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DIVERSITY ANALYSIS OF THE GERMPLASM OLEIFEROUS *Brassica* species

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ABSTRACT

An experiment was carried out with 40 rapeseed and mustard germplasms in the experimental farm of Sher-e-Bangla Agricultural University, Dhaka during November 2005-March 2006 with a view to study the genetic divergence. Diversity was estimated by cluster distance. All the genotypes were grouped into six clusters. Principal component analysis, Cluster analysis and Canonical Variate analysis exhibited similar results. Significant variations were observed among the genotypes for all the parameters under study. Cluster II had the maximum 10 and cluster I and III had the minimum 5 number of genotypes. The highest intra-cluster distance was observed in cluster V. The highest inter-cluster distance was observed between cluster I and VI and the lowest was found between the cluster III and V. The characters secondary branches/plant, siliquae/plant and yield/plant contributed maximum towards divergence among the rapeseed and mustard genotypes. The genotypes which had moderate inter-cluster distance coupled with medium to high yield could be utilized for screening suitable materials from large population. Considering diversity pattern, genetic status and other agronomic performances some of the materials viz. BD-6948 and SAUYC from cluster I; BD-9063, BD-9064 and BD-9071 from cluster II; BD-9068 and BD-9077 from cluster III; BD-9078, BD-9106 and BD-6949 from cluster IV; BD-9079 and BD-9081 from cluster V and BD-9100 and BD-7812 from cluster VI were selected as superior parents for rapeseed and mustard improvement programme.

Key words: Germplasm, diversity, oleiferous, *Brassica*

INTRODUCTION

Brassica is an important genus of plant kingdom consisting of over 3200 species with highly diverse morphology. Rapeseed and mustard are the leading oilseed crops in Bangladesh.There are three cultivated species of *Brassica* in the country- *Brassica rapa*, *B. napus* and *B. juncea*. The per capita consumption of edible oil in the country is 8 g/day as compared to the total need of 40 g/day (Kaul and Das, 1986). The big gap is mainly due to poor performance of the available short duration varieties. Thus, to fulfill our huge demand, we should develop short duration varieties with higher seed yield and higher oil percentage in the seed. The variability among different genotypes of a species is known as genetic diversity. Genetic diversity arises either due to geographical separation or due to genetic barriers of crossability. D^2 statics proposed by Mahalanobi's (1936) is one of the potent techniques for measuring the genetic divergence both in intra and inter cluster level. Genetic diversity plays an important role in plant breeding because hybrid between lines of diverse origin generally displays a great heterosis than those closely related strains (Singh, 1983). Such a study also permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. The study was undertaken in order to find out or select suitable genotypes of rapeseed and mustard on the basis of genetic diversity.

MATERIALS AND METHODS

The experiment was undertaken in the experimental farm, Sher-e-Bangla Agricultural University (SAU), Dhaka during November 2005-March 2006. The experiment was set up in a RCBD

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design with three replications following 30 cm x 10 cm spacing. The unit plot size was 21m×55 m and block to block distance was 1.5 m. The plot was fertilized with 250, 170, 85, 150, 5 kg/ha Urea, TSP, MP, Gypsum and Borax, respectively. Standard agronomic practices were carried out to raise healthy crop. Data were recorded on plant height, number of primary branches/plant, number of secondary branches/plant, length of siliqua, number of seeds/siliqua, number of siliquae/plant, days to 50% flowering, days to maturity, 1000 seed weight and yield/plant from ten plants selected at random from each line in each replication. The data were analyzed by GENSTAT program. However, genetic diversity was measured through Mahalanobi's (1936) generalized distance (D^2) extended by Rao (1952) and Principal component analysis was done by Rao (1964) for graphical presentation of the genotypes.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the entries for all the ten characters. The principal component analysis showed that the first two components accounted for 55.80% and it was 80.47% in the four components of the total variation.

