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GENETIC DIVERGENCE IN OLEIFEROUS *Brassica species*

M. I .Zahan[1], M. S. R. Bhuiyan[2] and M. S. Hossain[3]

ABSTRACT

Genetic divergence among 41 genotypes of rapeseed and mustard was estimated using D^2 analysis. In each case of three species *B. napus, B. rapa and B. juncea* the genotypes under study fell into six clusters. The inter-cluster distances were larger than the intra-cluster distances in each species suggesting wider genetic diversity among the genotypes of each species. In *Brassica napus* Cluster II had the highest intra-cluster distance. Cluster I and III had no intra cluster distance because only one genotype was under each of the both clusters. Inter cluster distance was maximum between clusters II and IV. In *Brassica rapa* Cluster II had the highest intra-cluster distance and Clusters I, V and VI had the lowest intra cluster distances. Inter cluster distance was maximum between clusters I and IV. In *Brassica juncea* Cluster I had the highest intra-cluster distance while clusters II and VI had the lowest or no intra cluster distance. Inter cluster distance was maximum between clusters I and IV. The results revealed that genotypes chosen for hybridization from clusters with highest distances would give high heterotic F_1 and broad spectrum of variability in segregating generations.

Key words: genetic divergence, Oleiferous *Brassica*, intra and inter class distance and variability

INTRODUCTION

The oleiferous *Brassica* viz. rapeseed and mustard is one of the leading oilseed crops in our country. In Bangladesh more than 210.57 thousand metric ton of rape and mustard seeds are produced from 279.23 thousand hectares of land cultivated in the year 2003-2004 (BBS, 2005). In the oleiferous *Brassica* group, a considerable variation of genetic nature exists among different species and varieties within each species also vary from each other in respect of different morpho-physiological characters (Malik *et al.*, 1995; Nanda *et al.*, 1995; Kakroo and Kumar, 1991; Singh *et al.*, 1991, Li, *et al.*, 1989). Hybridization is one of the major tools for the improvement of a crop. Before hybridization genetic diversity of the existing varieties need to be known. It is well established that the greater the genetic diversity the higher the chance of getting better hybrid or useful recombinant. It is a major tool being used in parent selection for efficient hybridization program (Bhatt, 1973; Khanna and Chaudhary, 1974, Chandra, 1977). The present study was therefore undertaken to categorise the various germplasm and analyze the genetic diversity of the genotypes in respect of different morphological characters.

MATERIALS AND METHODS

Forty one genotypes of three species of oleiferous *Brassica* were grown in a randomized complete block design (RCBD) with 3 replications at the experimental field of Sher-e Bangla Agricultural University, Dhaka, Bangladesh during the period from November 2005 to March 2006.

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[1]Intern in R&D, ACI Seed, Dhaka, [2&3]Professor, Dept. of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

There were 123 plots, each measuring 1.5 m × 1.0 m. The 41 genotypes of the experiment were assigned at random into 41 plots of each replication. Optimum amount of fertilizers were applied for growing the crops. The other intercultural operations were done timely to raise the crop properly. The crop was harvested depending upon the maturity of each genotype. Observations were recorded from 10 randomly selected plants of each entity in each plot for days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, length of siliquae (cm), number of seed per siliquae, 1000 seed weight per plant, yield/plant. Genetic divergence among the genotypes study was assessed by using D^2 statistics.

RESULTS AND DISCUSSION

The composition of different clusters with their corresponding genotypes based on genetic divergence study among the genotypes under each of three oleiferous *Brassica* species are shown in Table 1.

Table1. Clustering pattern of 15 *Brassica napus,* 13 *B. rapa* and 13 *B. juncea* genotypes by Tocher's method

Cluster group	Number of genotypes	Name of the genotypes
B. napus		
I	1	BD-7789
II	2	BD-7834, BD-7830
III	1	BD-7836
IV	3	BD-7833, BD-9101, BD-9102
V	2	BD-7128, BD-7832
VI	6	BD-7815, BD-7831, BD-7126, BD-7788, BD-7835, BD-7790
B. rapa		
I	1	BD-7102
II	2	BD-7958, BD-7114
III	4	BD-7129, SAU-YC, BD-7118, BD-7125
IV	4	BD-6955, BD-7113, BD-7115, BD-9061
V	1	BD-7837
VI	1	BD-7116
B. juncea		
I	2	BD-7127, BD-8884
II	1	BD-7136
III	4	BD-7131, BD-7132, BD-7107, BD-7104
IV	2	BD-7133, BD-7135
V	3	BD-7137, BD-7117, BD-7138
VI	1	BD-7134

The 15 genotypes of *B. napus* fell into 6 clusters. Cluster VI was the largest cluster comprising of 6 genotypes followed by cluster IV with 3 genotypes. The 13 genotypes of *B. rapa* fell into 6 clusters. Cluster III and IV was the largest cluster comprising of 4 genotypes. The 13 genotypes of *B. juncea* fell into 6 clusters. Cluster III was the largest cluster comprising of 4 genotypes.

