GENETIC DIVERGENCE IN RAPESEED-MUSTARD (*Brassica rapa* L.)

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Abstract

An experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2009 to February 2010 to study the genetic divergences of 32 genotypes of *Brassica rapa* L. through principal component analysis and Mohalanobis D^2 analysis. Analysis of variance indicated that considerable genetic variability were existed among the 32 genotypes. On the basis of D^2 analysis, the genotypes were grouped into 6 clusters. Cluster III had the maximum number of 11 genotypes, while the cluster IV and cluster V had only 2 genotypes each. The highest inter-cluster distance was observed between cluster I and V (21.871), while the lowest in the cluster II and III (4.237). The intra cluster distance was the maximum in cluster V (0.469) and minimum in cluster III (0.116). The characters yield per plant, number of siliquae per plant, and days to maturity were found prominent towards the genetic divergence. The genotypes G-15 and G-19 from cluster IV and G-1, G-3, G-4, G-10, G-18, and G-24 from cluster I were suitable for creating more variability for higher yield per plant through hybridization.

Keywords: Genetic divergence, rapeseed-mustard, *Brassica rapa* L.

Introduction

Rapeseed-mustard is a major oilseed crop in Bangladesh. It contributes a lion's share to the total edible oil production in the country. Most of the developed varieties take long duration to mature except a few. As a result, they do not fit well in the existing T. aman - mustard - Boro cropping pattern. There is no scope of horizontal expansion of cultivation of rapeseed-mustard. So, for increasing rapeseed-mustard production, yield per unit area must be increased. Rapeseed-mustard production can be enhanced through the development of short duration and high yielding varieties. Such high yielding and short duration varieties can also fit into the existing cropping pattern. Therefore, emphasis should be given to develop high yielding varieties with short duration through hybridization followed by selection. Genetic variability in respect to genetic diversity is the prerequisite for the crop improvement through selection of high yielding progenies. Genetic diversity arises either due to geographical separation or due to genetic barriers to cross ability. The quantification of genetic diversity by biometrical approaches can help choose diverse parents for a successful hybridization programme.

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Genetic diversity plays an important role in plant breeding because hybrids between lines of diverse origin generally display a greater heterosis than those between closely related strains (Singh, 1986) which permits to select the genetically divergent parents to obtain the desirable recombination in the segregating generations (Uddin and Chowdhury, 1994). Selection of parents based on genetic divergence has become successful in several crops (Ashana and Pandey, 1980; Ananda and Rawat, 1984). Evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm (Tomooka, 1991). Therefore, the present investigation was carried out to determine the divergence among the different genotypes of rapeseed-mustard.

Materials and Method

The present experiment was conducted at the experimental farm of Sher-e-Bangla Agricultural University, Dhaka, during November 2009 to February 2010. A total of 32 rapeseed-mustard germplasm along with two released varieties were used in the experiment. The crop was fertilized at the rate of 10 tons of cowdung, 250 kg Urea, 175 kg Triple Super Phosphate (TSP), 85 kg Muriate of Potash (MoP), 250 kg Gypsum, 3 kg Zinc oxide and 1 kg Boron per hectare. The half amount of urea, total amount of cowdung, TSP, MoP, Gypsum, Zinc Oxide, and Boron were applied during final land preparation. The rest amount of urea was applied as top dressing after 25 days of sowing. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The spacing between line to line 30 cm was maintained. Intercultural operations, such as weeding, thinning, irrigation, pest management, etc. were done uniformly in all the plots when necessary.

For studying different genetic parameters and inter-relationships, ten characters were taken into consideration from the randomly selected ten plants. Mean data of each character was subjected to multivariate analysis viz, Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Canonical Vector Analysis (CVA), and Cluster Analysis (CLA) using Genstat released 13 Programme by a IBM Computer following the method of multivariate analysis of Mohalanobis, 1936.

Results and Discussion

Analysis of variance showed significant difference among the genotypes studied in the experiment. Thus, it indicated that considerable genetic variability existed among the 32 genotypes. Highly significant differences were also found among the mustard genotypes for nine characters by earlier workers (Chauhan *et al.,* 2008). The D^2 value and principal component scores also revealed a good (Islam and Islam, 2000 and Vivek et al., 2007) genetic diversity among the genotypes.

Cluster analysis

On the basis of non-hierarchical clustering using covariance matrix, the 32 genotypes of *Brassica rapa* were grouped into six clusters (Table 1). Islam and Islam, 2000 and Vivek *et al.* (2007) reported similar findings in mustard where 42 cultivars grouped into 4 clusters and 81 mustard cultivars into 13 clusters). Cluster III contained the highest number of 11 genotypes. The cluster I and cluster II had six genotypes each. Five genotypes were obtained by the cluster VI. The cluster IV and cluster V were constituted by two genotypes each.

Table 1. Distribution of 32 genotypes of *Brassica rapa* in six clusters.

