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Genetic diversity analysis of mustard germplasm based on phenotypic traits for selection of short duration genotypes

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The present research was undertaken to determine the genetic variability and diversity among different mustard genotypes, to estimate the Genotype-environment (G×E) interaction in yield and yield contributing characters of mustard genotypes to select short duration mustard genotypes. The experiments were carried out at the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh during the period of 2011-2012 and 2012-2013. Analysis of variance demonstrated significant variations for all the characters studied among the genotypes. In case of genotype-environment interaction, it was found that (G×E) interaction was non-significant for number of siliqua plant^{-1}, 1000 seeds weight and days to maturity among the studied parameters for different genotypes of mustard. Among the genotypes, BARI Sarisha-15, BINA Sarisha-4 and BARI Sarisha-14 were found suitable for cultivation across all the environments under study, while other genotypes varied in performance especially in days to maturity and seed yield plant^{-1}. BARI Sarisha-8, Tori-7 and NAP-0763 were found to be more sensitive to environmental fluctuations. All the characters demonstrated high heritability (>80%) irrespective of any genotypes. Plant height, number of seeds siliqua^{-1}, number of siliqua plant^{-1} and length of siliqua were significantly correlated with seed yield plant^{-1} suggesting that genotypes with high partitioning efficiency gave increase in seed yield plant^{-1}. Among the characters, number of siliqua plant^{-1}, number of seeds siliqua^{-1} and 1000 seeds weight had high positive direct effects on grain yield plant^{-1} so those characters should be included owing to importance in selecting the genotypes for higher seed yield in mustard. Using Euclidean distance following Ward's method, the genotypes were grouped into four clusters. The cluster III had higher intra cluster distance and the maximum inter cluster distance was observed between genotypes of clusters I and IV followed by clusters III and IV.

Key words: Mustard, genotype-environment interaction, heritability, co-relation of coefficient, path analysis, diversity analysis.

INTRODUCTION

Oilseed *Brassica* is commonly known as rapeseed and mustard, and it occupies an important position in the rainfed agriculture of our country. Among the *Brassica* species, the varieties of *B. nigra, B. carinata* and *B. juncea* are commonly known as mustard, while those of *B. campestris* and *B. napus* are known as rapeseed (Yarnell, 1956). In most of the regions of the world, its cultivation has increased dramatically during last decades and, presently, it is the third largest contributor of the world supply of vegetable oil. Rapeseed is one of the most important oil and protein rich annual crops in the world. Seed provides oil both for industrial and culinary

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purpose. The oils extracted from mustard contain high protein (37%) feed concentrate which is highly palatable to livestock. Bangladesh is facing acute shortage in edible oil. At present, the oil seed production is about 0.26 million tons, which covers only 30% of the domestic need. About 70% of requirement of oil has been imported every year by spending huge amount of foreign currency (BBS, 2011). In Bangladesh, the seed yield of mustard/rapeseed is about 740 kg/ha, which is very low in comparison to other developed countries (2400 kg/ha) (FAO, 2011). On the other hand, the area of cultivation of mustard in Bangladesh is lower due to rice based cropping system which is difficult to change.

Most of the released mustard cultivars are generally long in duration (90-108 days) and thus, did not fit well for cultivation between *Aman* and *Boro* rice cropping system. Where a long duration mustard crop is grown after *Aman* and prior to the *Boro*, however, the transplanting of *Boro* may be pushed into February, resulting in a later harvest and greater exposure to early flood risk. So, if we can develop the short duration (75-80 days) lines which would be successfully cultivated between *Aman* and *Boro* rice rotation without affecting this popular cropping pattern, after *Aman* rice harvest and before the transplantation of *Boro* rice, 70-80 days would be available for cultivating gap filling crop. So, it is urgent to analyze the genetic diversity and its response for the selection of short duration mustard genotypes for increasing our cropping intensity.

Yield of mustard and its component being quantitative in nature would be useful to gain knowledge about the nature and magnitude of genetic variability and its interaction with environment. Interactions between genotypes and environments are particularly interesting because they reflect the fluctuations in environment if genetic makeup is known and in most cases prediction can be made in advance (Allard and Bradshaw, 1964). Therefore, to estimate heritability including the genotype×environment interaction variation for the total variance is more appropriate for prediction of genetic advance due to selection. Genotypes, which can adjust its phenotypic state in response to environmental fluctuations in such a way that it gives maximum stable economic return, can be termed as well "buffered" or stable (Allard and Bradshaw, 1964). It is necessary to identify the stable genotypes suitable for wide range of environments. Experiments for this purpose have been carried out by Wu et al. (2006), Escobar et al. (2011), Jeromela et al. (2011) and Zhang et al. (2013).

Grain yield in mustard is correlated with different yields contributing traits. These traits are also correlated between themselves. Therefore, the relationship between grain yield and different contributing traits establishes a complex chain. The complex chain of such relationship is further analyzed in more simple way through path coefficient. The path coefficient breaks the correlation coefficient of the yield with its contributing traits into direct and indirect effects. Estimates of genetic variability, heritability, genetic advance trait correlations and path coefficient analysis (Ali et al., 2003; Khan and Khan, 2003; Akbar et al., 2003, 2007; Aytaç and Kinaci, 2009; Sadat et al., 2010) will help to devise efficient selection criteria in the present study.

Genetic diversity is the basic for genetic improvement. It is widely accepted that information about germplasm diversity and genetic relatedness among elite breeding material is a fundamental element in plant breeding (Mukhtar et al., 2002). Genetic diversity is a very important factor for any hybridization program aiming at genetic improvement of yield especially in self pollinated crops (Joshi and Dhawan, 1966). Genetic diversity among individuals or populations can be determined using morphological, biochemical and molecular approaches (Mohammadi and Prasanna, 2003). Assessment of genetic diversity in *B. juncea* using phenotypic characters has previously been done by many researchers (Gupta et al., 1991; Vaishnava et al., 2006; Alie et al., 2009; Singh et al., 2010). With the development of advanced biometrical method such as multivariate analysis (Rao, 1952) based on Mahalanobis (1936), D^2 statistics and Ward's no-hierarchical squared Euclidean distance method have become possible to quantity magnitude of diversity among germplasm for their evaluation in respect of breeding program.

Keeping in mind the available genetic diversity and widely practiced breeding programs for developing variety for any trait, the present study was undertaken to achieve the following objectives: to determine the genetic variability and diversity among different mustard genotypes, to estimate the Genotype-environment (G×E) interaction in yield and yield contributing characters of mustard genotypes to select short duration mustard genotypes.

MATERIALS AND METHODS

The present study included two experiments. The experiments were carried out at the Experimental Farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh during the period of 13 November 2011 to March 2012 and 27 November 2012 to March 2013. The experiments were laid out in Randomized Complete Block Design (RCBD) with 3 replications. The plot sizes were 2.0 m × 1.0 m. The distance regarding block to block was 1 m, plot to plot was 50 cm and line to line was 30 cm. Inter cultural operations and other agronomic practices were done same in both experiments.

In the 1st experiment (Expt.-1), the performance of yield and yield contributing characters of 38 mustard genotypes (Table 1) were evaluated through Francis and Kannenberg (1978) method of selection to select the superior genotypes to be grown in the 2nd experiment. According to the method of Francis and Kannenberg

Table 1. List of mustard genotypes used in the experiments.

