

Genetic Divergence in Relation to Fatty Acids in Oilseed Brassica

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Analysis of genetic diversity using Mahalanobis D^2 analysis was carried out on 50 genotypes of *Brassica* and grouped into 12 clusters. Studies indicated that geographical isolation might not be the only factor causing genetic diversity. Oleic acid and erucic acid were the most potential traits contributing to the total genetic divergence. Clusters III and V were important because they comprised accessions with high and low erucic acid content, respectively and by utilizing accessions from these clusters there is a sufficient scope for varietal improvement through hybridization.

Key Words: *Brassica*, Fatty Acids, Genetic Divergence

To bring genetic improvement in the oil quality of *Brassica*, it becomes imperative to know the fatty acid composition of the available germplasm. There is a great scope to improve oil quality, provided genetically diverse parents are involved in hybridization. In this context, D^2 analysis has been found to be a potent biometrical tool in quantifying the degree of divergence (Rao, 1952) and has successfully been used in many crops (Arunchalam and Bandopadhyay, 1989). The present study was undertaken to estimate the genetic divergence among 50 genotypes of *Brassica* in relation to fatty acid composition.

Material and Methods

Brassica germplasm collection maintained at Crop Research Centre of G.B. Pant University of Agriculture and Technology, Pantnagar, were evaluated for fatty acid content. Harvested seeds of 50 genotypes were subjected to fatty acid determination by Gas Liquid Chromatography after converting different fatty acids into their respective esters (Luddy *et al.*, 1968). Genetic divergence was determined using Mahalanobis D^2 statistics (Mahalanobis, 1928, 1949) and the genotypes were grouped into clusters according to Tochar's method (Rao, 1952).

Results and Discussion

The analysis of variance showed highly significant differences between genotypes for each of the seven characters studied. Based on D^2 value the genotypes were grouped into 12 clusters (Table 1). Cluster III has maximum number of twenty-one genotypes followed by cluster I, nine genotypes, cluster V and VI had 4 genotypes each, cluster II and IV had 3 genotypes each and the rest of the clusters had one genotype each. The pattern of clustering demonstrated that the geographical origin of these genotypes is not related to genetic diversity as genotypes of different geographical areas were

distributed in different clusters and many genotypes of different geographical origin were grouped into same cluster (Table 1). Similar results have been reported by Alarmelu and Ramanathan (1998) in sesame.

Table 1. Clustering of 50 Brassica genotypes

Cluster No.	Number of genotypes	Genotype
I	9	BNLP-3, BNLP-4, BNLP-6, Hyola-401, EC-339014, BNLP-1, EC-339013, BNLP-5, BNLP-10
II	3	BNLP-11, BNLP-12, EC-339017
III	21	Pusa Bahar**, Kranti**, Krishna, Pusa Jaikisan, PRT-1, Kiran**, Vaibhav, RC781, Domo, PT-303, Vardan, YST-151, PYS-841, PYS-842, T-9, Orn. Rai, PYS-843, Pusa Bold, CSR-122 and Zem-2
IV	3	EC-339008, EC-339015, EC-339012
V	4	PRQ-9701, PRQ-9707*, PRQ-9701-2*, PRQ-9705-6*
VI	4	EC-338985, NCN-13, TRL-93, EC-339016
VII	1	EC-339012
VIII	1	PRQ-9705*
IX	1	EC-339001
X	1	EC-339000
XI	1	PRQ-9707-19*
XII	1	Zem-1

* Potential donor for low erucic acid

** Potential donor for high erucic acid

Intra- and inter-cluster distance are presented in Table 2. Intra-cluster values ranged from 0.00 to 19.37. The inter-cluster distance based on mean standard deviation of D^2 value ranged from 20.29 (between VII and IX) to 97.96 (between I and III) and classified into three divergent classes. Highest inter-cluster distance was observed between cluster I and III (97.96) which indicates that these clusters are highly divergent. The next higher

