Evaluation of genetic diversity in different genotypes of *Brassica juncea* by SDS-PAGE

Anupreet Kour and S.P. Singh

Department of Genetics and Plant Breeding
G.B. Pant University of Agriculture and Technology
Pantnagar-263 145 (U.A.) Email: anu_kour@rediffmail.com

Abstract

The objective of this study was to assess the genetic divergence available in different genotypes of *Brassica juncea* based on analyses of seed storage proteins, for the identification of genetically diverse and agronomically superior accessions of rapeseed, which may generate putative transgressive segregates on hybridization. Diversity within species of *Brassica juncea* can be analyzed at molecular level with the help of seed storage protein by using SDS-PAGE. On the basis of banding pattern on the gel zymogram (Diagrammatical representation of different protein bands) was sketched. By which, Euclidean distances were measured and a dendogram was formed on the basis of Rf values of different bands on the gel. With the help of this dendogram genotypes were clustered into different groups, by applying UPGMA (Unweighed paired group mean analysis).

Media Summary:

Fourteen genotypes of *Brassica juncea* were used to study genetic diversity by SDS-PAGE .The genotypes were grouped into three clusters .on the basis of seed protein profile.

Key words

Clusters analysis, Seed storage protein, germplasm,Rape seed Mustard

Introduction

Rapeseed Mustard crops account for almost 14 per cent of the edible vegetable oil supply of the world.. *Brassica* species. partially cross-pollinated, have evolved by natural and artificial selections over a long period of time and most of them have developed several sub species, which differ morphologically and physiologically. Rapeseed Mustard group includes *Brassica napus* L. (Gobhi sarson); *Brassica rapa* L. var. *toria*, *yellow sarson* and *Brown sarson*; *Brassica juncea* L. (Mustard); *Eruca sativa* (Taramira) and *Brassica carinata* (Karan Rai). In order to further upgrade the yield potential of these crops and to impart resistance to biotic and abiotic stresses, it is imperative to introduce desirable attributes in a good agronomic base. For this, an inevitable requirement is to genetically characterize the available variability in the germplasm. The ordination techniques like principal component analysis followed by cluster analysis was found to be useful tool for getting multi-correlated variables into another set of uncorrelated variables which can be utilized for classification of genotypes into homogenous groups. Likewise UPGMA [Unweighed paired group mean analysis] can be used to identity diversity within different species of *Brassica*. On the basis of Rf values, dendogram was sketched and clusters of different genotypes were formed with the help of this dendgram.

Materials and methods

The experimental material consisted of fourteen genotypes of *Brassica juncea*, which includes varieties released from different states in India and different strains. Protein profile was analysed by sodium dodecyl sulphate poly acrylamide gel electrophoresis (SDS-PAGE) of seed storage protein. Nykifourk and Flanagan (1994) method with certain modifications was used for extraction of protein from seeds.

On the basis of banding pattern on the gel, Rf values were calculated for different genotypes. 0, 1 pattern was prepared with the help of Rf values. If a band of particular Rf value was present then given the

number ‘1’ and if absent then ‘0’. Applying UPGMA [Unweighed paired group mean cluster analysis] different genotypes were classified into different clusters according to their Euclidean distances measured.

Result and discussion

The findings of seed protein electrophoresis was described under electrophoregram , Zymogram , Euclidean distance (Table-1) and dendogram (Fig.-1).In zymogram the banding pattern of different genotypes can be divided into three zones X, Y and Z, on the basis of Rf values of different bands.

