

*Full Length Research Paper*

## Genetic divergence in mustard (*Brassica* spp. L)

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Accepted 3 June, 2011

A field experiment was conducted with 25 mustard (*Brassica* spp. L) genotypes on the farm of Hajee Mohammad Danesh Science and Technology University, Dinajpur, Bangladesh from November 2009 to February 2010, to study the genetic diversity present among the genotypes. Eleven quantitative characteristics, namely plant height, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, diameter of siliqua, length of siliqua, number of seed per siliqua, 100 seed weight and yield per plant were taken into consideration. The analysis of variance revealed a remarkable variability among the genotypes in terms of the specified characteristics. Cluster analysis was used for grouping the 25 mustards (*Brassica* sp. L) genotypes into six clusters. Cluster II had the maximum number (13) of genotypes, while Clusters IV, V, and VI had the minimum number (2) of genotypes. The highest inter-cluster distance was observed between Clusters I and IV, while the lowest inter-cluster distance was observed between Clusters V and VI. Cluster II ( $D = 4.91$ ) had the highest intra-cluster distance, while Cluster II (5.607) had the lowest intra-cluster distance. The characteristics such as plant height, number of secondary branches per plant, and number of siliqua per plant contributed greatest towards the divergence in the mustard genotypes. Considering diversity analysis, the genotypes, BARI-11, BARI-12, and BARI-9 from cluster III had the highest yield, early flowering, and fruit maturity; the genotypes DAULAT and BARI-14 from Cluster IV had the highest number of siliqua per plant, number of secondary branches per plant, and yield per plant and may be considered as the best parents for future hybridization program.

**Key words:** *Brassica* spp. L, genotypes, cluster, Bangladesh.

### INTRODUCTION

The cultivated mustard (*Brassica* spp. L) is an ancient crop of the new world which originated in Asia, Europe and perhaps Africa, where it is cultivated in 1200 B.C. Canada is the largest producer of mustard seed in the world, and accounts for about 97% of world exports (Man and Weir, 2009). The acreage production of rape seed and mustard in Bangladesh during 2007 to 2008 fiscal year was 431078 and 153588 metric tones respectively. The average yield of *Brassica* oilseed in Bangladesh is around 356 kg/acre (BBS, 2008). Global mustard seed output is forecast at 50 million tons in 2008 to 2009 from 49 million in the previous year where mustard oil production is at 20 million tons (SMDC, 2009).

A large number of edible oil seed crops are growing in

Bangladesh. But acute edible oil in the country is increasing every year with the increase in population growth. Majority of Bangladesh people are suffering from an acute shortage of protein calorie malnutrition. The seed has oil as high as 46 to 48% which seed meal has 43.6% protein. Mustard protein value is 24.94 g (USDA, 2005). The family contains species of great economic importance, providing much of the World's winter vegetables. Mustard is a cool season crop that can be grown in short growing season. As a major oil producing crop, per acre yield of mustard seed is considerably lower than those of other developing countries. The yield potentiality of our varieties is now at stagnant position. To overcome this situation we have to emphasize on the physiology of the crop. Identification of physiological characteristics and their relationship with yield modification according to our choice are nowadays very important. Keeping this idea in mind a good number of

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physiological characteristics have been included in the present study.

Genetic divergence is essential to select the parents for future breeding program. If the parent is more diverse, the chances of obtaining high erotic  $F_1$  and broad spectrum variability in segregating generations are greater (Arunachalam, 2006). Genetic divergence has been measured successfully by many researchers, following Mahalanobis (1936)  $D^2$ -Analysis. With the development of advancement biometric techniques such as multivariate analysis, quantification of degree of divergence among the biological population and assessing the relative contribution different component to the total divergence at intra and inter cluster levels have now become possible. Limited work has been done on genetic divergence of mustard with physiological characteristics. The present study was undertaken to analyze the genetic divergence of 25 genotypes mustard.

## MATERIALS AND METHODS

The experiment was laid out in a Randomized Complete Block Design with three replications at the experimental field of the Department of the Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, during the period from November, 2009 to February, 2010 to study the genetic divergence of mustard. The 25 indigenous variety of mustard were taken as experimental crop and that is why each replication contained 25 plots. Each plot contained 5 line seedlings and each line contained 20 plants. The unit plot size was  $1 \times 0.75$  m. Plant to plant distance was 5 cm while row to row was 15 cm. The spaces between replications and between plots were  $0.5 \times 0.5$  respectively. There were  $57.25 \text{ m}^2$  plots in the experiment. Weeding was done as and when necessary to keep the crop free from weeds. Flood irrigation was given to the plants when necessary.