Genotypes	Name of the species	Place of origin and identity	Experiment	Genotypes	Name of the species	Place of origin and identity	Experiment
BARI Sarisha-2	*Brassica campestris* L.	BARI	1	NAP-0824	*Brassica napus* L.	RARS, Jamalpur	1
BARI Sarisha-5	*Brassica campestris* L.	BARI	1	NAP-206xNAP-248	*Brassica napus* L.	RARS, Jamalpur	1
BARI Sarisha-7	*Brassica napus* L.	BARI	1	BARI Sarisha-4	*Brassica campestris* L.	BARI	1 and 2
BARI Sarisha-10	*Brassica campestris* L.	BARI	1	BARI Sarisha-6	*Brassica campestris* L.	BARI	1 and 2
BARI Sarisha-11	*Brassica juncea* L.	BARI	1	BARI Sarisha-8	*Brassica napus* L.	BARI	1 and 2
BARI Sarisha-12	*Brassica campestris* L.	BARI	1	BARI Sarisha-9	*Brassica campestris* L.	BARI	1 and 2
BARI Sarisha-13	*Brassica campestris* L.	BARI	1	BARI Sarisha-14	*Brassica campestris* L.	BARI	1 and 2
Shambol	*Brassica juncea* L.	BAU	1	BARI Sarisha-15	*Brassica campestris* L.	BARI	1 and 2
Agrani	*Brassica campestris* L.	BINA	1	Tori-7	*Brassica campestris* L.	BARI	1 and 2
Safal	*Brassica campestris* L.	BINA	1	Sampad	*Brassica campestris* L.	BAU	1 and 2
BINA Sarisha-5	*Brassica campestris* L.	BINA	1	BINA Sarisha-3	*Brassica campestris* L.	BINA	1 and 2
BINA Sarisha-6	*Brassica campestris* L.	BINA	1	BINA Sarisha-4	*Brassica campestris* L.	BINA	1 and 2
NAP-0757	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0763	*Brassica napus* L.	RARS, Jamalpur	1 and 2
NAP-0740-2	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0762-2	*Brassica napus* L.	RARS, Jamalpur	1 and 2
NAP-0839	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0838	*Brassica napus* L.	RARS, Jamalpur	1 and 2
NAP-0724-2	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0721-1	*Brassica napus* L.	RARS, Jamalpur	1 and 2
NAP-0760	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0758-2	*Brassica napus* L.	RARS, Jamalpur	1 and 2
NAP-0741-1	*Brassica napus* L.	RARS, Jamalpur	1	NAP-0842-2	*Brassica napus* L.	RARS, Jamalpur	1 and 2

(1978), genotypes were grouped into four classes, drawing lines passing through the average mean and coefficient of variation (CV) value of the genotypes. Thus data were analyzed and classified into 4 groups. These were:

i) Low coefficient of variation (CV) and low mean.
ii) High coefficient of variation (CV) and low mean.
iii) Low coefficient of variation (CV) and high mean.
iv) High coefficient of variation (CV) and high mean.

In the case of days to maturity, the genotypes that showed low mean value with low coefficient of variation (CV) were selected. But in the case of the other characters, the genotypes which showed higher mean value with low coefficient of variation (CV) were selected. Giving emphasis on yield parameter, for example, seed yield plant^{-1}, 1000-grain weight and days to maturity, 16 genotypes which performed better were selected for the 2nd experiment. Therefore, Expt.-1 and Expt.-2 were considered as two different environments to study genotype-environment interaction of the selected 16 genotypes (Table 1).

Data collection

Five plants were randomly selected from each unit plot of both experiments for collecting data during growth stage. The selected plants were marked and the following characters on plot and individual plant basis were taken. The criteria used in recording of data were as follows: days to maturity, plant height (cm), number of primary branches, number of secondary branches, number of tertiary branches, length of raceme (cm), number of siliquae plant^{-1}, length of siliqua, number of seeds siliqua^{-1}, thousands (1000) seeds weight (g) and seed yield plant^{-1}(g).

Statistical analysis

Estimation of genotype × environmental interaction

Pooled analysis of variance for genotype-

environment interaction was performed by the Plant Breeding Statistical Program (PLABSTAT, Version 2N, Utz 2007) using the following model:

$$Y_{ijk} = \mu + g_i + e_j + r_{ik} + ge_{ij} + \varepsilon_{ijk}$$

Estimation of heritability

Heritability in broad sense (h^2_b) was estimated according to the formula suggested by Johanson et al. (1955) and Hanson et al. (1956):

$$\text{Heritability, } h^2_b = \frac{\delta^2 g}{\delta^2 p} \times 100$$

Estimation of correlation coefficient

The genotypic and phenotypic correlations were estimated by the formula suggested by Miller et al. (1958):

$$\text{Genotypic correlation, } r_{g1.2} = \frac{CoV.g_{1.2}}{\sqrt{\delta^2 g_1 \times \delta^2 g_2}}$$

Similarly, phenotypic correlation was:

$$r_{p1.2} = \frac{CoV.p_{1.2}}{\sqrt{\delta^2 p_1 \times \delta^2 p_2}}$$

Estimation of path co-efficient

Direct and indirect path coefficients were calculated as described by Lynch and Walsh (1998) as:

$$r_{yi} = P_{yi} + \sum_{\substack{i'=1 \\ i' \neq i}}^{k} r_{ii'} P_{yi'} \quad for\ i \neq 1$$

Analysis of genetic divergence

Genetic divergence plays a vital role in existing germplasm in mode and source of origin. Mahalanobis' D^2-statistics may be applied for such study. It also measures the distance for a number of traits between two populations. First the difference between the means in respect of the pooled effect of all characters between different populations was tested.

Calculation of D^2 values

The Mahalanobis' distance (D^2) values were calculated from transformed uncorrelated means of characters

according to Rao (1952) and Singh and Chaudhury (1985). For each combination, the mean deviation, that is, $Y^1_i - Y^2_i$ with $i = 1, 2 \ldots p$ was estimated and the D^2 was calculated as sum of the squares of these deviations, that is, $\sum (Y^1_i - Y^2_i)^2$. The D^2 values were estimated for all possible pairs of combinations between genotypes.

Clustering

The D^2 values of genotypes were arranged in order of relative distances from each other by the method suggested by Rao (1952), while the method suggested by Singh and Chaudhary (1985) was used for cluster formation.

Calculation of average intra-cluster distances

Average intra-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985):

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2}{n}$$

Calculation of average inter-cluster distances

Average inter-cluster distances were calculated by the following formula as suggested by Singh and Chaudhury (1985):

$$\text{Average intra-cluster } D^2 = \frac{\sum D^2 ij}{ni \times nj}$$

Estimation of contribution of individual characters towards divergence

In all the combinations, each character was ranked on the basis of $d_i = y^j_i - Y^k_i$ values. Rank 1 was given to the highest mean difference and rank p to the lowest mean difference, where p is the total number of characters. Thus, the number of times appearing first in ranking was calculated for each character and finally a table was prepared and the percent contribution was calculated.

RESULTS AND DISCUSSION

The performance of yield and yield contributing characters of 38 mustard genotypes were evaluated through Francis and Kannenberg (1978) method of selection to select the superior genotypes to be grown in the 2nd year experiment. Considering all 38 lines of the genotypes with their mean value and coefficient of variation (CV), about 32 lines performed better for various yield contributing characters. But analyzing all these 32 lines in the second year experiment is difficult and

Table 2. Analysis of variance for 11 plant characters in a G×E interaction study in 16 mustard genotypes.

Items	df	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/plant	Length of siliqua (cm)	Number of seeds/siliqua	1000 seeds weight (g)	Days to maturity	Seed yield/plant (g)
Genotypes	15	849.03**	3.89**	10.03**	4.89**	427.87**	934.09**	4.23**	99.68**	1.42**	437.02**	26.53**
Environments	1	1809.26**	2.04	0.01	0.15	745.38**	1008.09	3.07**	1.56	0.05	16.67	9.53
Replications	2	116.54	0.59	0.13	0.24	3.44	197.40	0.27	1.16	0.14	3.63	0.53
G × E	15	66.70**	0.54*	0.67*	0.28*	33.47**	141.54	0.29**	18.83**	0.18	3.39	4.12**
Error	60	19.46	0.25	0.32	0.15	7.48	94.63	0.07	3.71	0.16	2.90	1.21

* and ** indicate significance at 0.05 and 0.01 level of probability, respectively.

impractical. Based on yield parameter-seed yield per plant, 100-grain weight and days to maturity characters, about 16 lines (Table 1) which performed better were selected for the 2nd year experiment.

