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

D. SWAIN AND U. N. DIKSHIT

*Department of Plant Breeding and Genetics, Orissa University of Agriculture and ·
Technology, Bhubaneswar 751003*

ABSTRACT

Multivariate analysis of divergence among 40 genotypes of sesame (*Sesamum indicum* L.)
for 13 quantitative characters revealed considerable genetic diversity in the material and
led to their grouping into 14 clusters. No relationship between geographic origin and
genetic diversity was observed. Seed oil content contributed maximum, accounting for
44.9% of the total divergence. For varietal improvement programme in rabi season, strains
like Uma of cluster VIII, TY 66 of cluster XIV, and TY 35 of cluster XIII were important on
the basis of their genetic distances and higher cluster means.

Key words: Genetic divergence, sesame.

Sesame, which is the second important oilseed crop in Orissa, covers about 40% of the total sesame area in rabi (winter) season, characterized by short day length and low temperature. Systematic breeding efforts are necessary to evolve high yielding rabi sesame cultivars on the basis of photoperiod- and thermosensitivity. The information about the nature and magnitude of genetic divergence in a given population is essential for selection of diverse parents which upon hybridization lead to a wide spectrum of gene recombinations for quantitatively inherited traits. Since published work on rabi sesame is scanty, the present study has been undertaken with 40 sesame genotypes to understand the nature and magnitude of genetic divergence and the characters contributing to genetic diversity by using D^2 statistic.

MATERIALS AND METHODS

Forty genotypes representing different states of India (Table 1) were chosen for the study on the basis of thermo- and photoperiod-sensitivity as well as their performance in rabi season, from among 350 germplasm collections maintained under the All India Coordinated Research Project on Sesame at O.U.A.T., Bhubaneswar. These included six lines from Orissa

and 34 introductions from 12 States of India. They were evaluated in a four-row plot of 3.5 m length in randomized block design with three replications at the spacing of 30 x 10 cm during rabi season. Observations were recorded on 10 random plants from the two central rows for 13 quantitative characters and mean values from three replications were used for analysis. The data were subjected to Mahalanobis's D^2 statistic as described by Rao [2] and the genotypes were grouped into different clusters following Tocher's method [2].

RESULTS AND DISCUSSION

The analysis of variance revealed significant differences among the 40 strains for all the 13 characters. The aggregate effect of all the 13 characters was tested by the Wilk's criterion, indicating highly significant differences among the genotypes. Hence, the analysis of genetic divergence based on D^2 values was considered relevant.

On the basis of D^2 values, the 40 genotypes were grouped into 14 clusters (Table 1). Cluster II was the largest with 10 genotypes, followed by cluster I with seven genotypes, clusters V and VI with four each, clusters III and IV with three each, cluster VII with two, and the remaining seven clusters with one genotype each. The lack of correspondence between genetic diversity and geographical origin, as observed from the present study and also reported by other workers [3, 4], could possibly be due to the fact that varietal diversity in different geographical area is getting broadened and repeated through mutual exchange of breeding materials. Genetic drift