Table 2. Average inter- and intra-cluster in *Brassica* germplasm

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	11.005	42.580	97.956	42.740	64.792	68.419	38.406	83.301	55.488	53.186	81.509	74.989
II		17.915	75.415	37.237	39.036	46.332	27.883	50.745	41.482	32.261	68.465	40.233
III			13.062	71.923	79.154	34.927	61.983	68.683	46.713	79.434	87.431	52.820
IV				13.172	66.981	45.756	32.390	70.587	45.704	62.030	87.799	54.208
V					17.778	56.338	48.759	32.333	49.455	27.599	26.725	38.675
VI						19.372	33.418	53.305	23.939	54.004	70.064	35.505
VII							0.000	60.945	20.297	36.650	65.897	46.512
VIII								0.000	56.997	51.638	41.036	23.184
IX									0.000	41.852	61.282	42.935
X										0.000	40.270	48.599
XI											0.000	54.028
XII												0.000

DC1: Highly divergent = >70

DC2: Moderately divergent = 40-70

DC3: Closely related = <40

distance was observed between cluster IV and XI (87.70). Minimum inter-cluster distance was recorded between cluster VII and IX (20.29) which indicates close relationship between these two clusters. The inter-cluster distance was higher than the intra-cluster distance in all the cases indicating more divergence of genotypes between the clusters. Gondane and Lal (1993) observed similar relationship in okra.

The cluster mean and coefficient of variation also provided an interesting information of the nature of diversity (Table 3). Considerable differences in cluster means occurred for almost all the characters. The coefficient of variation for different characters indicated that major forces of discrimination were erucic acid (93.4%), linolenic acid (76.68%) and eicosanoic acid (71.65%). Maximum

cluster mean was observed in cluster number IV for oleic acid content and minimum cluster mean was observed in cluster number IV for linolenic acid. Cluster mean for erucic acid content ranged from 1.71 (cluster V) to 44.45 (cluster III). In order to enhance the usefulness of mustard oil as a food crop, a further increase in level of oleic acid along with decreases in erucic and linolenic acid is desirable. Reduction of linolenic acid is necessary to improve the shelf life of the mustard oil while reduction in erucic acid decreases blood cholesterol. (Renard and Mc Gregor, 1976). Oleic acid is the common precursor of erucic acid as well as linolenic acid. Increased oleic acid concentration and its further desaturation gives rise to higher concentration of linoleic linolenic acid. On other hand erucic acid accessions

Table 3. Mean cluster values for different traits in *Brassica*

Cluster	Palmitic acid 16:1	Stearic acid 18:0	Oleic acid 18:1	Linoleic acid 18:2	Linolenic acid 18:3	Eicosanoic acid 20:1	Erucic acid 22:1
I	4.942	1.018	78.194	10.389	0.422	0.443	4.652
II	4.965	0.423	43.917	23.917	7.017	13.220	6.162
III	3.688	0.796	13.101	17.546	13.264	7.718	44.446
IV	4.318	0.660	61.243	5.110	2.893	12.097	14.182
V	6.117	0.606	27.726	34.552	21.950	7.586	1.714
VI	5.207	0.694	30.710	18.400	10.194	7.914	30.011
VII	3.615	0.550	50.165	18.010	4.000	4.600	20.885
VIII	7.945	0.965	13.550	31.100	29.440	15.390	2.125
IX	2.920	0.625	40.080	18.990	9.500	1.005	28.510
X	4.345	0.755	33.770	35.980	8.525	6.005	83.335
XI	6.410	0.230	19.335	41.895	30.240	0.735	2.030
XII	4.460	0.550	18.160	28.895	20.850	16.685	12.520
CD	1.382	0.217	20.245	10.745	10.115	53.508	13.660
CV%	37.059	33.020	56.370	45.900	76.680	71.550	93.420

are important for industrial purpose. Cluster III, V, VIII and XI could be regarded as useful sources of genes for different traits and some of the promising germplasm accessions for desired traits are mentioned in Table 1.

Contribution of individual character towards divergence (Table 4) revealed that maximum contribution to total divergence is recorded by oleic acid (45.39%) and erucic acid (33.47) followed by linolenic, eicosenoic,

palmitic and stearic acid in decreasing order. In view of considerable genetic diversity in *Brassica* germplasm there is ample scope for varietal improvement through hybridization.

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Table 4. Contribution of each character to genetic divergence

Cluster	Palmitic acid	Stearic acid	Oleic acid	Linoleic acid	Linolenic acid	Eicosenoic acid	Erucic acid
No. of time appearing first in ranking	6	5	556	75	87	86	410
% Contribution	0.49	0.41	45.39	6.12	7.10	7.01	33.47

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