

**GENETIC DIVERSITY IN *Brassica rapa* L**

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**ABSTRACT**

The genetic diversity was assessed in 42 *Brassica rapa* genotypes for identifying parental genotypes having distant relationship for hybridization. All the genotypes were analyzed through principal component analysis, principal coordinate analysis canonical variate analysis and non-hierarchical clustering which compute Mahalanobis's  $D^2$  statistics. The genotypes under study were grouped into six clusters. The cluster V contained the maximum numbers of genotypes (15) and cluster III had the minimum number of genotypes (3). The highest intra-cluster distance was observed in cluster V that represented maximum variability within the cluster and Cluster VI had the lowest intra-cluster distance. The maximum inter cluster distance was noticed between the clusters II and III and the lowest between clusters II and VI. Cluster with large distances were considered more diverged than those with small distances. Yield and yield contributing characters such as days to 1<sup>st</sup> flowering, number of siliquae on main racemes, number of siliquae per plant, number of seeds per siliqua, 1000 seeds weight and seed yield per plant contributed more towards genetic divergence considering diversity pattern. Considering cluster distance, inter-genotypic distance, cluster mean and other agronomic performances genotypes BC-200502, BC-200505, BC-200506, BC-200510, BC-200512, BC-200515, BC-200519, BC-200521, BC-200529, BC-200530, BC-200531B, BC-200531Y, BC-200536, BC-200537, BC-200542, BC-200543, BARI Sarisha 12, and BARI Sarisha 14 may be selected from different clusters for hybridization program.

**Key words:** Genetic divergence, *Brassica rapa*, cluster analysis,  $D^2$ -statistics

**INTRODUCTION**

Rapeseed and Mustard belong to the family Cruciferae (Brassicaceae). The tribe has 51 genera including *Brassica* consisting 37 species (Gomez-Campo and Hinata, 1980). The primary center of origin for *Brassica campestris* recently known as *Brassica rapa* is near the Himalayan region and the secondary center of origin is located in the European-Mediterranean area and Asia (Downey and Robbelen, 1989). The seeds of mustard contain 42% oil, 25% protein (Khaleque, 1985). The oil is mainly used as edible oil. The oil serves as solvent of vitamin A, D, E and K. The oil cake contains proteins of high biological value and appreciable quantities of calcium and phosphorus and used as a very good animal feed as well as fertilizer for various crops. Annual requirement of edible oil in Bangladesh is high against the total production. Oilseed crops play a vital role in human diet; the consumption rate of oil in our country is far below than that of

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balanced diet (8 g oil per day per capita) against the optimum requirement of 40 g per head per day (Kaul and Das, 1986). Genetic diversity plays an important role in plant breeding because hybrid between lines of diversified origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent plants to obtain the desirable recombination of the segregating generation. Multivariate analysis is a useful tool in quantifying the degree of divergence between biological population at genotypic level and to assess relative contribution of different components to the total divergence both at intra- and inter-cluster levels (Jatasra and Parada, 1978; Zahan *et al.* 2008). Therefore, the present study was undertaken to identify divergent parents for hybridization program, which would provide superior segregates in mustard genotypes.

## MATERIALS AND METHODS

The experiment was conducted at the experimental field of Genetics and Plant Breeding Department of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur-1706 during the winter season (November 2008 to March 2009) on upland soil. Forty two *Brassica rapa* genotypes were collected from Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur-1706 and Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur, Bangladesh. Randomized Complete Block Design (RCBD) with two replications was followed in this experiment. The plot size was 4m×1.2m and each plot had 4 rows with the distance between rows was 30 cm and between plants was 10 cm. On the other hand, block to block distance and plot to plot distance was 50 cm in each case. The crop was fertilized at the rate of 250, 170, 85, 150 and 10 kg/ha of Urea, TSP, MP, Gypsum and Borax, respectively according to BARI.