The analyses of variance for all characters under study are shown in Table 2. It was observed that genotypic effects were highly significant for all characters indicating the presence of variation among genotypes for all these characters. The environments were also shown to have highly significant difference for plant height, length of raceme and length of siliqua whereas other traits were non-significant for different genotypes in two environments. In the case of genotype environment interaction, it was found that (G × E) interaction was highly significant for plant height, length of raceme, length of siliqua, number of seeds per siliqua and seed yield per plant, and moderately significant for number of primary branches, number of secondary branches and number of tertiary branches and the rest of the characters were non-significant for different genotypes of mustard. The average environmental effects on yield and yield contributing traits summarized for the genotypes (Table 3) showed that in Environment-2, plant height, length of raceme and length of siliqua had significantly higher values than Environment-1. The remainder traits did not differ significantly between the two environments.

The mean performances of 16 mustard genotypes evaluated for eleven characters over two environments were presented in Table 4. From the tabular results, it was observed that Tori-7 took lowest days (84.33 days) which did not differ significantly with BARI Sarisha-15 and NAP-0762-2 took highest days (107.3 days) to maturity. BARI Sarisha-4 had the highest (11.70 g) and Sampad had the lowest (2.762 g) seed yield per plant. 1000 seeds weight was highest in NAP-0721-1 (4.853 g) and lowest in NAP-0838 (2.775 g). BARI Sarisha-6 had the longest

(100.7 cm) and Tori-7 had the shortest (48.19 cm) plant height. BARI Sarisha-15 had the highest (5.308) and BINA Sarisha-3 had the lowest (2.622) number of primary branches. Number of secondary branches was highest in Tori-7 (5.417) and lowest in Sampad (0.100). Number of tertiary branches was highest in Tori-7 (3.70). BINA Sarisha-3 had the longest (48.42 cm) length of raceme and Tori-7 had the shortest (14.99 cm). Highest number of siliqua per plant was observed in NAP-0758-2 (97.38) and lowest was observed in Sampad (47.37). NAP-0721-1 had the longest (6.425) length of siliqua and Tori-7 had the shortest (3.932). BARI Sarisha-4 had the highest (34.47) number of seeds per siliqua and Tori-7 had the lowest (19.47). Thus genotypes BARI Sarisha-15, BINA Sarisha-4 and BARI Sarisha-14 were suitable for cultivation across all the environments under study, while other genotypes varied in performance especially in days to maturity and seed yield plant[-1].

Different genotypes differed considerably with respect to their stability in different environments. Mean for genotype-environment (G×E) interaction was presented in Table 5. From the table, it was found that significant differences exist among genotypes for plant height, length of raceme and number of siliqua per plant in both environments. Variation was low in the case of the rest of the characters. The plant height of the genotypes BARI Sarisha-4 (91.87 and 90.59 cm), BARI Sarisha-14 (77.25 and 81.82 cm) and BARI Sarisha-6 (103.2 and 98.22 cm) were more or less same in both environment which indicate that they were less responsive to environmental fluctuation. The plant height of BARI Sarisha-8 (80.13 and 99.53 cm) and NAP-0758-2 (83.60 and 101.1 cm) highly fluctuated in two environments. BARI Sarisha-9 (35.33 and 35.91 cm), BARI Sarisha-14 (36.73 and 37.19 cm) and Tori-7 (14.27 and 15.71 cm) had more or less same length of raceme for both environments, whereas

Table 3. Summary mean and LSD value of different plant characters of 16 mustard genotypes in two environments.

Items	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/plant	Length of siliqua (cm)	Number of seeds/siliqua	1000 seeds weight (g)	Days to maturity	Seed yield/plant (g)
Environment 1	77.69	3.79	2.57	0.67	34.69	72.86	5.29	25.44	3.54	96.77	6.58
Environment 2	86.38	4.08	2.55	0.59	40.26	79.34	5.65	25.70	3.50	95.94	7.21
Mean	82.03	3.94	2.56	0.63	37.48	76.10	5.47	25.57	3.52	96.35	6.89
LSD at 5%	4.49	0.73	0.52	0.25	2.49	12.87	0.23	1.83	0.35	4.02	1.36

NAP-0758-2 (32.47 and 45.49 cm), BINA Sarisha-4 (38.13 and 50.94 cm) and Sampad (21.27 and 30.97 cm) showed greater fluctuation in two environments. BARI Sarisha-8 (56.93 and 82.89) and BINA Sarisha-3 (62.07 and 77.85) were more responsive to environmental fluctuation and BARI Sarisha-14 (83.88 and 82.31) and NAP-0763 (62.53 and 61.85) were less responsive for number of siliqua per plant. From all the characters studied, it was found that among all the genotypes, BARI Sarisha-8, Tori-7 and NAP-0763 were more sensitive to environmental fluctuation. On the other hand, BARI Sarisha-14 and BARI Sarisha-9 were comparatively more stable.

The heritability (h^2_b) for all the characters over the environments under study is presented in Table 6. All the characters except number of primary branches, number of siliqua per plant, 1000 seeds weight and seed yield per plant estimated more than 94% heritability. Similar observations were also made by Ghosh and Gulati (2001), Khulbe et al. (2000), Pant and Singh (2001) and Bikram (2004). However, in contrast Singh et al. (1987) recorded low and medium heritability for number of primary branches per plant and plant height.

Relationship between physiological and yield contributing characters was studied through analysis of correlation between them. The correlation coefficients between all the nine characters were presented in Table 7. The correlation of seed yield plant[-1] with different characters was presented in Figure 1. Only number of tertiary branches was negatively correlated with seed yield plant[-1] indicating that seed yield plant[-1] would be increased with the decrease of that character. Similar results were obtained by Sirohi et al. (2004).

Study of correlation at yield component levels exhibited that plant height showed positive and significant correlation with length of raceme, length of siliqua and number of seeds per siliqua. Similar associations for plant height with length of siliqua (Basalma, 2008, Azadgoleh et al., 2009), plant height with length of raceme (Sadat et al., 2010) and plant height with number of seeds per siliqua (Azadgoleh et al., 2009) were reported earlier. Number of tertiary branches was negatively and significantly correlated with plant height. By contrast, Kumar et al. (1984) recorded positive and significant correlation between plant height and days to maturity. Number of primary branches showed positive and significant correlation with number of siliqua per plant and showed negative and significant correlation with length of raceme and length of siliqua. Similar observation was also made by Chowdhary et al. (1987), Kumar et al. (1987), Srivastava and Singh

(2002) and Rai et al. (2005). Number of secondary branches showed positive and significant correlation with number of tertiary branches and number of siliqua per plant. Chowdhary et al. (1987), Nagaraja (1990), Srivastava and Singh (2002) observed positive significant correlation of seed yield with number of secondary branches. Number of tertiary branches plant[-1] showed negative and significant correlation with length of raceme. Length of raceme showed positive and significant correlation with siliqua length and days to maturity. Similar association was reported by Chowdhury et al. (2007). Length of siliqua showed positive and significant correlation with number of seeds per siliqua and days to maturity. Xu and Yao (2006) studied the inheritance of siliqua length among several lines of *B. napus* and observed that lines with the longest siliqua generally showed significantly higher correlation with seed yield. 1000 seeds weight showed positive correlation with days to maturity. This is in conformity with the findings of Srivastava and Singh (2002). In contrast, Sandhu and Gupta (1996) reported that days to 50% flowering and 1000-seed weight exhibited negative correlation with seed yield. According to Kumar and Kakroo (2009), 1000 seed weight showed positive correlation with seed yield. As such from existing agro climatic situation based

Table 4. Mean performance of 16 mustard genotypes for yield and yield contributing characters averaged over two environments.

