

**MULTIVARIATE ANALYSIS OF DIVERGENCE IN ADVANCED LINES OF
MUSTARD (*Brassica spp*)**

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ABSTRACT

A field experiment was conducted comprising eighteen advanced lines of mustard in a randomized block design with three replication at Regional Agricultural Research Station, BARI, Hathazari, Chittagong during Rabi season (December 2009 to April 2010) for estimation of divergence among advanced lines of mustard. The genotypes were grouped into four clusters. Cluster I contained the highest number of genotypes (6) and the cluster III contained the lowest (3). The inter-cluster distances in all cases were larger than the intra-cluster distance which indicated that wider diversity was present among the genotypes of distant grouped. The highest intra cluster distance was observed in cluster II and the lowest in I. The highest inter cluster distance was observed between the cluster III and II followed by III and I and the lowest between cluster IV and III. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed maximum towards the total divergence which suggested that these characters were highly responsible for genetic divergence in the present materials. But the highest cluster means for primary branches per plant and maximum seeds per siliquae with minimum seed yield per plant were obtained from the cluster II. The genotypes from cluster I had dwarf plant along with earliness in days to 50% flowering, days to maturity and maximum number of primary branches per plant. Therefore, the genotypes from cluster I and III could be utilized in the hybridization programme for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration.

Key words: Multivariate analysis, Divergence and Mustard

INTRODUCTION

Mustard has been grown in the Indian sub continent for hundreds of years as an oil seed crop (Labana and Gupta, 1993). Rape seed mustard crop account for almost 14 percent of the edible vegetable oil supply of the world demand (Kour and Singh 2004). The annual production of rapeseed mustard in our country is 203 thousand metric tons from 578 thousand acres of land during 2008-09 (BBS, 2010). The seed of rapeseed mustard contain 42% oil and 25% protein (Khaleque, 1985). Its oil is mainly used for food cooking purpose Its oil and fat are not only the source of energy but also contain fat-soluble vitamins A, D, E, and K (Mahmud *et al.*, 2008). The oil cake is used as a very good animal feed as well as fertilizer for better improvement of soil status because of its high biological protein value as well as source of calcium and phosphorus.

Genetic diversity is the pre-requisite for hybridization programme to obtain desirable genotypes. Genetic diversity is very much essential to meet the diverse goals in plant breeding such as for producing cultivars with increased yield (Joshi and Dhawan, 1966), wider adoption, desirable quality and pest resistance (Nevo *et al.*, 1982). Obtaining the high heterotic F_1 and broader spectrum of variability in succeeding segregating generations depends upon the using of more diverse parents (Arunachalm, 1981). According to Tomooka (1991), the evaluation o diversity is important to know the source of genes for particular trait within the available germplasm. So, to know the genetic diversity of the existing genotypes is essential before undertaking any crop improvement programme. Therefore, the present study was carried out to estimate the nature and magnitude of genetic diversity present in a collection of 18 advanced lines of mustard.

MATERIALS AND METHODS

An experiment comprising 18 mustard genotypes was conducted in a randomized block design with three replication at Regional Agricultural Research Station, BARI, Hathazari, Chittagong during Rabi season November 2009 to February 2010. The unit plot size was six rows of 4 meter length. The inter row to row and plant to plant spacing were maintained at 30 cm and 5 cm, respectively. Recommended fertilizer doses, cultural practices and all plant protection measures were followed to ensure a good crop. The data on nine morphological characters namely days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of siliquae per plant, number seeds per siliquae, 1000 seeds weight (g), seed yield per plant (g) and seed yield per hectare (kg) were recorded. Genetic diversity were studied following Mahalanobis (1936) generalized distance (D^2) extended by Rao (1952). Based on the D^2 values, the studied genotypes were grouped into clusters according to the Tocher's method (Rao, 1952). The methods of Singh and Chowdhury (1985) were used for calculating the intra and inter cluster distances. Statistical analyses were carried out by Genstat Discovery edition 3.