**Table 1. Name and sources of collection of 42 *Brassica rapa* genotypes**

Genotype No.	Code Name	Sources of collection	Genotype No.	Code Name	Sources of collection
1	BC-200502	BSMRAU	22	BC-200526	BSMRAU
2	BC-200503	BSMRAU	23	BC-200527	BSMRAU
3	BC-200505	BSMRAU	24	BC-200528	BSMRAU
4	BC-200506	BSMRAU	25	BC-200529	BSMRAU
5	BC-200507	BSMRAU	26	BC-200530	BSMRAU
6	BC-200508	BSMRAU	27	BC-200531B	BSMRAU
7	BC-200509	BSMRAU	28	BC-200531Y	BSMRAU
8	BC-200510	BSMRAU	29	BC-200532	BSMRAU
9	BC-200511	BSMRAU	30	BC-200534	BSMRAU
10	BC-200512	BSMRAU	31	BC-200536	BSMRAU
11	BC-200513	BSMRAU	32	BC-200537	BSMRAU
12	BC-200514	BSMRAU	33	BC-200538	BSMRAU
13	BC-200515	BSMRAU	34	BC-200539	BSMRAU
14	BC-200516	BSMRAU	35	BC-200540	BSMRAU
15	BC-200517	BSMRAU	36	BC-200541	BSMRAU
16	BC-200518	BSMRAU	37	BC-200542	BSMRAU
17	BC-200519	BSMRAU	38	BC-200543	BSMRAU
18	BC-200520	BSMRAU	39	BC-200544	BSMRAU
19	BC-200521	BSMRAU	40	BARI Sarisha 12	BARI, BD
20	BC-200524	BSMRAU	41	BARI Sarisha 14	BARI, BD
21	BC-200525	BSMRAU	42	BARI Sarisha 15	BARI, BD

BSMRAU= Bangabandhu Sheikh Mujibur Rahman Agricultural University, BD=Bangladesh, BC=*Brassica campestris/rapa*, BARI= Bangladesh Agricultural Research Institute

The management of the crop including intercultural operations was done as per recommended practices. Data were recorded from 10 randomly selected plants in each plot for days to 1<sup>st</sup> flowering, days to 50% flowering, days to 100% flowering, days to last flowering, days to maturity, plant height, primary branches per plant, secondary branches per plant, leaf length (cm), leaf width (cm), petiole length (cm), root length (cm), length of main racemes (cm), number of siliquae on main racemes, length of siliqua (cm), length of beak (mm), number of siliqua per plant, number of seeds per siliqua, 1000 seeds weight (g), harvest index (%) and seed yield per plant (g). The data were analyzed following Mahalanobis's D<sup>2</sup>- statistics (Mahalanobis, 1936) and principal component analysis (PCA) for assessment of genetic divergence among the genotypes (Rao, 1952 and Singh and Chaudhary, 1985). All the statistical analysis was carried out using GENSTAT 5 computer based program.

## RESULTS AND DISCUSSION

The analysis of variance (ANOVA) for all the characters was studied showed in Table 2. Among the genotypes almost all characters showed highly significant variation indicating wide range of variability present among the genotypes. In the principal component analysis the eigen values were found as 55.28% in the first two components, whereas six of these eigen values above unity accounted for 79.51% of the total variance (Table 3).

**Table 2. Analysis of variance of the data of 21 important characters in respect of 42 *Brassica rapa* genotypes**

Sl. No.	Characters	Block	Genotype	Error	CV%	LSD (5%)
1	Days to 1 <sup>st</sup> flowering	1.71	5.45**	1.52	4.06	0.54
2	Days to 50% flowering	0.05	15.26**	2.95	4.70	0.76
3	Days to 100% flowering	21.00	15.05**	3.61	4.04	0.84
4	Days to last flowering	70.58	11.36**	2.49	2.14	0.69
5	Days to maturity	0.01	4.31**	1.70	1.55	0.57
6	Plant height (cm)	23.56	79.64**	35.30	5.89	2.62
7	Primary branches per plant	0.96	2.42**	0.54	10.97	0.32
8	Secondary branches per plant	13.04	12.09**	4.52	23.61	0.94
9	Leaf length (cm)	17.13	4.48**	1.42	10.28	0.53
10	Leaf width (cm)	4.70	3.15**	0.51	8.24	0.32
11	Petiole length (cm)	0.44	4.69**	1.94	16.82	0.61
12	Root length (cm)	0.49	2.22**	0.79	8.86	0.39
13	Length of main racemes (cm)	6.22	29.00**	9.82	7.46	1.38
14	No. of siliquae on main racemes	0.32	78.96**	11.74	8.55	1.51
15	Length of siliqua (cm)	0.01	0.28**	0.10	7.87	0.14
16	Length of beak (mm)	1.44	4.96**	1.71	12.17	0.58
17	No.of siliquae per plant	13255.3	1957.4**	803.8	17.4	12.5
18	No. of seeds per siliqua	16.63	7.16**	1.49	7.44	0.54
19	1000 seed weight (g)	0.10	0.11**	0.04	6.50	0.09
20	Harvest index (%)	5.64	21.10**	7.74	9.39	1.23
21	Seed yield per plant (g)	6.94	2.66**	0.57	13.8	0.33

\*\* indicates significant at 1% level of probability.