Genotypes	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/plant	Length of siliqua (cm)	Number of seeds/siliqua	1000 seeds weight (g)	Days to maturity	Seed yield/plant (g)
BINA Sarisha-4	81.68 b-f	2.886 ef	2.415 d-f	0.444 d	44.53 a-c	71.49 c-f	6.003 ab	26.97 b-d	3.664 bc	87.67 f	6.927 c-e
BARI Sarisha-14	79.54 d-f	3.748 c-e	2.336 d-f	0.034 d	36.96 cd	83.10 a-d	4.908 de	22.54 d-f	3.511 b-d	88.83 f	6.578 c-e
BARI Sarisha-4	91.23 a-c	4.500 a-c	2.570 c-f	0.234 d	34.72 de	88.36 ab	5.660 bc	34.47 a	3.812 b	96.00 d	11.70 a
NAP-0763	84.04 b-f	3.167 d-f	2.127 ef	0.333 d	42.31 a-d	62.19 e-g	5.820 a-c	24.42 c-f	3.685 b	104.0 b	5.603 de
NAP-0762-2	86.90 b-e	4.066 b-d	3.450 cd	1.467 b	40.60 a-d	82.60 a-d	6.441 a	29.49 a-c	2.917 e	107.3 a	7.159 b-e
Tori-7	48.19 h	4.667 a-c	5.417 a	3.700 a	14.99 g	76.28 b-f	3.932 f	19.47 f	3.542 bc	84.33 g	4.618 ef
BARI Sarisha-15	75.00 fg	5.308 a	0.967 gh	0.167 d	28.35 ef	74.49 b-f	4.319 ef	24.52 c-f	3.703 b	85.50 g	6.759 c-e
NAP-0838	84.04 b-f	3.718 c-e	2.520 c-f	0.333 d	46.40 ab	84.99 a-d	5.187 cd	23.20 d-f	2.775 e	107.0 a	5.552 de
NAP-0721-1	80.38 c-f	2.642 f	2.118 ef	0.360 d	42.44 a-d	60.49 fg	6.425 a	27.14 b-d	4.853 a	105.7 ab	7.939 b-d
NAP-0758-2	92.35 ab	4.803 ab	4.587 ab	1.135 bc	38.98 b-d	97.38 a	5.607 b-d	26.57 b-d	3.595 bc	107.3 a	9.365 a-c
BARI Sarisha-8	89.83 b-d	3.738 c-e	1.705 e-g	0.4000 d	42.11 a-d	69.91 d-f	6.444 a	27.08 b-d	3.502 b-d	97.83 c	6.566 c-e
BINA Sarisha-3	88.81 b-d	2.622 f	1.525 fg	0.234 d	48.42 a	69.96 d-f	6.140 ab	25.62 b-e	3.770 b	93.50 e	6.752 c-e

Table 4. Cont'd.

NAP-0842-2	76.18 e-g	3.968 d	2.632 c-f	0.602 cd	40.41 a-d	77.23 b-e	5.958 ab	27.02 b-d	3.248 b-e	104.3 b	6.839 c-e
BARI Sarisha-6	100.7 a	4.717 a-c	2.703 c-e	0.220 d	36.67 cd	83.76 a-d	5.728 a-c	30.73 ab	3.716 b	95.33 d	9.698 ab
BARI Sarisha-9	85.52 b-f	4.566 a-c	3.634 bc	0.400 d	35.62 de	87.90 a-c	4.940 de	20.12 ef	3.082 c-e	88.33 f	5.458 de
Sampad	68.14 g	3.863 b-e	0.100 h	0.00 d	26.12 f	47.37 g	3.991 f	19.74 ef	2.955 de	88.67 f	2.762 f
Mean	82.03	3.94	2.55	0.63	37.48	76.10	5.47	25.57	3.52	96.35	6.89
Minimum	42.62	1.75	0.00	0.00	12.70	32.60	3.16	17.80	2.71	83.00	1.88
Maximum	108.60	6.40	6.42	6.00	56.21	108.45	7.12	39.80	6.77	109.00	14.23
LSD at 5%	10.05	0.904	1.011	0.647	7.121	14.64	0.66	5.339	0.522	1.720	2.498

The mean values having common letters are statistically identical.

Table 5. Analysis of means for genotype-environment interaction study with 16 mustard genotypes.

Genotypes	Environment	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/ plant	Length of siliqua (cm)	Number of seeds/ siliqua	1000 seeds weight (g)	Days to maturity	Seed yield/plant (g)
BINA Sarisha-4	ENV-1	76.87	2.80	2.067	0.267	38.13	60.13	5.913	28.47	3.667	87.33	6.167
	ENV-2	86.50	2.973	2.763	0.620	50.94	82.85	6.093	25.46	3.660	88	7.687
BARI Sarisha-14	ENV-1	77.25	3.667	2.600	0.067	36.73	83.88	4.920	20.98	3.530	88.00	6.240
	ENV-2	81.82	3.830	2.073	0.000	37.19	82.31	4.897	24.10	3.493	89.67	6.917
BARI Sarisha-4	ENV-1	91.87	4.533	2.667	0.200	32.20	92.47	5.693	38.27	3.840	96.33	13.61
	ENV-2	90.59	4.467	2.473	0.267	37.25	84.25	5.627	30.68	3.783	95.67	9.800
NAP-0763	ENV-1	73.93	3.400	2.200	0.533	36.73	62.53	5.167	24.27	3.683	103.7	5.623
	ENV-2	94.15	2.933	2.053	0.133	47.89	61.85	6.473	24.56	3.687	104.3	5.583
NAP-0762-2	ENV-1	81.80	3.533	3.467	1.400	39.20	75.40	6.413	28.67	2.893	107.3	6.297
	ENV-2	92.01	4.600	3.433	1.533	42.00	89.81	6.470	30.32	2.940	107.3	8.020

Table 5. Cont'd.

Tori-7	ENV-1	44.81	4.600	6.000	4.467	14.27	74.67	3.567	18.93	4.197	85.00	4.763
	ENV-2	51.56	4.733	4.833	2.933	15.71	77.89	4.297	20.00	2.887	83.67	4.473
BARI Sarisha-15	ENV-1	70.73	5.667	1.000	0.133	23.13	74.40	3.867	22.07	3.693	86.33	6.070
	ENV-2	79.26	4.950	0.9333	0.200	33.56	74.57	4.770	26.97	3.713	84.67	7.447
NAP-0838	ENV-1	80.73	3.333	3.000	0.400	45.60	86.40	5.320	24.53	2.777	108.3	6.077
	ENV-2	87.34	4.103	2.040	0.267	47.21	83.59	5.053	21.88	2.773	105.7	5.027
NAP-0721-1	ENV-1	75.20	2.667	2.200	0.350	39.93	59.80	6.007	27.93	4.830	105.7	7.997
	ENV-2	85.57	2.617	2.037	0.370	44.96	61.19	6.843	26.35	4.877	105.7	7.880
NAP-0758-2	ENV-1	83.60	4.733	4.067	1.133	32.47	96.00	5.340	26.67	3.583	108.00	9.323
	ENV-2	101.1	4.873	5.107	1.137	45.49	98.77	5.873	26.47	3.607	106.7	9.407
BARI Sarisha-8	ENV-1	80.13	2.850	1.000	0.267	40.40	56.93	6.500	28.27	3.463	98.67	5.580
	ENV-2	99.53	4.627	2.410	0.533	43.81	82.89	6.387	25.90	3.540	97.00	7.553
BINA Sarisha-3	ENV-1	83.33	2.400	1.400	0.267	48.87	62.07	5.960	26.87	3.773	94.33	6.340
	ENV-2	94.28	2.843	1.650	0.200	47.98	77.85	6.320	24.37	3.767	92.67	7.163
NAP-0842-2	ENV-1	73.93	3.600	2.400	0.533	38.67	71.73	5.740	25.47	3.210	105.3	5.937
	ENV-2	78.42	4.337	2.863	0.670	42.15	82.73	6.177	28.57	3.287	103.3	7.740
BARI Sarisha-6	ENV-1	103.2	4.667	2.733	0.333	32.13	79.73	5.413	27.20	3.583	96.00	7.747
	ENV-2	98.22	4.767	2.673	0.107	41.20	87.79	6.043	34.26	3.850	94.67	11.65
BARI Sarisha-9	ENV-1	81.60	4.600	3.867	0.333	35.33	88.40	4.947	19.27	3.023	88.67	5.147
	ENV-2	89.44	4.533	3.400	0.467	35.91	87.41	4.933	20.97	3.140	88.00	5.770
Sampad	ENV-1	64.10	3.600	0.200	0.000	21.27	41.13	3.873	19.20	2.953	89.33	2.317
	ENV-2	72.18	4.127	0.000	0.00	30.97	53.61	4.110	20.28	2.957	88.00	3.207