On the basis of D^2 analysis, by the application of non-hierarchical clustering using co-variance matrix, the 40 *Brassica* germplasms were grouped into six different clusters. Cluster II had maximum ten genotypes followed by cluster V, VI, IV, III and I, which had seven, seven, six, five and five genotypes, respectively.

Table 1. Distribution of 40 *Brassica* germplasms in different clusters

Cluster	No. of genotypes	Name of genotypes	Numbering of genotypes
1	5	SAUYC, BD 9069, BD 9086, BD 9088, BD 6948	19, 37, 38, 39, 40
2	10	BD 9062, BD 9063, BD 9064, BD 9067, BD 9071, BD 9073, BD 9082, BD 9084, BD 7108, BD 9066	1, 2, 3, 4, 6, 7, 13, 15, 35, 36
3	5	BD 9068, BD 9075, BD 9083, BD 9085, BD 9077	5, 9, 14, 16, 23
4	6	BD 9070, BD 9078, BD 9099, BD 9106, BD 6949, BD 7810	21, 24, 25, 28, 29, 30
5	7	BD 9074, BD 9079, BD 9080, BD 9081, BD 9087, BD 6956, BD 9076	8, 10, 11, 12, 17, 18, 22,
6	7	BD 9065, BD 9100, BD 9104, BD 7811, BD 7812, BD 7813, BD 7814,	20, 26, 27, 31, 32, 33, 34

Distantly located genotypes of different clusters were considered for the identification of parental materials for future hybridization program. Canonical Variate analysis was done to calculate the intra and inter cluster distances (D^2) values. Results indicated that the inter cluster distance was larger than intra cluster distances suggesting wider genetic diversity among the germplasms. Islam (1995) obtained larger inter- cluster distances than the intra-cluster distances in a multivariate analysis.

Table 2. Average intra and inter-cluster distances (D^2) for rapeseed and mustard genotypes

Cluster	I	II	III	IV	V	VI
I	**0.8107**					
II	6.531	**0.0203**				
III	11.719	5.909	**0.6789**			
IV	7.835	5.297	5.501	**1.5367**		
V	9.272	4.016	2.513	3.332	**1.596**	
VI	12.443	9.402	6.139	4.715	5.796	**1.0987**

Underlined bold figures denote intra-cluster distances

The maximum inter-cluster distance (12.443) was recorded between clusters I and VI followed (11.719) by between I and III. Genotypes from these clusters could be used in hybridization program. The intra-cluster divergence varied from 0.0203 to 1.596, maximum for cluster V, which was comprised of five genotypes of diverse origin, while the minimum distance was observed in cluster II that comprised of ten genotypes.

These results confirmed the clustering pattern of the germplasms according to the Principal Component analysis (PCA). Based on Principal component axis I and II, a two dimensional chart (Z_1 $-Z_2$) of the genotypes are presented in (Fig. 1). The scatter diagram (Fig. 1) represented that apparently there were mainly six clusters and the genotypes were distantly located from each other.