**Table 3. Eigen values and percentage of variation in respect of 21 characters of 42 *Brassica rapa* genotypes**

Principal component axis	Eigen values	Total variation accounted (%)	Cumulative percentage of variation	Principal component axis	Eigen values	Total variation accounted (%)	Cumulative percentage of variation
1	7.086	33.74	33.74	12	0.321	1.53	94.88
2	4.524	21.54	55.28	13	0.247	1.18	96.06
3	1.684	8.02	63.3	14	0.211	1.01	97.07
4	1.313	6.25	69.55	15	0.169	0.81	97.88
5	1.067	5.08	74.63	16	0.119	0.57	98.45
6	1.025	4.88	79.51	17	0.104	0.50	98.95
7	0.861	4.10	83.61	18	0.074	0.35	99.3
8	0.623	2.97	86.58	19	0.060	0.28	99.58
9	0.567	2.70	89.28	20	0.052	0.25	99.83
10	0.495	2.36	91.64	21	0.039	0.19	100.02
11	0.360	1.71	93.35				

#### Cluster analysis

By application of non-hierarchical clustering using covariance matrix, the 42 genotypes were grouped into six different clusters (Table 4). Cluster V contained the maximum number of fifteen genotypes followed by cluster IV, I and II having eight, six and six genotypes, respectively. Cluster III contained the least number of three genotypes. Verma and Sachan (2000) reported 12 clusters in rapeseed and mustard.

**Table 4. Distribution of 42 *Brassica rapa* genotypes in six clusters**

Clusters	Number of genotypes	Genotypes
I	6 (5,15,16,18,25,37)	BC-200507, BC-200517, BC-200518, BC-200520, BC-200529, BC-200542
II	6 (10,11,19,36,38,40)	BC-200512, BC-200513, BC-200521, BC-200541, BC-200543, BARI Sarisha 12
III	3 (3,41,42)	BC-200505, BARI Sarisha 14, BARI Sarisha 15
IV	8 (1,7,8,13,23,26,31,35)	BC-200502, BC-200509, BC-2005010, BC-200515, BC-200527, BC-200530, BC-200536, BC-200540
V	15(2,6,9,12,17,20,22,24,27,28,29,30,32,33,39)	BC-200503, BC-200508, BC-200511, BC-200514, BC-200519, BC-200524, BC-200526, BC-200528, BC-200531B, BC-200531Y, BC-200532, BC-200534, BC-200537, BC-200538, BC-200544
VI	4 (4,14,21,34)	BC-200506, BC-200516, BC-200525, BC-200539

Canonical variate analysis was done to compute the intra and inter cluster distance ( $D^2$ ) values are presented in Table 6. Results indicated that the inter cluster distances were larger than intra cluster distances in most of the cases suggesting wider genetic diversity among the genotypes of different groups. Singh *et al.*, (1987) also reported about the cluster by using  $D^2$ -statistics. The maximum inter cluster distance was observed between clusters II and III (41.91) followed by III and VI (37.34), III and IV (29.77), I and II (24.15). The maximum inter cluster distance indicated the genotypes in these clusters were far diverse than those of other clusters. The minimum inter-cluster distance was observed between clusters II and VI (4.64) (Table 5) indicating a close relationship among the genotypes of these cluster.

**Table 5. Average intra- and inter-cluster distances ( $D^2$ ) for 42 *Brassica rapa* genotypes**

Cluster	I	II	III	IV	V	VI
I	<b>1.76</b>					
II	24.15	<b>1.56</b>				
III	19.52	41.91	<b>1.22</b>			
IV	10.63	14.04	29.77	<b>1.76</b>		
V	5.87	18.34	24.92	4.86	<b>3.33</b>	
VI	20.01	4.64	37.34	10.54	14.32	<b>0.87</b>

Bold and under line figures denote intra cluster distance

The highest intra-cluster distance was found in cluster V (3.33) followed by cluster IV and I (1.76). The lowest intra-cluster distance was noticed for cluster VI (0.87). These results revealed that the genotypes in cluster V were distantly related; on the other hand the genotypes in cluster VI were closely related. These results confirmed the clustering pattern of the genotypes according to principal component analysis. It is expected in our results that the crosses between the genotypes of cluster II and III, III and VI and III and VI would exhibit high heterosis and produce new combination with desirable traits. The genotypes of distant cluster could be used for further hybridization program.

