distance (D) was observed between clusters I and II ($D=39.75$) followed by clusters I and III ($D=26.06$) and II and III ($D=24.97$). The genotypes belonging to different clusters separated by high statistical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates. In this context, the genotypes from cluster I can be crossed with II and III in hybridization programme for obtaining a wide range of variation among the segregants.

A wide range of variation for several characters among single as well

as multi-genotype clusters was observed. However, the differences were clear for plant height, number of capsules per plant, height to first capsule, length of capsule, number of capsules per leaf axil, seed yield per plant and harvest index. The present findings are in conformity with those reported earlier in sesame by Kumhar *et al.* (2008) Parameshwarappa *et al.* (2009) and Jadhav and Mohrir (2012). The clustering pattern could be utilized in selecting the parents and deciding the cross combinations which may generate the highest possible variability for various traits.

The genotypes with high values of any cluster can be used in hybridization programme for further selection and improvement. In the present study, cluster I noted high cluster mean values for number of branches per plant (Table 3). Cluster II was good for length of capsule, width of capsule and number of capsules per leaf axil. Cluster III expressed the highest cluster mean values for days to flowering, days to maturity, plant height, number of capsules per plant, height to first capsule, number of seeds per capsule, 1000 seed weight, seed yield per plant and harvest index. Therefore, intercrossing of genotypes involved in these cluster would be useful for inducing variability in respective characters and their rational improvement for increasing the seed yield in sesame. High cluster means for various characters were also reported by Kumhar and Solanki (2009), Begum *et al.* (2011), Parameshwarappa *et al.* (2012) and Tripathi *et al.* (2013).

The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that height to first capsule followed by number of capsules per leaf axil, length of

capsule, seed yield per plant and number of seeds per capsule contributed maximum towards total genetic divergence in the present study, whereas remaining characters, number of capsules per plant, number of branches per plant, width of capsule, harvest index, days to maturity, plant height, days to flowering and 1000 seed weight contributed less towards total genetic divergence (Table 3). The present finding are supported with earlier reports of Kumhar and Solanki (2009), Bandila *et al.* (2011), Parameshwarappa *et al.* (2012), Narayanan and Murugan (2013) and Tripathi *et al.* (2013).

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981). Therefore, based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster I with the genotypes of cluster II and cluster III, which may lead to the generation of broad spectrum of favourable genetic variability for yield improvement in sesame.

REFERENCES

- Anonymous (2014). Status Paper on Oilseeds. Oilseeds Division, Department of Agriculture and Cooperation, Ministry of Agriculture, Government of India, New Delhi (http://nmoop.gov.in/Publication/Status_Paper.pdf).
- Arunachalam, V. (1981). Genetic distances in plant breeding. *Indian J. Genet.*, **41**: 226-236.
- Bandila, S.; Ghanta, A.; Natrajan, S. and Subramoniam, S. (2011). Determination of genetic variation in Indian sesame (*Sesamum indicum*) genotypes for agro-morphological traits. *J. Res. Agril. Sci.*, **7**(2): 88-99.
- Begum, S.; Islam, M. A.; Husna, A.; Hafiz, T. B. and Ratna, M. (2011). Genetic diversity analysis in sesame (*S. indicum* L.). *SAARC J. Agri.*, **9**(2): 65-71.
- Falconer, D. S. (1989). An Introduction to Quantitative Genetics. Longman, New York.
- Jadhav, R. S. and Mohrir, M. N. (2012). Genetic variability studies for quantitative traits in sesame (*Sesamum indicum* L.). *Electronic J. Plant Breed.*, **3**(4): 1009-1011.
- Joshi, A. B. and Dhawan, N. L. (1966). Genetic improvement of yield with special reference to self-fertilizing crops. *Indian J. Genet. Pl. Breed.*, **26**: 101-113.
- Kumhar, S. R. and Solanki, Z. S. (2009). Genetic diversity and variability in sesame, *Sesamum indicum* L. *J. Oilseeds Res.*, **26**(2): 162-164.
- Kumhar, S. R.; Solanki, Z. S. and Choudhary, B. R. (2008). Studies on genetic variability, character association and path coefficient analysis in sesame (*Sesamum indicum* L.). *Indian J. Pl. Genet. Resources*, **21**(2): 90-92.
- Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proc. Nat. Inst. Sci.*, **2**: 49-55.
- Mukhtar, M. S.; Rahman, M. and Zafar, Y. (2002). Assessment of genetic diversity among wheat (*Triticum aestivum* L.) cultivars from a range of

- localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica*, **128**: 417-425.
- Narayanan, R. and Murugan, S. (2013). Genetic divergence and stability analysis in sesame (*Sesamum indicum*). *Int. J. Adv. Doctoral Res.*, **2**(11): 16-19.
- Parameshwarappa, S. G.; Palakshappa, M. G.; Salimath, P. M and Parameshwarappa, K. G. (2009). Studies on genetic variability and character association in germplasm collection of sesame (*Sesamum indicum* L.). *Karnataka J. Agric. Sci.*, **22**(2): 252-254.
- Parameshwarappa, S. G.; Palakshappa, M. G. and Shinde, Gayatree G. (2012). Studies on genetic divergence for yield and yield attributing traits in sesame (*Sesamum indicum* L.) germplasm. *Int. J. Agric. Sci.*, **8**(2): 441-444.
- Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research. John Willey and Sons, New York.
- Tripathi, A.; Bisen, R.; Ravindra, P. A.; Paroha, Seema; Sahu, Roshni and Ranganatha, A. R. G. (2013). Study on genetic divergence in sesame (*Sesamum indicum* L.) germplasm based on morphological and quality traits. *The Bioscan*, **8**(4): 1387-1391.
- Weiss, E. A. (1983). Oilseed Crops, Longman, New York.

Table 1: Grouping of 40 genotypes of sesame in various clusters on the basis of D^2 –statistic

Cluster	No. of Genotypes	Name of the genotypes
I	36	Nesadi Selection, Wild Dhandhuka (<i>w</i>), Nana Bhamodra, Kashmiri Til, JR 22, IS 196, RSS 106, B 90-1, U 76-I0, J 68-3, VCS 76-3, csm-1, Shelna 5, AT 178, AT 213, AT 222, AT 229, AT 231, AT 235, AT 238, AT 242, AT 253, AT 255, AT 262, AT 282, AT 306, AT 324, AT 336, AT 338, AT 345, Patan 64, GT 1, GT 2, GT3, GT 4, GT 10
II	3	AT 164, AT 332, RSE 3
III	1	China

Table 2: Average inter and intra-cluster distance ($D=\sqrt{D^2}$) values 40 genotypes of sesame.

	I	II	III
I	9.69	39.75	26.06
II		10.45	24.97
III			0.00

Table 3: Cluster mean for 13 different characters in 40 genotypes of sesame.

Clusters	Days to flowering	Days to maturity	Plant height (cm)	Number of branches per plant	Number of capsules per plant	Height to first capsule (cm)	Length of capsule (cm)	Width of capsule (cm)	Number of capsules per leaf axil	Number of seeds per capsule	1000 seed weight (g)	Seed yield per plant (g)	Harvest index (%)
	(1)	(2)	(3)	(4)	(5)	(6)	(7)	(8)	(9)	(10)	(11)	(12)	(13)
I	46.55	84.85	55.74	2.61	45.73	19.44	2.84	0.58	1.00	78.46	2.88	16.71	36.79
II	45.89	85.22	47.54	2.30	42.21	20.10	3.21	0.58	2.87	77.72	2.93	17.90	37.88
III	47.67	86.00	78.37	2.02	64.27	31.88	2.12	0.56	2.00	81.33	3.16	22.70	45.42
Mean	46.52	84.91	55.69	2.57	45.93	19.81	2.85	0.58	1.16	78.47	2.89	16.95	37.09
S.Em. $\pm$	1.29	2.47	4.73	0.26	4.42	0.62	0.08	0.03	0.03	4.80	0.20	1.05	2.39
C.V. %	4.80	5.04	14.71	17.71	16.66	5.43	5.01	8.57	4.70	10.59	11.71	10.75	11.16
Percentage contribution of characters towards total divergence													
	1	2	3	4	5	6	7	8	9	10	11	12	13
No. of times appearing first	1	3	2	8	20	285	119	8	149	67	1	110	7
% contribution	0.13	0.38	0.26	1.03	2.56	36.54	15.26	1.03	19.10	8.59	0.13	14.10	0.90

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