RESULTS AND DISCUSSION

The analysis of variance and dispersion showed highly significant variations among the different genotypes for all the eight characters under study, which revealed the presence of considerable variability among the genotypes. The eighteen genotypes were grouped into four clusters using the closer genetic distance in such a way that the genotypes within the cluster had smaller D^2 values among themselves than those belonging to different clusters (Table 1). Pattern of distribution of genotypes among various clusters reflected the considerable genetic variability present in the genotypes under study. The maximum number of genotypes (6) were comprised into cluster I followed by five in cluster IV. The minimum genotypes (3) comprised into cluster II. The *Brassica campestris* genotypes were grouped into cluster I and II whereas the *Brassica juncea* genotypes were grouped into cluster III and IV respectively, which indicated that genotypes of quite different pedigree may fall into the same cluster, due to unidirectional selection pressure that could yield the genotypes, which were genetically closer than their parents. This was due to homogeneity in parental sources. Bansal *et al.* (1990) reported that clustering pattern was influenced by the pedigree of breeding lines. Similar results were found in case of *Brassica juncea* (Singh *et al.*, 2010). The D^2 analysis showed intra and inter-cluster distance (Table 2). The inter-cluster distances in

all cases were larger than the intra-cluster distance which indicated that wider diversity was present among the genotypes of distant grouped.

Table 1. Distribution of mustard genotypes in different clusters

Cluster no.	No. of Genotypes	No. of population	Mustard Genotypes
I	1, 2, 3, 4, 5, 15	6	BC-9922, BC-9909, BC-9917, BC-9921, BC-9907, Tori-7
II	6, 7, 8, 17	4	BC-05115, JBC-05118, JBC-05117, BARIsarisha-15
III	10, 14, 18	3	BJDH-05, BJDH-20, BARIsarisha-16
IV	9, 11, 12, 13, 16	5	BJDH-01, BJDH-11, BJDH-12, BJDH-17 BARIsarisha-11

Table 2. Intra (Bold) and inter cluster distances (D^2) for 18 mustard genotypes

Cluster	I	II	III	IV
I	0.054	6.39	29.49	25.79
II		0.212	32.30	28.24
III			0.153	5.38
IV				0.082

The maximum inter-cluster distance of 32.30 existed between cluster II and III followed by 29.49 between cluster I and III and 28.24 between cluster II and IV suggesting wide diversity between them and the genotypes in these cluster could be used as parents in hybridization programme for getting transgressive segregates. The genotypes were apparently distributed into four clusters; it was also revealed that the genotypes of cluster III were more diverse from the genotypes of cluster II and I. The lowest inter-cluster distance of 5.38 existed between cluster III and IV followed by 6.39 between cluster II and I indicating a close relationship between the same grouped. The highest intra-cluster distance was observed 0.212 in cluster II and the lowest (0.054) in cluster I.

Table 3. Cluster mean values of 8 different characters of 18 mustard genotypes

Characters	Clusters			
	I	II	III	IV
Days to 50% flowering	34.28	36.83	49.78	50.33
Days to maturity	81.00	81.75	93.11	91.47
Plant height (cm)	90.52	93.45	185.78	166.87
Primary branches/Plant	5.19	5.23	4.71	3.93
Siliqueae/Plant	109.40	61.33	222.78	158.31
Seed /Siliqueae	15.24	25.07	10.51	10.94
1000 seed weight (g)	3.71	3.90	4.55	3.93
Yield /Plant (g)	3.96	3.83	6.67	5.62

The mean values of cluster III ranked first for the highest plant height (185.78 cm), the longest maturity (166.27 days), maximum number of siliqueae per plant (223), the highest 1000 seed weight (4.55 g) and the highest seed yield per plant (6.67 g) (Table 3). The mean values of cluster IV ranked second for late maturity (91.47 days), plant height (166.87 cm), siliqueae per plant (158.31), 1000 seed weight (3.93 g) and seed yield per plant (5.62 g). The genotypes from cluster II ranked first for primary branches per plant (5.23) and minimum seeds per siliqueae with minimum seed yield per plant (3.83 g). The genotypes from cluster I had dwarf plant (90.52 cm) along with the earliness in days to 50% flowering (34.28 days), day to maturity (81.00 days) and the maximum number of primary branches per plant (5.19) (Table 3).

