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Short communication

Genetic diversity for quality traits in Indian mustard [*Brassica juncea* (L.)]

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Abstract

Genetic diversity analysis in Indian mustard (*Brassica juncea* L. Czern & Coss.) was carried out by using Mahalanobis D^2 analysis. Thirty five genotypes were grouped in to V clusters for different quality characters. Cluster means revealed that the cluster I showed the highest mean value for stearic acid. Cluster II for protein content, palmitic acid and for linoleic acid. Cluster III for oil content, and oleic acid and for linolenic acid. Cluster IV for fibre content. Cluster V for erucic acid and for ash content. The clustering pattern did not establish a clear-cut relationship between genetic diversity and geographical diversity. The analysis of data revealed that the intercluster distance (D) ranged from 3.3 to 9.5 the maximum intercluster distance was observed between clusters IV and cluster I. The protein content (28.6%) and oil content (26.9%) were the main contributors to the total divergence. The characters such as palmitic acid (14.1%) and stearic acid (10.6%) had contributed moderately.

Key words: Genetic diversity, quality, Indian mustard

Introduction

Indian mustard [*Brassica juncea* (L) Czern & Coss] is the second largest oilseed crop in India after soybean. It is cultivated in *rabi* (post-rainy) season mainly in Northwest India and contributes nearly 27 per cent to edible oil pool of the country. The oil is mainly used for edible purposes, accounting for nearly 30 percent of the total oilseeds produced in the country. The fatty acid composition of the oil determines its nutritional quality. Rapeseed-mustard seed contain 35-45 percent oil. Oil contain 92-98 percent triacylglycerol of fatty acids (C:16-C:22) and the remaining portion is composed of lipid compounds like unsaponifiable hydrocarbons, tarpins, sterols, tocopherols, glycolipids and phospholipids. Oil contains lowest saturated fat and possesses more proportion of linoleic and linolenic acid which are not synthesized by the human body. Erucic acid (C:22) comprises nearly 50 % of total fatty acid which is undesirable and not well metabolized thus increases blood cholesterol. Linolenic acid is an essential dietary fatty acid, but undesirable in edible oil because of prone to auto-oxidation resulting in off-flavors and reduced shelf life of the oil. To accomplish success in Indian mustard improvement programme it is necessary to collect information on genetic diversity as it provides the basis for an efficient selection of genotypes for hybridization.

Materials and methods

Thirty-five genotypes of Indian mustard selected from the Main Castor and Mustard Research Station, S.D. Agricultural University, were grown in Randomized Block Design with three replications during *rabi* (winter*)* 2008-09 at the Agronomy Instructional farm, C. P. College of Agriculture, S.D. Agricultural University, Sardarkrushinagar, Gujarat. Each replication consisted of a single row of 3m for each entry with row to row and plant to plant spacing being 45 cm and 15 cm respectively.

Recommended agronomic practices were followed to raise a good crop. Ten competitive plants were randomly selected in each entry for recording observation on oil content (%), protein content (%), palmitic acid (%), stearic acid (%), oleic acid (%) linoleic acid (%), linolenic acid (%) erucic acid (%) fiber content (%) and ash content (%) . A random sample (Approximately 12.0 g) of bulk seeds from each genotype in each replication was taken for the oil and protein analysis by NIR (Near Infrared Reflectance) method. Fatty acids Palmitic acid, stearic acid, oleic acid, linoleic acid, linolenic acid, Erucic acid, fiber content and ash content of the oil were determined in percentage by Liquid Gas Chromatography (GLC). However, observations were recorded on plot basis for days to 50% flowering and days to maturity. Following the analysis of variance the data were subjected to multivariate analysis of genetic divergence using Mahalanobis D^2 statistic (Mahalanobis, 1936). Grouping of entries was done by following Tocher's method (Rao, 1952).

Results and discussion

In the present study, analysis of variance for thirty five Indian mustard genotypes showed significant differences for all the characters, indicating the existence of genotypic variability and validated further genetic analysis. Mahalanobis's D2-statistic helped in grouping thirty five genotypes of Indian mustard into five clusters (table 1). The cluster II was the largest comprising 19 genotypes followed by cluster V (7) genotypes and cluster III (6). The genotypes of the same geographical area were grouped in another cluster indicating that there is no formal relationship between geographical diversity and genetic diversity. Ghosh and Gulati (2002), Arha *et al*. (2006), Patel *et al*. (2006) and Singh *et al.* (2007) were of the same opinion.