on the present study, it could be stressed that more emphasis should be given for number of siliqua per plant, number of seeds per siliqua, length of siliqua and plant height as they showed very high to fair degree of positive association with seed yield. The path coefficient analysis was

Table 6. Heritability (h^2_b) of 11 traits of 16 mustard genotypes.

Traits	Heritability, h^2_b (%)
Plant height (cm)	96.66
Number of primary branches	91.06
Number of secondary branches	95.40
Number of tertiary branches	95.57
Length of raceme (cm)	97.43
Number of siliqua/plant	86.45
Length of siliqua (cm)	97.57
Number of seeds/siliqua	94.66
1000 seeds weight (g)	85.10
Days to maturity	99.01
Seed yield/plant (g)	93.52

Table 7. Coefficients of correlation among different yield components of 16 mustard genotypes.

Characters	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/plant	Length of siliqua (cm)	Number of seeds/siliqua	1000 seeds weight (g)	Days to maturity
Number of primary branches	-0.08									
Number of secondary branches	-0.144	0.345								
Number of tertiary branches	-0.610*	0.278	0.773**							
Length of raceme (cm)	0.716**	-0.631**	-0.236	-0.563*						
Number of siliqua/plant	0.385	0.540*	0.661**	0.184	0.084					
Length of siliqua (cm)	0.672**	-0.526*	-0.019	-0.262	0.815**	0.083				
Number of seeds/siliqua	0.666**	-0.007	-0.023	-0.243	0.412	0.307	0.692**			

Table 7. Cont'd.

1000 seeds weight (g)	0.097	-0.314	-0.063	-0.082	0.099	-0.205	0.327	0.342		
Days to maturity	0.457	-0.235	0.136	-0.097	0.596*	0.177	0.651**	0.429	0.019	
Seed yield/plant (g)	0.651**	0.19	0.213	-0.167	0.282	0.576*	0.508*	0.883**	0.459	0.315

P.H.=Plant height
P.B.=No. of primary branches
S.B.=No. of secondary branches
T.B.=No. of tertiary branches
L.R.=Length of raceme
S/P=No. of siliqua/plant
L.S.=Length of raceme
S/S=No. of seeds/siliqua
S.W.=1000 seeds weight
D.M.=Days to maturity
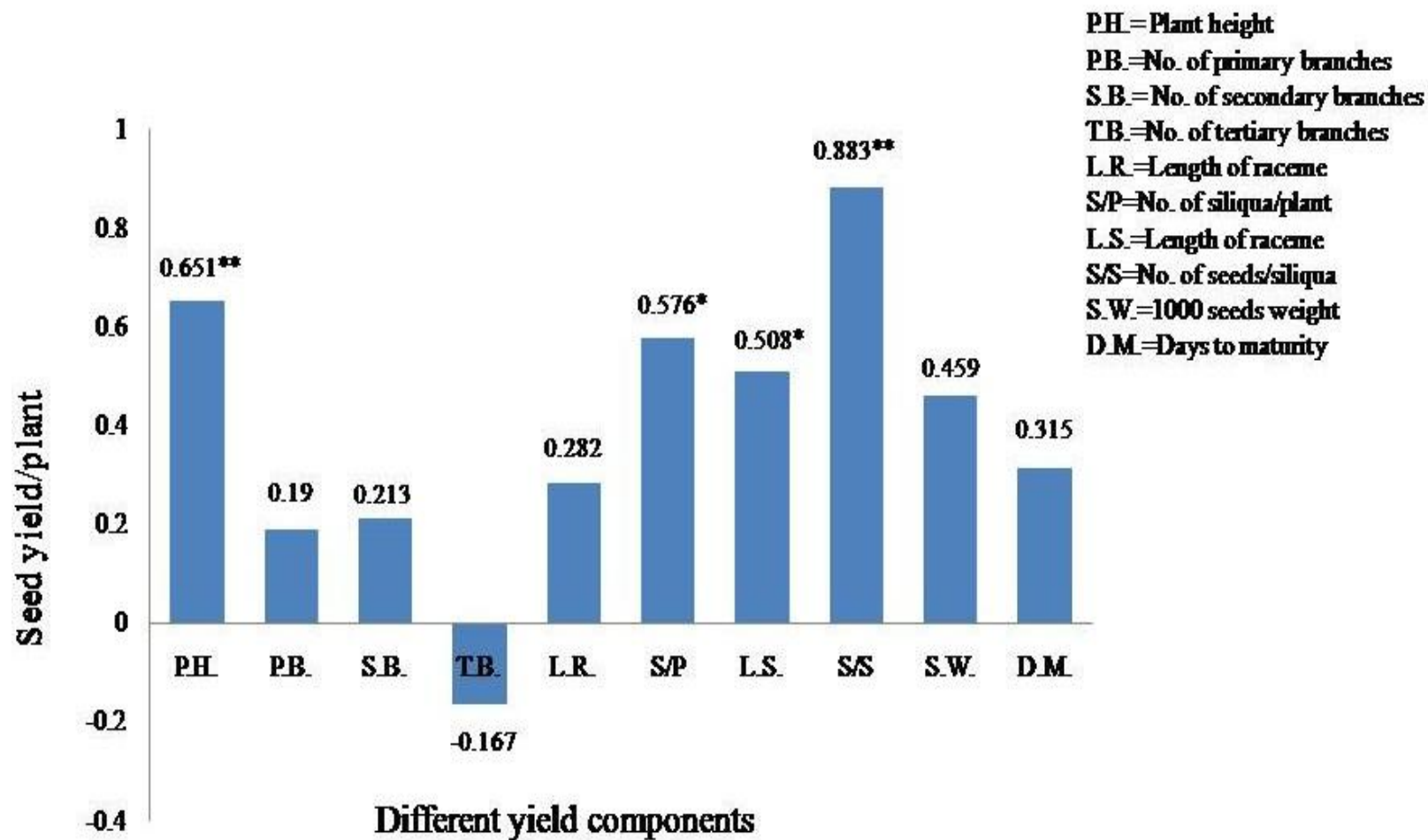
Figure 1. Correlation for 10 characters with seed yield/plant in 16 genotypes of mustard.

Table 8. Partitioning of phenotypic correlations into direct and indirect effects of ten important characters by path analysis.