Table 1. Distribution of sesame genotypes into different clusters

Cluster	Number of genotypes	Genotypes	Origin
I	7	TKG 21, JLSC 8, TKG 84	Tikamgarh (M.P.)
		AT 34	Amreli (Gujarat)
		RT 121	Mandore (Rajasthan)
		Purulia 1	Purulia (W.B.)
		Sekhara	Kanpur (U.P.)
II	10	Kanak, Kalika, Usha	Bhubaneswar (Orissa)
		AHT 79, ABT 6	Amreli (Gujarat)
		Krishna	Sabour (Bihar)
		JLT 26	Tikamgarh (M.P.)
		TC 398	Gurudaspur (Punjab)
		B 67	Berhampore (W.B.)
		Thilak	Kayakulam (Kerala)
III	3	T4	Kanpur (U.P.)
		TSE 4	Trombay (Maharashtra)
		TKG 55	Tikamgarh (M.P.)
IV	3	VS 339	Virdhachalam (T.N.)
		YLM 17	Yellamanchali (A.P.)
		OMT 32	Bhubaneswar (Orissa)
V	4	TY 1, TY 3, TY 20, PY 76	Trombay (Maharashtra)
VI	4	Rajeswari	Yellamanchali (A.P.)
		DES 1	Dharwad (Karnataka)
		AKT 60	Akola (Maharashtra)
		TNAU 12	Coimbatore (T.N.)
VII	2	VS 9104, VS 9003	Virdhachalam (T.N.)
VIII	1	Uma	Bhubaneswar (Orissa)
IX	1	Vinayak	Bhubaneswar (Orissa)
X	1	TMV 3	Virdhachalam (T.N.)
XI	1	MT 11	Mauranipur (U.P.)
XII	1	TY 33	Trombay (Maharashtra)
XIII	1	TY 35	Trombay (Maharashtra)
XIV	1	TY 66	Trombay (Maharashtra)

and selection forces under diverse environments could cause even greater diversity than caused due to geographical distance [5].

Cluster V showed maximum intracluster distance (Table 2). As regards intercluster distances, cluster VIII showed maximum genetic distance from cluster XIV. Clusters IX, X, XIII, VII and II were also most distant from cluster XIV. The magnitude of heterosis depends largely on the degree of genetic diversity in the parental lines. Therefore, the genotypes belonging to diverse clusters could be used in hybridization programme to derive a broad spectrum of genetic variability in the segregating generations [3].

Based on intercluster distances (Table 2) and character means of different clusters (Table 3), the crosses between the strains of cluster IX, VIII, V, XIII and XIV may combine high seed yield with high oil content.

The characters contributing maximum to the divergence should be given more emphasis for the purpose of further selection and choice of parents for hybridization. The maximum contributors to genetic divergence were seed oil content (44.9%), 1000-seed weight (10.6%), capsule length (8.9%), and days to flowering (7.1%) (Table 4). Working on kharif sesame, Thangavelu and Rajasekaran [4] reported that oil content contributed

Table 2. Intracluster (in bold) and intercluster distances (D^2) among 14 clusters in sesame

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
I	159.5	415.6	416.3	335.7	640.9	618.6	944.9	859.0	759.9	999.0	368.6	654.3	721.4	848.4
II		195.4	1014.9	434.8	991.4	340.4	684.7	303.0	304.8	435.9	759.2	656.5	408.7	1650.2
III			108.8	425.3	444.2	954.8	1313.6	1222.6	1476.3	1404.7	318.1	607.3	1382.2	321.5
IV				183.3	433.1	390.0	547.1	799.3	577.8	536.0	456.0	337.7	648.8	737.1
V					223.6	656.9	1237.8	1810.3	1218.0	1288.2	285.5	296.3	841.1	343.9
VI						188.2	631.5	737.0	418.6	402.0	611.1	296.4	365.4	1340.5
VII							221.9	674.1	725.6	401.7	1352.4	815.0	1034.1	1754.8
VIII								0.0	297.1	395.7	1539.1	1282.3	776.9	2622.0
IX									0.0	348.3	1112.0	844.5	270.4	2090.6
X										0.0	1317.9	622.6	822.1	2142.4
XI											0.0	398.2	737.4	502.6
XII												0.0	688.4	773.6
XIII													0.0	1616.8
XIV														0.0