#### Cluster means for the characters

The mean performances of 21 characters in six clusters are shown in Table 6. Most of the characters showed distinct difference among the clusters. In cluster I, it contained the highest values for the character length of siliqua and the lowest values for the characters days to 100% flowering, days to maturity and 1000 seeds weight. The lowest days to maturity indicated that short durated *Brassica rapa* genotypes could be found from this cluster.

**Table 6. Cluster means for 21 characters of *Brassica rapa* genotypes**

Characters	Cluster					
	I	II	III	IV	V	VI
Days to 1 <sup>st</sup> flowering	30.25	29.92	33.17	30.06	30.13	30.50
Days to 50% flowering	36.08	36.25	39.17	36.13	36.97	35.25
Days to 100% flowering	46.00	46.92	46.83	47.25	47.67	46.00
Days to last flowering	73.50	73.92	68.33	74.12	74.13	74.00
Days to maturity	82.92	84.08	83.67	84.50	84.57	83.75
Plant height (cm)	100.77	103.70	88.65	106.20	99.59	100.16
Primary branches per plant	7.00	6.44	6.95	7.08	6.48	6.19
Secondary branches per plant	6.19	10.48	5.28	10.54	8.27	11.49
Leaf length (cm)	11.05	12.31	7.88	12.45	11.87	11.41
Leaf width (cm)	7.79	8.95	5.78	9.25	9.10	9.35
Petiole length (cm)	7.65	8.34	5.46	9.55	8.38	8.29
Root length (cm)	9.11	11.09	9.00	10.37	9.84	10.78
Length of main racemes (cm)	40.31	44.40	33.41	44.01	42.50	41.75
No. of siliqua on main racemes	38.84	44.70	23.75	42.10	40.34	41.90
Length of siliqua (cm)	4.27	4.14	3.37	3.91	3.90	3.79
Length of beak (mm)	11.02	10.80	7.22	11.37	11.08	10.43
Number of siliquae per plant	138.92	207.94	82.12	172.29	158.27	191.24
Number of seeds per siliqua	17.71	15.67	20.79	16.07	15.69	15.50
1000 seed weight (g)	2.96	2.97	2.98	3.12	3.07	3.08
Harvest index (%)	28.86	31.17	24.83	29.94	29.78	30.84
Seed yield per plant (g)	4.96	6.24	3.69	6.07	5.21	6.18

Cluster II produced the highest cluster mean for the characters root length, length of main racemes, number of pods on main racemes, number of siliqua per plant, harvest index and seed yield per plant and the lowest mean values observed from the character days to 1<sup>st</sup> flowering. Cluster III had the maximum cluster mean for the character days to 1<sup>st</sup> flowering, days to 50% flowering and number of seeds per siliqua and the lowest for the characters days to last flowering, plant height, secondary branches per plant, leaf length, leaf width, petiole length, root length, length of main racemes, number of siliquae on main racemes, length of siliqua, length of beak, number of siliquae per plant, harvest index and seed yield per plant.

Cluster IV comprised the highest mean for the characters plant height, primary branches per plant, leaf length, petiole length, length of beak and 1000 seeds weight. Cluster V had the maximum range of variability for the characters days to 100% flowering, days to last flowering and days to maturity. Finally, cluster VI showed the highest mean for the characters secondary branches per plant and leaf width and the lowest mean values the characters days to 50% flowering days to 100% flowering and primary branches per plant.

#### Contribution of characters towards divergence of the genotypes

Contribution of characters towards divergence of the genotypes is presented in Table 7. Days to 1<sup>st</sup> flowering, number of pods on main racemes, number of siliquae per plant, number of seeds per siliqua, 1000 seeds weight and seed yield per plant in both the vectors had positive signs which indicated that they were the important component characters having higher contribution to the genetic divergence among genotypes studied.