Characters	Plant height (cm)	Number of primary branches	Number of secondary branches	Number of tertiary branches	Length of raceme (cm)	Number of siliqua/plant	Length of siliqua (cm)	Number of seeds/ siliqua	1000 seeds weight (g)	Days to maturity	Correlation to yield
Plant height (cm)	**0.147**	0.010	-0.010	0.081	-0.136	0.172	-0.135	0.462	0.033	0.026	0.651**
Number of primary branches	-0.012	**-0.128**	0.023	-0.037	0.120	0.242	0.105	-0.005	-0.105	-0.013	0.190
Number of secondary branches	0.021	-0.044	**0.066**	-0.103	0.045	0.296	0.004	0.016	-0.021	0.008	0.213
Number of tertiary branches	-0.090	-0.036	0.051	**-0.133**	0.107	0.082	0.053	-0.169	-0.028	-0.005	-0.167
Length of raceme (cm)	0.106	0.081	-0.016	0.075	**-0.191**	0.038	-0.163	0.286	0.033	0.034	0.282
Number of siliqua/plant	0.057	-0.069	0.044	-0.025	-0.016	**0.447**	-0.017	0.213	-0.069	0.010	0.576*
Length of siliqua (cm)	0.099	0.067	-0.001	0.035	-0.155	0.037	**-0.200**	0.480	0.110	0.037	0.508*
Number of seeds/siliqua	0.098	0.001	-0.002	0.032	-0.078	0.137	-0.139	**0.694**	0.115	0.024	0.883**
1000 seeds weight (g)	0.014	0.040	-0.004	0.011	-0.019	-0.092	-0.066	0.237	**0.336**	0.001	0.459
Days to maturity	0.067	0.030	0.009	0.000	-0.001	0.079	-0.131	0.298	0.006	**0.056**	0.315

Residual effect, R = 0.63

* and ** indicate significant at 0.05 and 0.01 level of probability, respectively. Bold figures indicate the direct effect.

performed using correlation coefficient to determine direct and indirect influence considering ten characters. Seed yield being the complex outcome of different characters was considered as the resultant variable and other characters as causal variable. Estimates of direct and indirect effects of ten yield contributing characters are shown in Table 8. Among the characters that have positive direct effect on seed yield per plant number of siliqua per plant (0.447), number of seeds per siliqua (0.694) and 1000 seeds weight (0.336) had high positive direct effects on grain yield plant[-1].

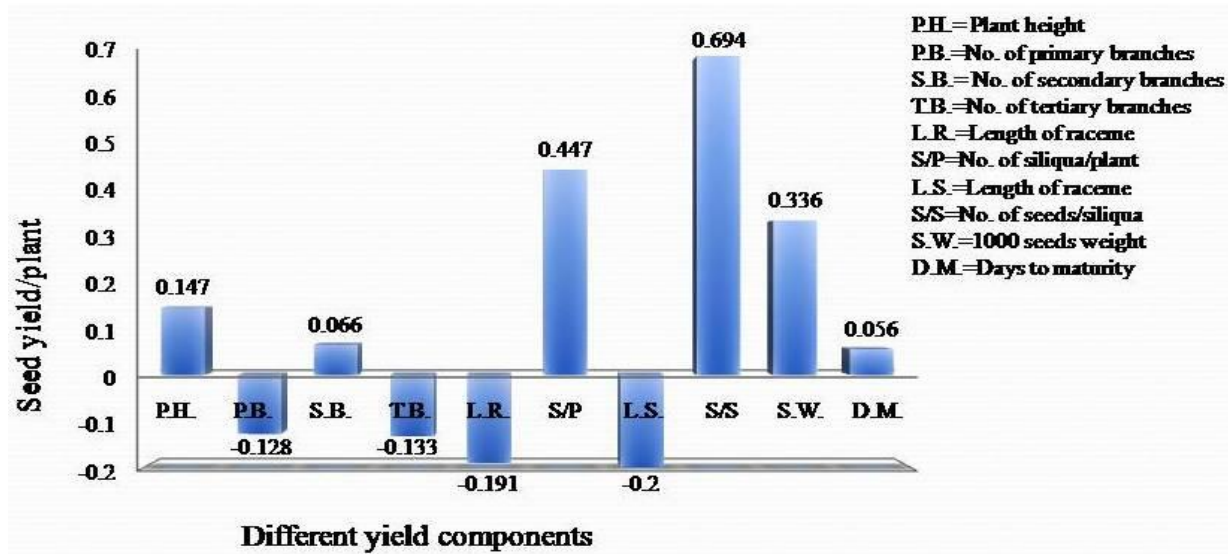The phenotypic correlation of number of siliqua per plant, number of seeds per siliqua and plant

Figure 2. Partitioning of phenotypic correlations into direct effects of ten important characters with seed yield/plant in 16 genotypes of mustard.

Table 9. Clustering pattern of 16 genotypes of mustard based on Euclidean distance following Ward's method and the member present in each respective cluster.

Cluster number	Number of genotypes	Percent	Name of genotypes
I	5	31.25	BINA Sarisha-4, NAP-0763, NAP-0721-1, BARI Sarisha-8 and BINA Sarisha-3
II	4	25.00	BARI Sarisha-14, BARI Sarisha-15, BARI Sarisha-9 and Sampad
III	6	37.50	BARI Sarisha-4, NAP-0762-2, NAP-0838, NAP-0758-2, NAP-0842-2 and BARI Sarisha-6
IV	1	6.25	Tori-7

height with seed yield per plant was also high. Such high correlation with seed yield plant^{-1} was mainly due to the high positive direct effect of number of seeds per siliqua and considerable positive indirect effects were number of siliqua per plant and plant height. Similar results were in accordance with studies of Dastidar and Patra (2004). The residual effect was 0.63, indicating that the ten characters contributed 37% of variability in seed yield plant^{-1} studied in path analysis. The residual effects towards seed yield in this study may be due to several reasons such as, may be other causal factors (characters) that are not included in the analysis contribute more towards yield and sampling errors. Both correlation and path co-efficient studies revealed for number of siliquae per plant, number of seeds per siliqua, length of siliqua and plant height were the most important components for getting higher yield. Recent breeding research also emphasized on giving importance of these characters. Therefore, the present study suggested that number of siliqua per plant, number of seeds per siliqua

and 1000 seeds weight should be included owing to importance in selecting the genotypes for higher seed yield in mustard.