Cluster	No. of genotypes	Name of Genotypes
I	6	G-1, G-3, G-4, G-10, G-18 and G-24
II	6	G-2, G-11, G-17, G-20, G-26 and G-32
III	11	G-5, G-7, SAU Sarisha- 1 S_3 (G-8), G-9, G-12, G-13 G-14,G-22, G-25, G-30 and G-31
IV	2	SAU Sarisha- 1 S_1 (G-15), SAU Sarisha- 1 S_2 (G-19)
V	2	BINA - 6 P_1 (G-16) , BINA Sarisha- 6 P_2 (G-21)
VI	5	G-6 G-23, G-27, G-28 and G-29

Principal component analysis (PCA) was carried out with 32 genotypes of *Brassica*. A two dimensional scattered diagram (Fig. 1) was developed on the basis of the principal component score, Z_1 and Z_2 of two principal coordinates axes I and II of Fig. 2. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA (Fig. 1). So the results obtained through PCA were confirmed by non-hierarchical clustering. Uddin and Chowdhury (1994) reported similar findings on genetic divergence among 34 genotypes of mustard in which genotypes were grouped into four clusters.
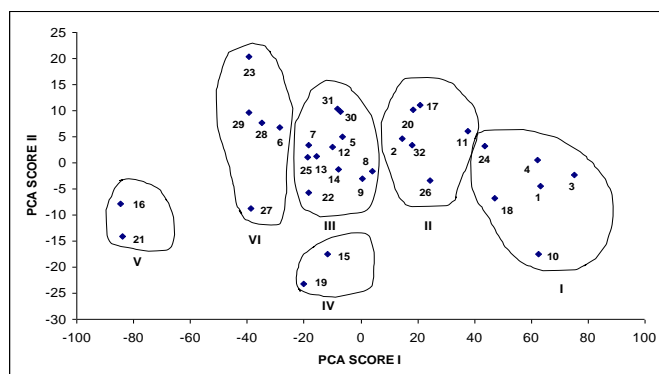

Fig. 1. Scatter distribution of 32 *Brassica rapa* genotypes based on their principal component scores superimposed with clustering.

The inter and intra cluster distance of the 32 genotypes are shown in (Table 2). The highest inter-cluster distance (21.871) was observed between cluster I and V followed by the cluster II with V (16.251) and I with IV (15.048). It is noted that the genotypes grouped into this clusters were highly divergent from each other. Parent selection from highly divergent cluster is expected to manifest high heterosis in hybridization. The lowest inter cluster distance (4.237) was observed between the cluster II and III followed by the cluster III and VI (4.760), cluster I and II (5.756) suggesting close relationship among these four clusters. Moderate or intermediate distance was found between cluster III and V (12.718), cluster II and IV (10.372). This result is similar with previous findings (Ashwini *et al.,* 2004).

Table 2. Average intra (bold) and inter cluster distance of 32 *Brassica rapa* genotypes.

Cluster	I	II	III	IV	V	VI
I	**0.343**	5.756	9.913	15.048	21.871	14.415
II		**0.432**	4.237	10.372	16.251	8.661
III			**0.116**	8.941	12.718	4.760
IV				**0.243**	8.867	7.020
V					**0.267**	8.015
VI						**0.469**

It is mentioned that crossing involving parents belonging to the medium divergent clusters may also exhibited significant and positive heterosis (Mian and Bahl, 1989). The inter cluster distance varied from 4.237 to 21.871 indicating the wide diversity among the genotypes. The intra cluster distance (0.469) was the highest in the cluster V, while the minimum was found in the cluster III. The inter cluster distances were higher than the intra cluster distances suggesting the wider genetic diversity among the genotypes of different groups.

A comparison of cluster means has been shown in Table 3. Cluster I had the highest cluster mean value for three characters viz., days to 50% flowering (33.50), number secondary branches per plant (6.78) and number of siliquae per plant (211.79). The cluster IV obtained the highest cluster mean value for five characters viz., plant height (115.50 cm), number of primary branches per plant (8.74), length of siliquae (6.21), 1000-seed weight (4.15), and yield per plant (8.97). This cluster was able to lead in respect of the highest cluster mean value for maximum characters. Among 10 characters, this cluster stood first for five characters. Cluster II and III failed to show the

highest or second highest mean values for yield or any other yield contributing characters. Cluster V contained two genotypes had the highest mean value for days to 80% maturity (92.16) and number of seeds per siliquae (22.16). Cluster VI also had no highest or second highest mean values for yield or any other yield contributing characters.

Table 3. Cluster means for ten characters of 32 *Brassica rapa* genotypes.