Intra and inter cluster distances among the different genotypes under each of three species are presented in Table 2.

Table 2. Average intra (bold) and inter-cluster D^2 and D values of 6 clusters for 15 *B. napus*, 13 *B. rapa* and 13 *B. juncea* genotypes formed by Tocher's method

Clusters	I	II	III	IV	V	VI
B. napus						
I	**0.00** **(0.00)**	5.258 (2.293)	6.212 (2.492)	7.111 (2.667)	4.485 (2.118)	2.358 (1.536)
II		**0.789** **(0.888)**	6.478 (2.545)	3.133 (1.770)	8.114 (2.849)	3.587 (1.894)
III			**0.00** **(0.00)**	9.557 (3.091)	5.879 (2.425)	6.000 (2.449)
IV				**0.645** **(0.803)**	3.515 (1.875)	9.335 (3.055)
V					**0.333** **(0.577)**	6.582 (2.566)
VI						**0.666** **(0.816)**
B. rapa						
I	**0.00** **(0.00)**	5.336 (2.310)	7.558 (2.749)	8.557 (2.925)	4.892 (2.212)	6.223 (2.495)
II		**0.901** **(0.949)**	5.328 (2.308)	7.665 (2.769)	5.712 (2.390)	3.598 (1.897)
III			**0.666** **(0.816)**	6.325 (2.515)	7.253 (2.693)	3.278 (1.811)
IV				**0.421** **(0.649)**	5.444 (2.333)	5.478 (2.341)
V					**0.00** **(0.00)**	6.195 (2.489)
VI						**0.00** **(0.00)**
B. juncea						
I	**0.779** **(0.883)**	4.225 (2.055)	5.212 (2.283)	8.912 (2.985)	5.221 (2.285)	2.958 (1.719)
II		**0.00** **(0.00)**	7.526 (2.743)	3.558 (1.886)	8.332 (2.887)	5.558 (2.358)
III			**0.748** **(0.865)**	2.338 (1.529)	5.338 (2.310)	7.338 (2.709)
IV				**0.488** **(0.699)**	2.552 (1.597)	3.889 (1.972)
V					**0.763** **(0.874)**	5.111 (2.261)
VI						**0.00** **(0.00)**

In *B. napus* cluster II had the highest intra-cluster distance (0.789) and Cluster I and III had no intra cluster distance (0.00) because only one genotype was included in each of both the cluster. Inter cluster distance was maximum between cluster II and IV (9.557). In *B. rapa* clusters II had the highest intra-cluster distance (0.901) and cluster I, V and VI had the lowest intra cluster distance . Inter cluster distance was maximum (8.557) between clusters I and IV. Golakiya and Makne (1991) while assessing genetic diversity of 23 genotypes of rapeseed grouped them into six clusters. Inter and intra cluster values (D) were reported to be ranged from 9.50 to 22.20 and 5.18 to 8.45. In *B. juncea* cluster I had the highest intra-cluster distance (0.779) followed by cluster V (0.763), cluster III (0.748) and IV (0.488) while cluster II and VI had no intra cluster distance. Inter cluster distance was maximum (8.912) between clusters I and IV, followed by clusters II and V (8.332). The results revealed that genotypes chosen for hybridization from clusters with highest distances among each species would give high heterotic F_1 and broad spectrum of variability in segregating generations.

From the cluster mean value of different characters of *B. napus* genotypes (Table 3) it was observed that the mean value of cluster I ranked first for days to 50% flowering, days to maturity, plant height, primary branches per plant, number of siliquae per plant, seed per siliquae, 1000 seed weight per plant and yield per plant. Cluster II ranked first for secondary branches per plant. Cluster III ranked for length of siliquae.