Assemblage and assessment of divergence in the germplasm is essential to know the spectrum of diversity. In the present investigation, 16 genotypes of mustard were considered for the assessments of genetic diversity by multivariate analysis as per Mahalanobis' (1936) concept of generalize distance (D²) considering eleven important quantitative characters. Using Euclidean distance following Ward's method, the genotypes were grouped into 4 clusters (Figure 2 and Table 9). The average intra and inter cluster distances are presented in Figure 3 and Figure 4. It was observed that inter cluster distance was always higher than those of intra cluster distance. The intra cluster distance of cluster III had 114.73 containing 6 genotypes which was the highest value that indicates the highest amount of genetic divergence within the group. Similarly, Verma et al. (2000) got 5 clusters. Aunwinithul et al. (2004) obtained 8
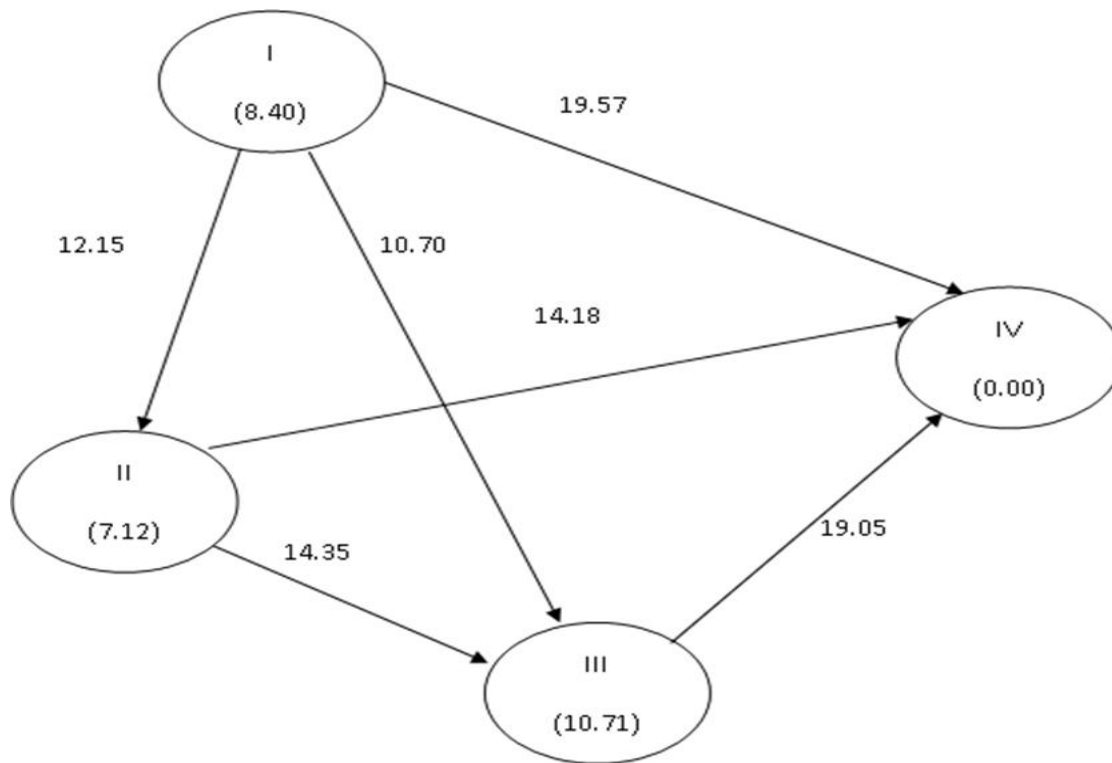
Figure 3. Cluster diagram showing the average intra and inter cluster distances (D= $\sqrt{D^2}$ values) of 16 mustard genotypes.
The values along the lines are inter cluster distances and the values within the circle are intra cluster distances.
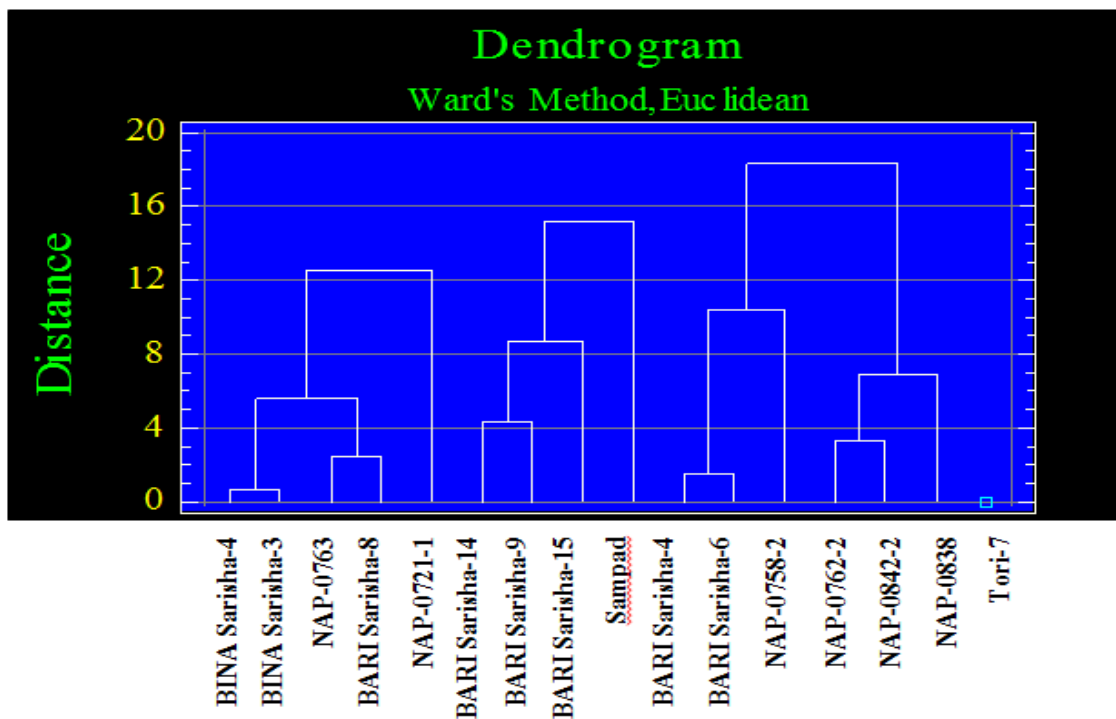

Figure 4. Dendrogram based on summarized data on differentiation among 16 genotypes of mustard according to Ward's method.

Table 10. Cluster mean for 11 yield and yield related characters in 16 mustard genotypes.

Characters	I	II	III	IV
Plant height (cm)	84.95 (I)	77.04 (I)	88.56 (H)	48.18 (L)
Number of primary branches	3.01 (L)	4.36 (I)	4.29 (I)	4.66 (H)
Number of secondary branches	1.97 (I)	1.75 (L)	3.07 (I)	5.41 (H)
Number of tertiary branches	0.35 (I)	0.15 (L)	0.66 (I)	3.7 (H)
Length of raceme (cm)	43.96 (H)	31.75 (I)	39.62 (I)	14.98 (L)
Number of siliqua/plant	66.81 (L)	73.21 (I)	85.72 (H)	76.27 (I)
Length of siliqua (cm)	6.16 (H)	4.3 (I)	5.76 (I)	3.93 (L)
Number of seeds/siliqua	26.24 (I)	21.72 (I)	28.58 (H)	19.46 (L)
1000 seeds weight (g)	3.89 (H)	3.31 (L)	3.34 (I)	3.53 (I)
Days to maturity	97.73 (I)	87.83 (I)	102.89 (H)	84.33 (L)
Seed yield/plant (g)	6.75 (I)	5.38 (I)	8.38 (H)	4.61 (L)

clusters. Hence, there is a lot of scope for exchange of genes among genotypes within these clusters.

The maximum inter cluster distance was observed between genotypes of clusters I and IV (383.02) followed by clusters III and IV (362.99). Thus, hybridization among genotypes drawn from these widely divergent clusters with high yield potential would likely to produce heterotic combinations and wide variability in segregating generations. Therefore it could be concluded that the genotypes present in combination of those clusters could be utilized for successful breeding programme.

The mean values of each cluster for eleven characters are presented in Table 10. There was wide range of variation in the cluster mean values for all the characters. The mean values of all characters for the respective clusters were categorized into low (L), intermediate (I) and high (H) classes.

The present study revealed that clusters I and III possessing high mean values for most of the desirable traits are desired to be crossed with cluster IV which possessed low mean values of days to maturity. This finding was strongly supported with identification of similar cluster combinations from interpretation of intercluster distance made in the present study and thereby the expected progenies inculcate traits in a positive direction and further selection would be more effective.

CONCLUSIONS AND RECOMMENDATIONS

Best performing genotypes were BARI Sarisha-15, BINA Sarisha-4 and BARI Sarisha-14. BARI Sarisha-8, Tori-7 and NAP-0763 were found to be more sensitive to environmental fluctuations. Tori-7 was totally different from other genotypes. The results of the present experiment revealed that the variability which existed among the selected mustard genotypes were much wide. Among these cultivars, the superior genotypes may be used in future breeding program to develop short duration cultivar of mustard. This variability may be used for the

selection of superior and short duration genotypes for commercial cultivation and at the farmer's level as well as for breeding new genotypes of mustard in our country.