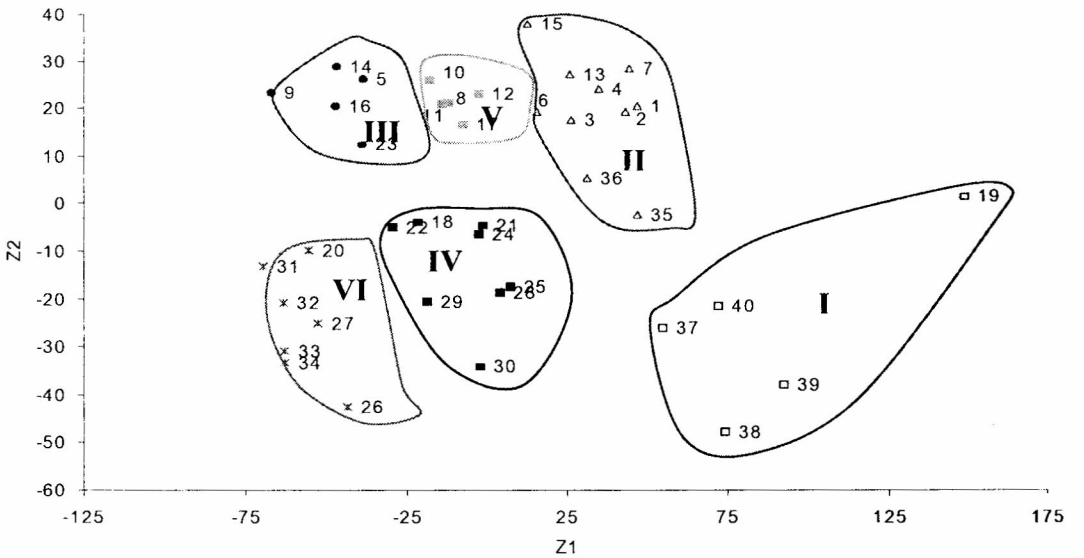

Figure 1. Scatter diagram with clustering pattern of forty mustard germplasms

In the diagram the number indicates the germplasm numbers 1=BD 9062, 2=BD 9063, 3=BD 9064, 4=BD 9067, 5=BD 9068, 6=BD 9071, 7=BD 9073, 8=BD 9074, 9=BD 9075, 10=BD 9079, 11=BD 9080, 12=BD 9081, 13=BD 9082, 14=BD 9083, 15=BD 9084, 16=BD 9085, 17=BD 9087, 18= BD 6959, 19=SAUYC, 20=BD 9065, 21=BD 9070, 22=BD 9076, 23=BD 9077, 24=BD 9078, 25=BD 9099, 26=BD 9100, 27=BD 9104, 28=BD 9106, 29=BD 6949, 30=BD 7810, 31=BD 7811, 32=BD 7812, 33=BD 7813, 34=BD 7814, 35=BD 7108, 36=BD 9066, 37=BD 9069, 38=BD 9086, 39=BD 9088, 40=BD 6948, respectively.

The mean performances of 10 characters in six clusters are shown in Table 3. Most of the characters showed distinct differences among the clusters. According to the above discussion it could be recommended that the materials present in the cluster II are early maturing and simultaneously high yielding as other yield contributing characters are also high in this group.

From the class mean values it was observed that all the cluster mean values for number of primary branches/plant, number of secondary branches/plant, length of siliqua, seed per siliqua, 1000 seed weight, total weight were more or less similar. The maximum range of variability was observed for the characters plant height (50.359-110.999 cm), days to 50% flowering (29.433-60.619 days) and days to maturity (77.267-92.619 days) among all the characters in six clusters.

Table 3. Cluster means for ten characters in mustard

Characters	Cluster					
	I	II	III	IV	V	VI
Plant height (cm)	110.999	64.916	50.359	88.350	62.831	83.433
Primary branch/plant	7.919	6.151	4.431	6.350	5.310	6.142
Secondary branches/plant	4.261	4.674	2.441	2.049	2.095	2.014
Siliqua length (cm)	3.101	3.597	3.256	3.761	3.295	4.180
Seed/siliqua	12.234	13.786	12.017	15.308	13.226	12.932
Siliqua/plant	174.495	124.267	45.079	86.064	76.230	30.327
1000 wt. (g)	2.029	2.750	2.013	2.699	2.032	2.650
Total weight (g)	2.375	1.967	1.374	1.637	1.337	1.032
Days to 50% flowering	51.602	29.433	31.468	51.110	32.856	60.619
Days to maturity	86.534	77.267	77.536	87.557	79.906	92.619

Cluster IV and VI mainly late flowering and late maturing genotypes with low yield, but they were highly heterogeneous in nature. The high yielding lines belonged to the group I and II. To develop high yielding varieties/lines, genotypes of the group could be used in hybridization program.