Observations were recorded on the ten randomly selected plants from each plot for eleven characteristics, namely plant height, days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, diameter of siliqua (mm), plant length of siliqua (cm), number of seed per siliqua, 1000 seed weight (g), yield per plant (g) of 25 genotypes of mustard. The data were analyzed on June, 2010 using Mahalanobis- $D^2$  statistics and principal component analysis (PCA) by utilizing GenStat, seventh edition and version- 7.2.2.222 programme.

## RESULTS AND DISCUSSION

Results of analysis of variance showed significant differences among the genotypes suggested the presence of sufficient variability in the genotypes selected for the study. Highly significant differences were also found among the genotypes for 9 characteristics in mustard genotypes by earlier findings (Chauhan et al., 2008). Based on the degree of divergence among twenty five genotypes were grouped into six clusters (Table 1).

The computation from covariance matrix gave non-hierarchical clustering based on Mahalanobis- $D^2$  values among 25 genotypes and grouped them into six

clustering. 40 rapeseed-mustard cultivars were grouped into 8 clusters while 81 mustard cultivars grouped into 13 clusters by Chauhan et al. (2008) and Vivek et al. (2007) respectively. The clusters occupied by 25 genotypes of mustard are presented in Table 1. It explained that Cluster II contained highest thirteen genotypes followed by Cluster I and III each having 3 genotypes, Cluster IV, V, and VI each having 2 genotypes in Table 1.

According to Mahalanobis- $D^2$  statistics the intra and inter cluster distance ( $D^2$ ) values are presented in Table 2. Results indicated that the highest inter cluster distance was observed between I and IV ( $D = 4.62$ ) followed by IV and V ( $D = 4.15$ ), IV and VI ( $D = 4.13$ ). The lowest inter cluster distance was observed between the Clusters V and VI ( $D = 0.46$ ) followed by II and VI ( $D = 1.74$ ), II and V ( $D = 1.76$ ), suggesting close relationship among these three clusters. However, the maximum inter cluster distance were recorded between I and IV ( $D = 4.62$ ) followed by IV and V ( $D = 4.15$ ), IV and VI ( $D = 4.13$ ). Intra cluster distance was highest in Cluster II (2.36). This result is similar with previous findings (Ashwini et al., 2004). Genotypes from these four clusters if involve in hybridization may occur a wide spectrum of segregating population as genetic diversity is very distinct among the groups.

From the clusters studied in Table 3, Clusters I, II, III and VI were the early maturing types and Clusters IV, V were the late maturing types. Moreover, Cluster IV took maximum time of flowering (41.00) days of flowering and others took less days of flowering on the other hand number of seed per siliqua was highest in Cluster V (20.69) and lowest in Cluster III (12.02). Finally, yield per plant was highest in Cluster III (5.01) and IV (4.52), lowest in VI (2.22). To develop high yielding varieties geno-types of these two groups can be used for further hybridization programme (Table 3).

Group constellations were also independently developed by using principal component analysis (PCA) to verify grouping obtained through  $D^2$  statistics. The scores obtained through first two components were plotted against two main axes and then superimposed with clustering (Figure 1). Therefore, this clustering pattern confirmed the results obtained by  $D^2$ -analysis.

The PCA revealed that in both Vectors 1 and 2, the important characteristics responsible for divergence were length of siliqua, days to maturity, number of primary branches per plant, number of secondary branches per plant, number of siliqua per plant, diameter of siliqua, number of seed per siliqua (Table 4). In both vectors, there was a high and positive value which indicated that these characteristics contributed maximally towards divergence (Rahman and Al Munsur, 2009). On the other hand, negative values for Vectors 1 and 2 for the characteristics such as days to 50% flowering, 1000 seed weight, and yield per plant indicated the lowest contribution to the total divergence. The greater divergence in the present materials is due to these three