REFERENCES

Akbar M, Mahmood T, Yaqub M, Anwar M, Ali M, Iqbal N (2003). Variability, correlation and path coefficient studies in summer mustard (*B. juncea* L.). Asian J. Plant Sci., 2(9): 696-698.

Akbar M, Saleem U, Tahira M, Yaqub, Iqbal N (2007). Utilization of genetic variability, correlation and path analysis for seed yield improvement in mustard, *B. juncea* L. J. Agric. Res., 45(1): 25-31.

Ali N, Javidfar F, Elmira JY, Mirza MY (2003). Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). Pak. J. Bot., 35(2): 167-174.

Alie FA, Singh T, Sharma PK (2009). Genetic diversity analysis in Indian mustard *[Brassica juncea* (l.) czern & coss]. Progressive Agriculture-An International Journal, 9, 50-53.

Allard RW, Bradshaw AD (1964). Implications of genotype-environment interaction in applied plant breeding. Crop Sci. 4: 503-508.

Aunwinithul, Patil S, Charjan SU, Thakare PG, Wankhade M (2004). Genetic divergence studies in Indian mustard. Soil and Crops, 14(2): 297-304.

Aytaç Z, Kınacı G (2009). Genetic variability and association studies of some quantitative characters in winter rapeseed (*B. napus* L.). Afr. J. Biotechnol., 8(15): 3547-3554.

BBS. (2011). Hand book of Agricultural Statistics, December 2010. Bangladesh Bureau of Statistics (BBS), Ministry of Planning Govt. People's Republic Bangladesh. p.14.

Chowdhary MA, Miah AJ, Rahman L, Rahman A (1987). Correlation and path coefficient analysis of nine important characters of Mustard (*Brassica juncea* L. Czern and Coss). Bangladesh J. Agric., 12: 149-154.

Chowdhury N, Javidfar F, Elmira JY, Mirza MY (2007). Relationship among yield components and selection criteria for yield improvement in winter rapeseed (*Brassica napus* L.). Oilseed Research Program, National Agricultural Research Centre, Islamabad, Pakistan. 35(2): 167-17.

Dastidar KKG, Patra MM (2004). Character association for seed yield components in Indian mustard (*Brassica juncea* L. Czem and Coss), 8(2): 155-160.

Escobar M, Berti M, Matus I, Tapia M, Johnson B (2011). Genotype Environment Interaction in Canola (*Brassica napus* L.) Seed Yield in Chile. Chilean J. Agric. Res. vol.71 number2.

FAO. 2011. FAO Production Year Book. Basic data unit, Statistic Division, FAO Rome, Italy.

Ghosh SK, Gulati SC (2001). Genetic variability and association of yield components in Indian mustard (*Brassica juncea* L.). Crop Res., Hisar, 21(3): 345-349.

Gupta VP, Sekhon MS, Satija DR (1991). Studies on genetic diversity, heterosis and combining ability in Indian mustard [*Brassica juncea* L. (Czern and Coss*)]*. Indian J. Genetics, 51, 448-453.

Jeromela AM, Nagl N, Varga JG, Hristov N, Spika AN, Vasicand MM, Marinkovic R (2011). Genotype by environment interaction for seed yield per plant in rapeseed using AMMI model. Pesq. agropec. bras. vol. 46 (2).

Joshi AB, Dhawan NL (1966). Genetic improvement of yield with special reference to self fertilizing crop. Indian J Genet Pl Breed. 26A:101-113.

Khan RSAK, Khan FA (2003). Evaluation of genetic potential of some *Brassica* germplasm collections. Int. J. Agri. Biol., 5(4): 630-631.

Khulbe RK, Pant DP, Saxena N (2000). Variability, heritability and genetic advance in Indian mustard *(Brasisca juncea* L. Czern and Coss). Crop Res., Pant, S.C. and Singh, 2001, Genetic variability in Indian mustard, Agric. Sci. Digest, 21(1): 28-30.

Mohammadi SA, Prasanna BM (2003). Analysis of genetic diversity in crop plants salient statistical tools and considerations. Review & Interpretation. Crop Science, 43, 1235-1248.

Mukhtar MS, Rahman M, Zafar Y (2002). Assessment of genetic diversity among wheat (*Triticum aestivum* L.) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. Euphytica. 128: 417-425.

Nagaraja TE (1990). Genetic variability study in Rapeseed *(Brassica compestris* L.) and Mustard (*Brassica juncea* (L) Czern and Coss). M.Sc. (Agri.) Thesis*,* Univ. Agric. Sci*.* Bangalore.

Rai SK, Verma A, Pandey D (2005). Genetic variability and character association analysis in Indian mustard (*Brassica juncea* L. Czern and Coss). Ann. Agri. Bio. Res., 10(1): 29-34.

Rao CR (1952). Advance statistical method in biometrical research. Ednl John Willey and Sons, New York.

Sadat HA, Nematzadeh GA, Jelodar NB, Chapi OG (2010). Genetic evaluation of yield and yield components at advanced generations in rapeseed (*B. napus* L.). Afr. J. Agric. Res., 5(15): 1958-1964.

Sandhu SK, Gupta NP (1996). Genetic divergence and correlation studies in *Brassica* species. Crop Improv., 23(2): 253-256.

Singh B (2004). Character association and path analysis under dryland condition in India mustard (*B. juncea*). Cruciferae Newslet., 25: 99-100.

Singh BD (2000). Plant Breeding. Klyani Publishers, New Delhi. pp. 574-597.

Singh D, Arya RK, Chandra N, Niwas R, Salisbury P (2010). Genetic diversity studies in relation to seed yield and its component traits in Indian mustard (*Brassica juncea* L. Czern & Coss.). Journal of Oilseeds Brassica, 1, 19-22.

Singh RP, Malik BP, Singh DP (19870. Variation for morpho-physiological characters in genotypes of Indian mustard. Indian J. Agric. Sci., 57: 227-230.

Sirohi SPS, Sanjai M, kumar A (2004). Correlation and path analysis of Indian mustard (*Brassica juncea L.* Czern and Coss). Ann. Agric. Res., 25(4): 491-494.

Srivastava MK, Singh BP (2002). Correlation and path analysis in Indian mustard (*Brassica juncea L.* Czern and Coss*)*. Crop Res. Hisar, 23(3): 517-521.

Sun DL, Zhao QC, Song WQ, Chen RY (2001). Relationships analysis of Chinese cabbage species by AFLP. Acta Horticulture Sinica, *28*, 331-335.

Vaishnava A, Sachan JN, Tewari SK (2006). Genetic divergence for important quantitative traits in Indian mustard (*Brassica juncea* (L.) Czern and Coss). Agricultural Science Digest, 26, 269-272.

Verma OP, Kushwaha GD, Singh HK (2000). Heterosis in relation to genetic diversity on Indian mustard*,* Cruciferae Newslet., pp.93-94.

Wu JG, Shi CH, Zhang HZ (2006). Partitioning genetic effects due to embryo, cytoplasm and maternal parent for oil content in oilseed rape (*Brassica napus* L.). Genet. Mol. Biol. vol.29 number3.

Xu SQ, Yao X (2006). Study on the correlation between yield characters and yield of superior rape (*Brassica napus L.*) in north Zhejiang Province. Jiaxing Academy of Agricultural Sciences, Jiaxing 314016, China. 22(2): 65-67.

Yarnell SH (1956). Cytogenetics of Vegetable Crops. Bot. Rev. 22: 81-166.

Zhang H, Berger JD, Milroy SP (2013). Genotype x environment interaction studies highlight the role of phenology in specific adaptation of canola (*Brassica napus*) to contrasting Mediterranean climates. Field Crops Res. Vol. 144, Pages 77–88.