Zone ‘X’ (Rf-0.17-0.40) (X1-X9)
Zone ‘Y’ (Rf-0.43-0.77) (Y1-Y8)
Zone ‘Z’ from Z1-Z6 (Rf-0.80-0.98)

Table 1: Euclidean distances between fourteen genotypes of *Brassica juncea*

CLUSTER ANALYSIS
Imported data
Analyzing 23 variables ? 14 cases
UPGMA
Euclidean

Distance matrix

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	0													
2	2.449	0												
3	2.646	2.646	0											
4	3	3	2.449	0										
5	3.317	3.317	3.162	2.828	0									
6	2.449	2.828	2.236	2.236	3	0								
7	3.162	3.742	3.606	3	3	3.162	0							
8	3.742	4	**4.359**	3.873	3.606	4	2.828	0						
9	3.464	3.742	4.123	3.606	3	3.464	2	2.449	0					

10	3.606	3.873	4.243	3.742	3.162	3.606	2.236	2.236	**1**	0				
11	3.317	3.873	3.742	3.464	2.828	3.317	3.317	3	2.646	2.828	0			
12	3.317	3.606	3.742	3.464	2.828	3.317	3.317	3	3.317	3.464	2.449	0		
13	3.162	3.464	3.317	3	2.236	3.464	3.162	3.162	3.464	3.606	2.236	2.236	0	
14	3.606	3.606	3.162	3.464	2.449	3.873	3.606	3.606	3.873	4	2.828	2.449	1.732	0
	1	2	3	4	5	6	7	8	9	10	11	12	13	14

On the basis of this banding pattern, Euclidean distances between different genotypes were measured. Euclidean distance between different genotypes ranged from ‘1’ to ‘4.359’. It was ‘1’ between genotypes JM-1 and Pusabold; and was 4.359 between Zem-1and Karishna (Table-1).

On the basis of these Euclidean distances dendogram was formatted (Fig-1). Different genotypes were grouped into three clusters.

Cluster I	**Cluster II**	**Cluster III**
? *Varuna* var (Kanpur) NC	? *Urvashi* var (Kanpur)	? *Basanti* var (Kanpur)
? *Kranti* var (Pantnagar) NC	? PRQ-9705-6 (Strain)	? Pusa Bold (IARI)
? *Karishma* (Strain)	? PRQ-9707-3-2 (Strain)	? JM-1 var (MP)
? SEJ-2 var. (IARI) NC	? PR-9627 (Strain)	? Zem-1 (Strain) Introduced
? *Krishna* var (Pantnagar)	? RC-781 var	

NC = National Check

In cluster I, Varuna or selection from it is the common parent while, RC-781 is white rust resistant and three strains are involved from it. In cluster III, similarity is in maturity duration.

In cluster I Kranti and Krishna evolved from Varuna after selection.

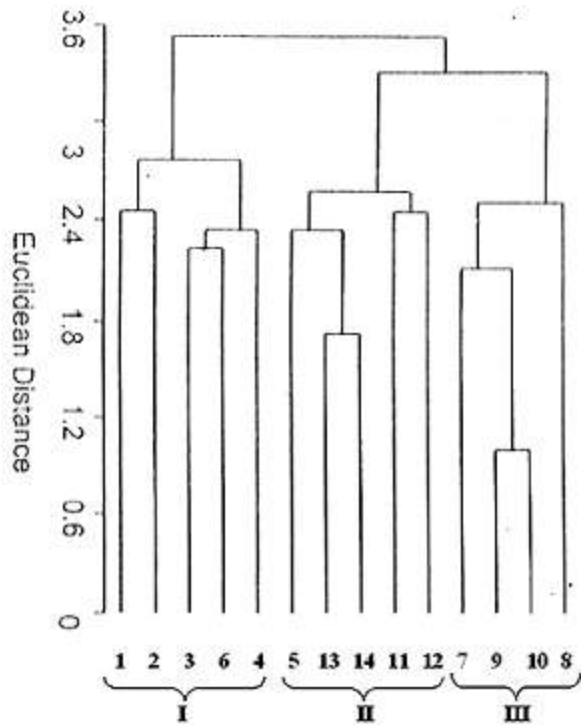

Fig 1: Dendogram of fourteen genotypes of Mustard (*Brassica juncea*)

Conclusion

It was possible to distinguish certain genotypes based on seed protein. Seed protein electrophoresis was proved to be useful in identifying genotypes and characterizing them. The screening of genotypes helped in identifying the promising genotypes for different traits, which may serve as good genetic donors for exploitation in further breeding programme.

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