**Table 1.** Distribution of 25 genotypes of mustard in six clusters.

Cluster no.	Number of genotypes	Genotypes	Accession no.	Source	Origin
I	3	SS-75	1	BARI, Joydebpur	Bangladesh
		BARI-14	2	BARI, Joydebpur	Bangladesh
		BD-7131	20	BARI, Joydebpur	Bangladesh
II	13	BARI-7	4	BARI, Joydebpur	Bangladesh
		TS-72	5	BARI, Joydebpur	Bangladesh
		TORI-7	10	BARI, Joydebpur	Bangladesh
		BARI-15	7	BARI, Joydebpur	Bangladesh
		BARI-6	8	BARI, Joydebpur	Bangladesh
		BC-2193	11	BARI, Joydebpur	Bangladesh
		BARI-13	12	BARI, Joydebpur	Bangladesh
		BD-7118	17	BARI, Joydebpur	Bangladesh
		BD-7112	19	BARI, Joydebpur	Bangladesh
		BD-7113	21	BARI, Joydebpur	Bangladesh
		BD-7800	22	BARI, Joydebpur	Bangladesh
III	3	BD-7127	24	BARI, Joydebpur	Bangladesh
		BD-7108	25	BARI, Joydebpur	Bangladesh
		BARI-11	9	BARI, Joydebpur	Bangladesh
IV	2	BARI-12	15	BARI, Joydebpur	Bangladesh
		BARI-9	16	BARI, Joydebpur	Bangladesh
V	2	DAULAT	13	BARI, Joydebpur	Bangladesh
		BARI-10	14	BARI, Joydebpur	Bangladesh
VI	2	NAP-9906	3	BARI, Joydebpur	Bangladesh
		BARI-8	6	BARI, Joydebpur	Bangladesh
VI	2	BD-116	6	BARI, Joydebpur	Bangladesh
		BD-7136	18	BARI, Joydebpur	Bangladesh

Where, BARI = Bangladesh Agricultural Research Institute.

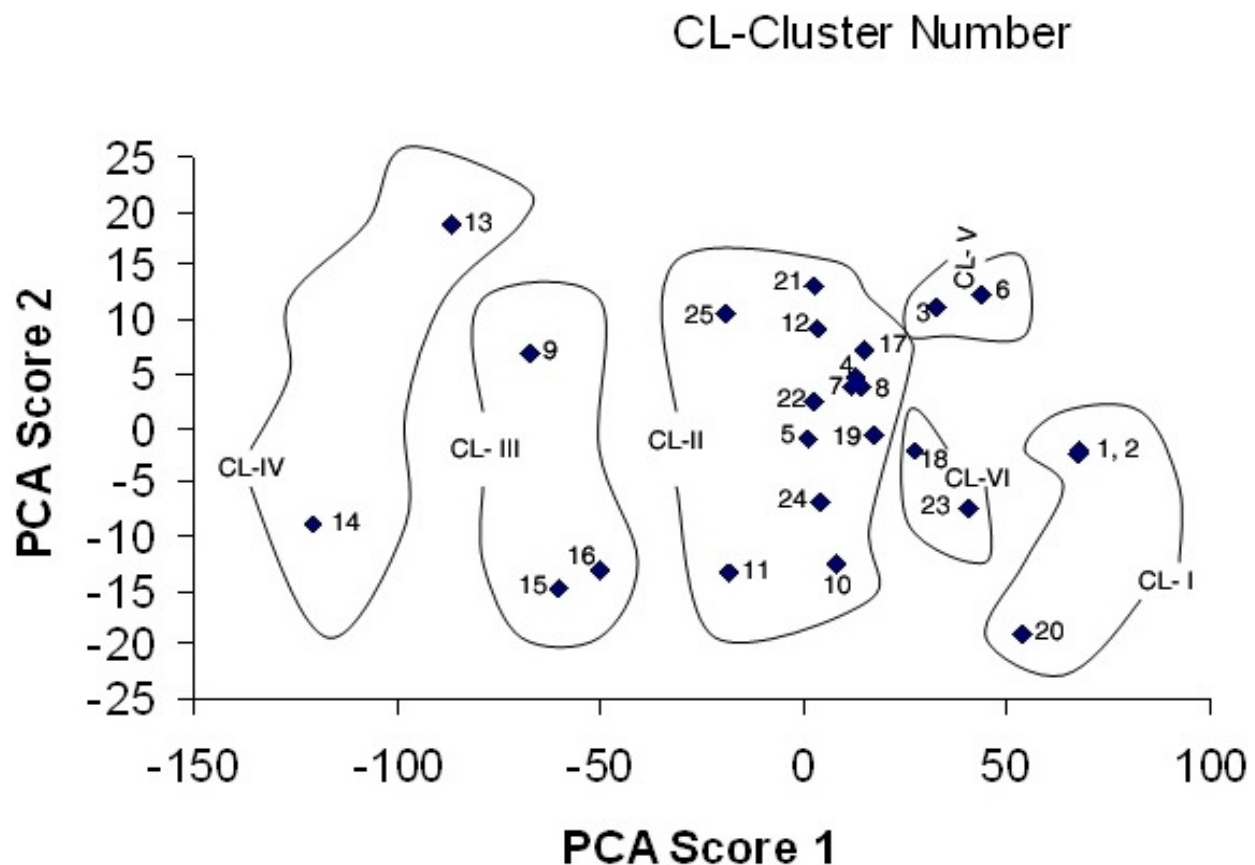
**Table 2.** Average intra (Bold) and inter distances ( $D^2$  and  $\sqrt{D^2} = D$ ) values for six clusters formed by Tocher's method.