**Table 7. Latent vectors for 21 characters in *Brassica rapa* genotypes**

Characters	Vector I	Vector II	Characters	Vector I	Vector II
Days to 1 <sup>st</sup> flowering	0.03	0.36	Root length (cm)	-0.34	-0.16
Days to 50% flowering	0.13	-0.12	Length of main racemes (cm)	-0.11	-0.53
Days to 100% flowering	-0.10	0.30	No. of siliquae on main racemes	0.20	0.08
Days to last flowering	0.37	-0.04	Length of siliqua (cm)	-0.79	-1.96
Days to maturity	-0.34	-0.48	Length of beak (mm)	-0.62	-1.18
Plant height (cm)	-0.06	-0.08	No. of siliquae per plant	0.35	0.09
Primary branches /plant	0.31	-1.27	No. of seeds per siliqua	0.51	0.12
Secondary branches / plant	0.20	-0.31	1000 seeds weight (g)	2.09	2.23
Leaf length (cm)	-0.23	0.21	Harvest index (%)	-0.21	-0.35
Leaf width (cm)	0.59	-0.66	Seed yield per plant (g)	0.39	1.55
Petiole length (cm)	-0.69	-0.55			

#### Selection of parents for future hybridization

The crossed involving parents belonging to maximum divergent clusters were expected to manifest maximum heterosis and also wide genetic variability. A higher heterosis could be produced from the crosses between genetically distant parents (Ghaderi *et al.*, 1984). Keeping this in view, it appears that crosses between genotypes belonging to cluster cluster II and III, III and VI and III and VI would give high manifestation of heterosis as well as wide spectrum of genetic variation in F<sub>2</sub> generation. Genotypes included in cluster I was important for earliness in maturity, cluster II for number of siliquae per plant, harvest index and seed yield per plant, cluster III for the number of seeds per siliqua and cluster IV for maximum plant height. Considering cluster distance, inter-genotypic distance, cluster mean and other agronomic

performances, genotypes BC-200502, BC-200505, BC-200506, BC-200510, BC-200512, BC-200515, BC-200519, BC-200521, BC-200529, BC-200530, BC-200531B, BC-200531Y, BC-200536, BC-200537, BC-200542, BC-200543, BARI Sarisha 12, and BARI Sarisha 14 may be selected from different clusters for hybridization program.

## REFERENCES

- Downey, R. K. and G. Roebbelen. 1989. *Brassica* species, *In*: G. Roebbelen, R. K. Downey, A. Ashri (eds). Oil crops of the world. Mc Graw Hill Pub. Co. pp. 339-362.
- Ghaderi, A., Shishegar, M., Regai, A. and Ehdaie, B. 1984. Multivariate analysis of genetic diversity for yield and its components in mungbean. *J. American Soc. Hort. Sci.* 104: 728-732.
- Gomez-Campo, C., K. Hinata. 1980. A check list of domestic number in the tribe Brassicaceae; *In*: S. Tsunoda, L. Hinata, C. Gomez-Campo (eds.), *Brassica Crops and wild Allies*. Japan Scientific Press, Tokyo. pp.51-63.
- Jatasra, D. S. and R. S. Parada. 1978. Genetic divergence in wheat under different environmental conditions. *Cereal Res. Comm.* 6: 307-317.
- Kaul, A. K. and M. L. Das. 1986. Oilseeds in Bangladesh. Bangladesh-Canada Agric. Sector term. Ministry of Agric. Govt. of the Peoples' Republic of Bangladesh. 1p.
- Khaleque, M. A. 1985. A Guide Book on Production of Oilcrops in Bangladesh. DAE and FAO/UNDP project BGD/79/034, strengthening the Agricultural Extension service Khamarbari, Framgate, Dhaka. 3p.
- Mahalonobis, P. C. 1936. A statistical study at Chinese head measurement. *J. Asiat. Soc. Bengal.* 25: 301-377.
- Rao, C. R. 1952. *Advanced statistical methods in biometrics research*. John Willey and Sons, Inc., New York.
- Singh R. P., D.P. Singh. and B. D. Chaudhury. 1987. Morphological variation in Indian mustard. *Annal. Biol.* 3(1): 26-31.
- Singh, P. 1983. Studies on genetic variability and diversity of rice. *Madras Agric. J.* 70(7): 436-440.
- Singh, R. K. and B. D. Chaudhary. 1985. *Biometrical methods in quantitative genetic analysis*. The Kalayni Publishers. New Delhi, India.
- Verma, S. K. and J. N. Sachan. 2000. Genetic divergence in Indian mustard [*Brassica juncea* (L.) Czern and Coss]. *Crop Res. Hisar.* 19 (2): 271-276.
- Zahan, M.I., M. S. R. Bhuiyan, and M. S. Hossain. 2008. Genetic divergence in Oleiferous *Brassica* species. *J. Sher-e-Bangla Agric. Univ.* 2(1):1-6.