Table 1: Distribution of thirty five Indian mustard genotypes to different clusters on the basis of D^2 statistics

Clusters	Number of genotypes	Name of genotype
I	2	BPR-6-166-43-6, SW-I-90-10
II	19	EC 222622 , BPR-380-1, EC 333591, EC 287711, EC 333575, RSK 28, SW-I-90-6, BIO-Q-442-99, BPR-6-91-65-4, T 9, EC 242647, B-11058, ISH 602, Tobin, EC 482999, Varuna, GM 1, GM 2, GM 3
III	6	Dhara, NUDH YJ 1, BPR-6-166-50-6, NUDH YJ 4, BPR-6-91-65-3, BPR-6-166-24-3
IV	1	ZEM 2
V	7	Tower 36, EC 302485, BIO-Q-1O8M, SW-91-1, SW-I-90-17, BIO-902, EC 333594

Table 2: Average Intra (Bold) and Inter cluster distance (D) values in Indian mustard

Clusters	I	II	III	IV	V
I	3.1				
II	4.4	3.7			
III	5.5	3.3	3.2		
IV	9.5	8.7	8.5	0.0	
V	4.9	3.3	4.0	8.1	3.7

Contribution of different characters towards total genetic divergence (table 4) revealed highest contribution of protein content (28.6%) followed by oil content (26.9%) The genetic divergence contribution was least by linoleic acid (0.4%). Cluster means of different clusters (table 3) observed maximum values for Cluster III for oil content (37.4%), oleic acid (20.0%) and for linolenic acid (5.7%)., Cluster II for protein content (15.8%), palmitic acid (1.0%) and for linoleic acid (14.0%), Cluster IV for fiber content (17.8%). Cluster V for erucic acid (51.9%) and for ash content (4.3%) and cluster I showed the highest mean value for stearic acid (3.2%).

Table 3: Cluster means for different characters in Indian mustard

Clusters	OIL	PRO	PMA	STA	OLA	LLA	LNA	EAA	FIB	ASH
I	31.3	15.0	1.0	3.2	15.8	11.5	5.4	29.3	16.4	4.1
II	36.2	15.8	1.0	2.9	19.5	14.0	5.5	49.8	16.6	4.2
III	37.4	15.8	0.8	2.6	20.0	11.9	5.7	5.2	16.6	4.2
IV	36.5	15.5	1.0	0.5	12.6	13.5	4.9	0.5	17.8	3.4
V	36.1	15.2	0.9	2.5	15.3	13.3	4.7	51.9	17.0	4.3

OIL=Oil content (%), PRO=Protein content (%), PMA= Palmitic acid (%), STA=Stearic acid (%), OLA= Oleic acid (%), LLA= Linoleic acid (%), LNA= Linolenic acid (%), EAA= Erucic acid (%), FIB= Fibre content (%), ASH= Ash content (%)

Table 4: Per cent contribution of different characters to total genetic divergence

	Number of times first characters ranked	Per cent contribution
Oil content	61	26.9
Protein content	65	28.6
Palmitic acid	32	14.1
Stearic acid	24	10.6
Oleic acid	17	7.5
Linoleic acid	1	0.4
Linolenic acid	4	1.8
Erucic acid	16	7.0
Fibre content	2	0.9
Ash content	5	2.2
Total	227	100

The analysis of data revealed (table 2) that the intercluster distance (D) ranged from 3.3 to 9.5. The maximum intercluster distance (D = 9.5) was observed between clusters IV and cluster I and minimum intercluster distance (D = 3.3) was observed between cluster V and cluster II. Intra cluster distance (D) ranged from 0.0 to 3.7. Cluster II had the highest value (D = 3.7) followed by cluster III, I, V and IV.

Hence, cluster mean values showed that clusters III, IV and II had the maximum divergence among five clusters, suggesting that for hybridization programme, genotypes from these clusters should be selected as parents for making crosses to obtain high heterotic expression in F_1's.

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