Table 3. Character means in different clusters of sesame genotypes

Character	Character means in different clusters													
	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII	XIV
Days to flowering	*41.2*	44.3	41.4	46.5	50.2	48.8	**56.8**	43.3	47.0	50.7	45.7	52.3	49.3	46.7
Days to maturity	*78.2*	84.3	79.4	87.8	91.4	90.2	**96.0**	81.3	88.7	92.3	85.0	91.3	91.7	86.7
Plant height (cm)	63.8	69.0	*57.4*	80.4	89.6	90.1	75.3	58.9	80.7	80.4	63.3	**91.1**	88.6	83.9
No. of branches	2.1	1.4	1.3	1.5	1.0	*0.6*	**3.1**	1.9	1.3	1.3	0.6	1.3	1.1	1.6
Nodes on main stem	19.9	22.3	16.5	25.1	**27.9**	24.4	22.7	22.8	25.4	23.3	*13.8*	25.6	26.9	25.3
Fruiting nodes	9.4	9.3	*7.8*	10.1	**10.8**	9.8	7.8	9.5	10.5	7.9	6.4	9.8	10.5	9.7
Capsules per plant	25.0	18.3	*12.9*	21.8	19.2	12.6	21.8	20.6	**27.4**	12.3	19.4	12.6	22.5	18.2
Capsule length (cm)	2.3	2.3	2.3	2.3	2.7	2.3	2.1	2.2	2.5	*2.0*	2.6	2.6	**2.8**	2.7
Capsule breadth (cm)	0.6	0.6	0.6	*0.5*	0.6	0.6	0.5	0.5	0.5	0.5	0.6	**0.7**	0.6	0.5
1000-seed weight (g)	3.4	3.1	3.2	2.9	3.3	3.0	2.4	2.6	2.7	*2.2*	3.4	2.7	3.4	**3.6**
Oil content (%)	45.6	47.9	48.7	44.9	43.7	47.1	46.2	**49.1**	48.4	47.3	44.6	45.2	48.5	*41.6*
Harvest index (%)	**51.6**	*46.0*	47.9	49.0	45.3	39.3	47.8	46.9	47.4	40.6	51.1	36.2	49.0	44.6
Seed yield (g)	5.8	3.4	2.9	4.4	4.7	2.9	3.4	3.0	6.5	*2.0*	3.5	2.7	**6.7**	4.1

Note. Maximum and minimum values of each character are printed in bold and italics, respectively.

maximum towards genetic divergence, followed by number of seeds per capsule and seed index, while Dikshit [3] reported maximum contribution of oil content, capsule number and seed weight to genetic divergence. Based on the mean performance for the aforesaid four characters of the present study, cluster VIII for seed oil content, cluster XIV for 1000-seed weight, cluster XIII for capsule length, and cluster I for days to flowering showed high potential for genetic upgradation of genotypes (Table 3). On the basis of intercluster distance and characters with high contribution to D^2 values, there is good scope for varietal improvement through hybridization of the vars. Uma of cluster VIII and TY 35 of cluster XIII with TY 66 of cluster XIV.

Table 4. Contribution of 13 quantitative characters to divergence (D^2) in sesame

Character	D^2	Percentage of total D^2
Days to flowering	43.7	7.1
Days to maturity	22.7	3.7
Plant height	29.2	4.7
Number of branches	29.0	4.7
Nodes on main stem	10.9	1.8
Fruiting nodes	3.7	0.6
Capsules per plant	23.0	3.7
Capsule length	55.1	8.9
Capsule breadth	22.9	3.7
1000-seed weight	65.8	10.6
Oil content	277.4	44.9
Harvest index	23.6	3.8
Seed yield	11.4	1.8

REFERENCES

1. C. R. Rao. 1952. Advanced Statistical Methods in Biometrical Research. John Wiley & Sons, New York.

2. C. R. Rao. 1960. Multivariate analysis — an indispensable statistical aid in applied research. Sankhya, **22**: 317–338.

3. U. N. Dikshit. 1992. Genetic Analysis in Sesamum: Genetic Divergence, Heterosis and Nature of Gene Action. Ph. D. Thesis. Orissa University of Agriculture & Technology, Bhubaneswar.

4. M. S. Thangavelu and S. Rajasekaran. 1983. Genetic divergence in *Sesamum*. Madras Agric. J., **70**(4): 211–214.

5. G. M. Bhatt. 1970. Multivariate analysis approach for selection of parents for hybridisation aiming at yield improvement in self-pollinated crops. Aust. J. Agric. Res., **21**: 1–7.