The PCA revealed that in vector I (Z_1) the important characters responsible for genetic divergence in the major axis of differentiation were number of secondary branches per plant (0.3267), seed per siliqua (0.0602), siliqua per plant (0.2829) and total yield (0.2787) (Table 4). In vector II (Z_2) that was the second axis of differentiation, plant height (0.4325), primary branch/plant (0.5343), secondary branches/plant (0.3242), siliqua length (0.0712), seed/siliqua (0.0447), number of siliquae/plant (0.4692), 1000 seed weight (0.0411), total weight (0.3759), days of 50% flowering (0.1768) and days to maturity (0.1450) were important. The role of number of secondary branches per plant, seeds per siliqua, siliqua per plant and total yield in both the vectors were positive across two axes indicating the important components of genetic divergence in those materials.

Table 4. Latent vectors for 10 morphological characters in rapeseed and mustard

Characters	Vector 1	Vector 2
Plant height (cm)	-0.3148	0.4325
Primary branches/plant	-0.0345	0.5343
Secondary branches/plant	0.3267	0.3242
Length of siliqua (cm)	-0.1728	0.0712
Seeds/siliqua	0.0602	0.0447
Siliquae/plant	0.2829	0.4692
1000 seed weight (g)	-0.1520	0.0411
Total weight (g)	0.2787	0.3759
Days to 50% flowering	-0.5355	0.1768
Days to maturity	-0.5403	0.1450

From the study it was assumed that maximum amount of heterosis will be manifested in cross combinations involving the germplasms belonging to most divergent clusters. Germplasms in cluster I if crossed with VI and III might exhibit high heterosis as well as higher level of production. Considering above discussion the genotypes BD-6948 and SAUYC, from cluster I; BD-9063, BD-9064 and BD-9071 from cluster II; BD-9068 and BD-9077 from cluster III; BD-9078, BD-9106 and

BD-6949 from cluster IV; BD-9079 and BD-9081 from cluster V and BD-9100 and BD-7812 from cluster VI were selected as promising germplasms.

REFERENCES

Anand, I.J. and Rawat, D.S. 1984. Genetic Diversity, combining ability and heterosis in brown mustard. *Indian J. Genet.* 44: 226-234.

Andrahennadi, C.P., Weerasena, L. A. and Aberyrantne, M.D.R.S. 1991. Evaluation of brown mustard germplasms in Srilanka. *Cruciferae Newsletter.* 14 (15): 62-63.

Golakia, P.R. and Makne, V.G. 1992. D^2 analysis in virginia runner groundnut genotypes. *Indian J. Genet.* 55(3): 252-256.

Islam, M.S. 1995. Genetic divergence in groundnut (*Arachis hypogaea* L.). M. S. thesis, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur.

Islam, M.S. and Islam, M.O. 2000. Genetic diversity in rapeseed and mustard (*Brassica* sp.). *Bangladesh J. Pl. Breed. Genet.* 13 (2): 25-30.

Jagadev, P.N., Samal, K.M. and Lenka, L. 1991. Genetic divergence in rape mustard. *Indian J. Genet. Pl. Breed.* 51: 465-466.

Kaul, A. K. and Das, M. L. 1986. Oilseeds in Bangladesh. Bangladesh-Canada Agric. Sector Team-MOA, Bangladesh. 323p.

Mahto, N.R. 1996. Diversity in Indian mustard. *Indian J. Agron.* 45(1): 95-98.

Mahalanobis. P.C.1936. On the generalized distance in statistics. *Indian Proc. Natl. Inst. Sci.* 2: 49-55.

Mitra, S.K. and Saini, S.A. 1998. D^2 and metroglyph analysis in mustard. *Indian J. Genet.* 50(1): 120-125.

Rao, C.R. 1952. *Advance Statistical Methods in Biometrical Research.* John Wiley and Sons. New York.

Rao, C.R. 1954. The use and interception of principal component analysis in applied research. *Sankhya.* 22:317-338.

Singh, P. 1983. Studies on genetic variability and diversity of rice. *Madras Agric. J.* 70(7): 436-440.