Therefore, the genotypes from cluster I and III could be utilized in the hybridization programme for getting desirable transgressive segregants and high heterotic response due to getting maximum yield along with short duration. The genotypes for hybridization might be chosen from widely separated clusters (Fig. 1), as it was observed that there were several genotypes included in the crossing programme from widely separated clusters e.g, 11 (BJDH-01), 15 (BJDH-17), 7 (JBC-05117) and 14 (BJDH-12).

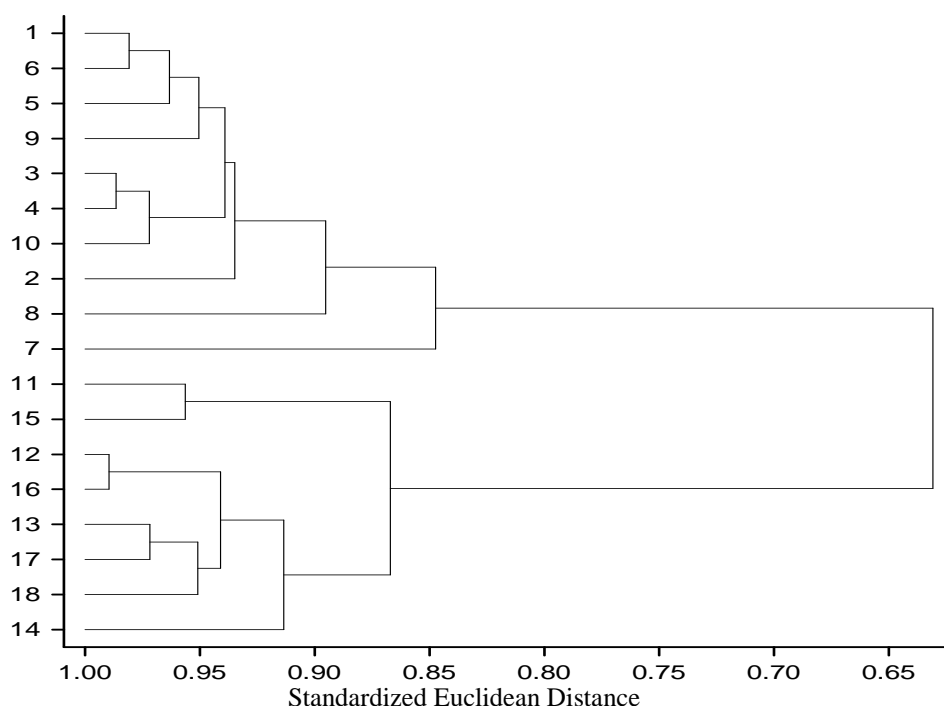


Fig 1. Euclidean average link dendrogram

Table 4. Percent contribution of characters towards divergence in 18 mustard genotypes

Characters	Latent Roots	Percent contribution
Days to 50% flowering	7.754	81.94
Days to maturity	0.779	8.24
Plant height	0.551	5.82
Branches /Plant	0.180	1.91
Siliquae /Plant	0.111	1.17
Seed /Siliquae	0.065	0.69
1000seed weight	0.018	0.19
Yield/Plant	0.004	0.04

The variance for the cluster means were calculated for 8 quantitative characters of mustard. Maximum variance for cluster mean was observed for days to 50% flowering, days to maturity, plant height, branches per plant and siliquae per plant. Days to 50% flowering (81.94%), days to maturity (8.24%), plant height (5.82%), branches per plant (1.91%) and siliquae per plant (1.17%) contributed the maximum towards the total divergence (Table 4) which suggested that these characters were highly responsible for genetic divergence in the present materials. This indicated that the parents selected for hybridization on the basis of these characters were represented to be genetically

diversed. Similar results were obtained by Verma and Sachan (2000), Goswami and Shiekh (2003), Kumar *et al.* (2007) and Yu-cheng *et al.* (2007).

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