Table 3. Cluster means for 10 characters of 15 *B. napus* genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50% flowering	51	41	38	39.78	43.17	47.58
Days to maturity	94	83.75	81.33	81.89	81.67	87.11
Plant height	112.5	82.1	83.36	79.94	85.52	87.86
Number of primary branches/plant	10.5	10	5.97	4.98	4.74	5.73
Number of secondary branches/plant	5.13	6.15	3.5	2.71	2.6	3.21
Number of siliquae/plant	145.25	71.74	66.73	60.86	61.38	37.78
Length of siliquae	5.46	5.6	6.03	4.95	4.92	4.13
Number of seed/siliquae	21.88	17.89	16.11	17.4	17.08	11.94
1000 seed weight / plant	3.31	3.2	3.27	3.12	3.19	2.66
Yield/plant	8.38	1.97	1.77	1.45	1.54	1.16

From the cluster mean value for the genotypes under *B. rapa* species (Table 4) it was observed that the mean value of cluster I ranked first for secondary branches per plant. Cluster II ranked first for siliquae per plant. Cluster III ranked for primary branches per plant and yield per plant and cluster IV ranked for number of seed per siliquae. However, cluster V ranked for days to 50% flowering, plant height, 1000 seed weight per plant. On the other hand, cluster VI ranked for days to maturity.

Table 4. Cluster means for 10 characters of 13 *B. rapa* genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50% flowering	27	30.33	41.36	36.8	43.33	42.33
Days to maturity	67.67	76	81.1	80.7	79.67	82.67
Plant height	57.78	71.52	93.01	75.20	103.3	88.77
Number of primary branches/plant	4.36	5.55	7.28	5.29	5.3	5.4
Number of secondary branches/plant	8.12	7.48	0	1.85	0	0
Number of siliquae/plant	144.33	146.65	97.4	76.61	65.3	73.3
Length of siliquae	3.58	4.21	4.37	4.08	3.52	4.51
Number of seed/siliquae	22.8	17.88	24.65	25.85	22	22.5
1000 seed weight / plant	3.09	2.74	3.14	2.68	3.48	2.72
Yield/plant	4.02	4.41	6.14	4.19	5.92	4.9

From the cluster mean value for the genotypes of the *B. juncea* (Table 5) it was observed that the mean value of cluster I ranked first for days to 50% flowering, days to maturity, plant height, primary branches per plant, siliquae per plant, seed per siliquae, and yield per plant. Cluster II ranked first for secondary branches per plant, length of siliquae, 1000 seed weight per plant.

Table 5. Cluster means for 10 characters of 13 *B. juncea* genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Days to 50% flowering	48.33	37	36.5	39.83	39.22	36.33
Days to maturity	86.67	79	80.5	81.33	83.11	86
Plant height	152.23	105.13	101.42	101.48	96.39	94.27
Number of primary branches/plant	6.23	9.4	7.93	6.52	5.97	7.6
Number of secondary branches/plant	8.93	6.43	7.59	6.38	3.34	4.2
Number of siliquae/plant	203.72	77.23	162.65	133.27	113.14	107.4
Length of siliquae	3.25	3.58	3.41	3.01	3.13	3.02
Number of seed/siliquae	14.17	14.77	13.68	13.11	12.58	13.4
1000 seed weight / plant	3.1	3.15	2.69	2.63	2.48	2.89
Yield/plant	7.62	5.95	5.35	5.84	4.66	3.62

Baydar and Bayraktar (1994) reported 35 genotypes of *Arachis hypogaea* which were divided into 6 clusters of different genetic divergences. Islam and Islam (2000) evaluated the genetic diversity in rapeseed and mustard using D^2 analysis of 42 genotypes. The genotypes were grouped into four clusters. The inter cluster distances were larger than the intra cluster distances. Badignnavar *et al.* (2002), Joel and Mylsamy (1998) also found the same results and observed that inter cluster distances were larger than that of intra cluster distances. Reddy *et al.* (1987) found maximum inter cluster distance between cluster I and II in his study. All these findings supported the results of the study.

The crosses involving parents belonging to the most diverged custers are expected to manifest higher heterosis (Mian and Bhal, 1989). Genotypes BD-7834 and BD-7830 from cluster amd genotypes BD-

7833, BD-9101, BD-9102 from cluster IV were found promising for improving the characters days to maturity, plant height and number of siliqua per plant in case of *B. napus*

For *B. rapa*, genotype BD-7102 from cluster I might give good result with genotypes BD-6955, BD-7133, BD-7115, BD-9061 from cluster IV for number of siliqua per plant. For *B. Juncea*, however, genotypes BD-7127 and BD-8884 from cluster I could show much better performance with genotypes BD-7133 and BD-7135 from cluster IV for the traits number of siliqua per plant and plant height. Therefore, considering cluster distance and other agronomic performances the genotypes of the two groups in each species could be selected for future breeding programme.

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