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Short Communication

GENETIC DIVERGENCE IN SESAME (*SESAMUM INDICUM* L.)

O.U.K. Reddy and N. Padmavathi

NRCS, Rajendranagar,
Hyderabad 500 030 (Andhra Pradesh)

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Genetic divergence among parents is essential for the expression of heterosis and for enlarging the variability in the subsequent segregating generatons. Generally, genotypes drawn from diverse geographical regions are preferred in the hybridization programmes, on the presumption of genetic diversity among such genotypes.

Fifty genotypes of sesame, both of indigeneous and exotic origin, were grown at the School of Genetics, Tamil Nadu Agricultural University, Coimbatore, during January 1987 in randomized block design with four replications. Selfed seeds of each genotype were sown with a spacing of 45 cm between rows and 30 cm between plants. Five adjacent plants per replication in the middle of the row were selected in each genotype and observations were recorded on individual plant for fifteen morphological and developmental characters.

The data were subjected to analysis of variance as well as multivariate analysis suggested by Mahalanobis (1936). Clusters were formed as suggested by Tocher (Rao, 1952) and canonical analysis was done as per the method suggested by Rao (1952).

The available divergence between genotypes for the characters studied was tested by Wilks lamda criterion (Wilks, 1932) and it was found to be significant (X 735 = 2683.78). The generalised D values ranged from 29.17 to 1813.69.

The fifty genotypes were grouped into eight clusters by the application of clustering techniques. Cluster I had as many as thirty two genotypes representing different geographical regions of the world. There were five genotypes in Cluster III, of which, one was indigeneous and others exotic.

Clusters II and IV had four genotypes each. Cluster II had three exotic genotypes from Chile, Japan and Greece, and one indigenous genotypes from Uttar Pradesh. Cluster IV had a single exotic genotype from Japan, while the other three genotypes were from Tamil Nadu. Two genotypes, one each from Greece and Palestine, constituted Cluster V. Clusters VI, VII and VIII had one genotype each. The clustering pattern failed to indicate any relationship between genetic divergence and geographical distribution. This is in agreement with the findings of earlier workers such as Trehan *et al.* (1975), Thangavelu and Rajasekharan (1983) and Dhamu *et al.* (1984).

Table 1. Inter and intra (diagonal) cluster average of D values and the extent of diversity among the clusters.

	I	II	III	IV	V	VI	VII	VIII
I	10.793	24.091	13.725	15.113	15.579	21.106	20.149	15.511
	-	M	C	C	C	C	C	C
II		10.953	23.923	29.172	24.886	37.314	30.074	27.672
		-	M	M	M	H	H	H
III			10.619	19.548	13.368	28.169	23.829	16.832
			-	C	C	M	M	C
IV				11.857	24.096	18.246	13.157	19.469
				-	M	C	C	C
V					10.834	30.142	30.407	18.758
					-	H	H	C
VI						-	20.637	23.232
							C	M
VII							-	21.504
								C
VIII								-

H : Highly divergent = Above 30; M : Moderately divergent = Between 21 and 30;
C : Closely related = 22 and below

The clustering pattern indicates the existence of wide genetic diversity among the genotypes chosen from the same geographic region. This is in agreement with earlier reports (Trehen *et al.*, 1974 and Dhamu *et al.*, 1974). They supposed that extremely variable environment within the same origin could have caused such diversity. Murty and Arunachalam (1966) explained that such a wide adaptation could be possible due to heterogeneity, genetic

Table 2. Cluster means for fifteen characters in *Sesamum*

Clusters	Plant height (cm)	No. of primaries	No. of secondaries	First capsule bearing node	Capsule on main stem	Capsule on branches	Capsule length (cm)	Seed per capsule	1000-seed weight (g)	Days to maturity	Oil content. (%)	LAI	DMP (q)	Harvest index (%)	Seed yield (g)
I	69.51	4.11	2.51	3.93	18.14	35.09	2.39	62.17	3.41	85.85	42.25	1.61	23.71	31.16	6.32
II	55.61	2.98	0.92	3.45	12.85	10.38	2.18	111.48	3.48	88.80	42.62	1.04	15.74	31.04	4.05
III	57.14	2.66	1.54	2.42	15.56	13.31	2.23	56.18	3.14	84.45	42.59	0.67	15.39	28.43	3.32
IV	74.09	5.75	4.12	5.05	19.79	48.42	2.26	52.22	3.54	96.13	43.17	1.55	26.51	32.33	7.63
V	56.44	2.00	0.89	3.00	17.55	20.15	2.61	63.18	3.61	75.13	41.22	0.62	16.33	28.57	3.71
VI	93.10	6.15	4.85	5.35	19.94	70.05	2.77	53.37	3.32	91.00	41.92	3.58	43.77	37.43	16.14
VII	74.10	5.30	4.30	4.70	16.75	49.85	2.26	57.07	2.65	108.75	41.45	1.74	27.47	30.28	6.96
VIII	74.10	4.00	1.04	3.40	17.80	27.97	2.42	52.00	2.53	6.25	35.85	1.53	20.11	28.70	4.63

LAI - Leaf area index

DMP - Dry matter production

architecture of the population, past history of selection, developmental factors and the degree of general combining ability. Such situation is desirable for the breeder to select parents with similar adaptability.

Canonical analysis suggested that primary axis was differentiated mainly by plant height, capsules on branches, leaf area index, number of secondaries and days to maturity. First capsule bearing node, plant height, number of primaries and harvest index constituted the secondary axis of differentiation.

The intra and inter cluster distances among the eight clusters are presented in Table 1. There did not exist much difference in the intra cluster distances. The inter cluster distance ranged from 13.157 (between clusters IV and VIII) to 37.314 (between clusters II and VI). It was found that Cluster II was highly divergent from Clusters VI and VII. Similarly, Cluster V was highly divergent from Clusters VI and VII. Between themselves, Clusters VI and VII appeared to be closely related. This indicates that hybridization programme of genotypes belonging to highly divergent clusters can be used for exploitation of hybrid vigour and for getting good recombinants.

Among the eight clusters, Cluster VI recorded the maximum values of cluster mean (Table 2) for most of the characters studied except seed per capsule, 1000-seed weight and oil content. Cluster II registered the maximum values for seed number per capsule and oil content. The 1000-seed weight was the highest and days to maturity was lowest indicating earliness in Cluster V. This crossing programme involving genotypes from these clusters could help in obtaining wide spectrum of variability for the above mentioned yield components in the subsequent segregating generations.

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