Clusters	I	II	III	IV	V	VI
I	1.119 (1.05)	6.819 (2.61)	13.054 (3.61)	21.387 (4.62)	4.160 (2.03)	4.364 (2.08)
II		5.607 (2.36)	6.235 (2.49)	15.553 (3.94)	3.126 (1.76)	3.039 (1.74)
III			0.571 (0.75)	11.284 (3.35)	9.188 (3.03)	9.046 (3.00)
IV				0.297 (0.54)	17.281 (4.15)	17.066 (4.13)
V					0.273 (0.52)	0.220 (0.46)
VI						0.764 (0.87)

Figures within parenthesis indicate D value.

**Table 3.** Cluster means for 11 characteristics of 25 mustard genotypes.

Components	Clusters					
	I	II	III	IV	V	VI
Plant height (cm)	69.34	95.01	103.65	126.70	94.65	80.94
Days to maturity	110.57	111.31	111.87	115.85	115.80	112.50
Days to 50% flowering	39.45	37.33	38.44	41.00	39.84	37.66
Number of primary branches/ plant	3.24	4.33	5.53	5.68	2.80	3.95
Number of secondary branches/ plant	0.78	1.51	4.62	8.08	0.72	2.18
Number of siliqua per plant	41.73	95.47	158.63	197.90	60.29	68.27
Diameter of siliqua (mm)	4.28	2.60	2.54	2.13	2.95	2.16
Length of siliqua (cm)	4.39	4.81	4.27	3.80	7.32	4.73
Number of seed per siliqua	19.11	15.76	12.02	13.05	20.69	13.54
1000 seed weight (g)	3.67	3.67	4.32	3.43	4.61	3.20
Yield per plant (g)	2.27	2.82	5.01	4.52	2.81	2.22

**Figure 1.** Scatter diagram on 25 genotypes of mustard based on their principal component scores superimposed with clustering.

characteristics which will offer a good scope for improvement of yield through rational selection of parents for producing heterotic mustard hybrid. Considering the previous findings of diversity analysis in the genotypes, BARI-11, BARI-12, BARI-9 from Cluster III for higher

yield, early flowering and fruit maturity; the genotypes DAULAT and BARI-14 from Cluster IV for higher number of siliqua per plant, number of secondary branches per plant, yield per plant might be considered to be better parents for future hybridization programme.

**Table 4.** Latent vectors for 11 characteristics of mustard (*Brassica* sp. L) genotypes.

Characteristics	Vector 1	Vector 2
Plant height (cm)	0.0485	-0.0657
Days to maturity	0.1602	0.3372
Days to 50% flowering	-0.0822	-0.0496
Number of primary branches/ plant	0.6090	0.4356
Number of secondary branches/ plant	0.9179	1.2195
Number of siliqua per plant	0.0879	0.0153
Diameter of siliqua (mm)	0.4477	1.0632
Length of siliqua (cm)	0.9537	1.1022
Number of seed per siliqua	0.1228	0.3034
1000 seed weight (g)	-1.1568	-1.7549
Yield per plant (g)	-0.9323	-1.9637

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