Character	Cluster					
	I	II	III	IV	V	VI
DTF	**33.50**	32.22	32.18	30.66	32.50	31.80
PHT	104.97	92.84	94.53	**115.50**	102.16	87.69
NPB	7.32	5.92	5.34	**8.74**	6.22	5.63
NSB	**6.78**	5.94	4.90	1.83	0.92	3.75
NPP	**211.79**	175.89	143.71	136.33	68.66	117.67
PLH	5.54	5.46	5.46	**6.21**	5.68	5.42
DEF	92.11	90.89	89.79	87.84	**92.16**	90.07
SPP	16.21	16.42	15.57	20.67	**22.16**	15.76
TSW	3.32	3.63	3.49	**4.15**	3.56	3.64
YPP	8.86	7.93	7.33	**8.97**	6.77	6.10

DTF = Days to 50% flowering, PHT= Plant height (cm), NPB =No. of primary branches/plant, NSB = No. of secondary branches/plant, NPP = No. of siliquae/plant, PLH = Length of siliquae (cm), DEF = Days to 80% maturity, SPP = No. of seeds/siliquae, TSW = 1000-seed weight (g) and YPP = Seed yield/plant (g).

Canonical Variate Analysis (CVA) indicates that the characters having positive values in both vector I and II contributed maximum towards divergence (Rahman and Munsur, 2009). The characters yield per plant, number of siliquae per plant, and days to maturity had the positive value in both   the   vectors (Table 4). Therefore, these characters had the maximum contribution towards the genetic divergence, while the character days to 50% flowering had negative contribution. Hence, these characters could offer a good scope for genetic improvement in rapeseed-mustard. Though the characters plant height and number of secondary branches per plant in vector I and number of primary branches per plant, siliquae length, number of seed per siliquae, and 1000-seed weight in II showed positive value only in one vector but negative value in other vector also played significant role towards the genetic divergence.

Table 4. Latent vectors for 10 principal component characters of 32 genotypes of
***Brassica*.**

Characters	Vectors 1	Vectors 2
Days to 50% flowering	-0.1279	-0.128
Plant height	0.0595	-0.025
No. primary branches/plant	-0.4644	1.0300
No. of secondary branches/plant	0.3637	-0.4368
No. of siliqua/plant	0.1284	0.0225
Siliqua length	-0.9130	0.0386
Days to maturity	0.0353	0.1086
No. of seeds/siliqua	-0.1358	0.3077
1000-seed wt	-1.9866	2.2513
Yield/plant	0.1541	0.2292

Selection of parents depends on the particular cluster from which the parents are selected and the relative contribution of characters to the total divergence (Choudhury *et al.,* 1975). Therefore, the parents in the cluster V if crossed with Cluster I and II might exhibit heterosis as well as higher level of genetic variation. The crosses involving parents belonging to intermediate diverse parents may also have chance to produce significant and positive heterosis in the subsequent generations. Considering the magnitude of genetic distance, contribution of different characters towards the total divergence, magnitude of cluster means for different characters and field performance, the genotypes G-15 and G-19 from cluster IV and G-1, G-3, G-4, G-10, G-18 and G-24 from cluster I may be suitable for creating higher yield per plant through hybridization which will eventually offer more scope of selection of plants with higher per plant yield.

References

Anand, I. J. and D. S. Rawat. 1984. Genetic diversity, combining ability and heterosis in brown mustard. *Indian J. Genet. Pl. Breed.* **44(2)**: 226-234.

Ashwini, T., P. Shanti, S.U. Charjan, P. G. Thakare, W. Meena. 2004. Genetic divergence studies in Indian mustard (*Brassica juncea* L). *J. Soil Crops*. **14(2)**: 297-304.

Ashana, A. N. and V. K. Pandy. 1980. Genetic divergence in linseed. *Indian J. Genet. Pl. Breed.* **40**: 247-250.

Chauhan, J. S, V. P. S. Bhadauria, K. H. Singh, S. Maharaj and K. Arvind. 2008. Genetic diversity analysis in rapeseed-mustard using quality characteristics. *Annals of Arid Zone*. **47(2)**: 145-149.

Chowdhury, B. D., R. K. Singh and N. K. Kakar. 1975. Estimation of genetic parameters in barley (*Hodeum vulgare L.*) Triallel anlysis. *J. Cytol*. Genet. Congr. Suppl. Pp. 54-57.

Islam, M. S. and M. O. Islam. 2000. Genetic diversity in rapeseed and mustard (*Brassica sp*.). *Bangladesh J. Genet. Pl. Breed.* **13 (2)**: 25-30.

Mahalanobis, P.C. 1936. On the generalized distance in statistics. *Proc. Natl. Inst. Sci*. **2** : 49-55.

Mian, M. A. K. and P. N. Bahl, 1989. Genetic divergence and hybrid performance in chickpea. *Indian J. Genet*. **40(1)**: 119-129.

Rahman M. M. and M. A. Z. Munsur. 2009. Genetic divergence analysis of lime. *J. Bangladesh Agric. Univ*. **7(1)**: 33-37.

Singh, H. 1986. Genetic variability, heritability, and drought indices analysis in *Brassica* species. *J. Oilseeds Res*. **3(2)**:170-177.

Tomooka, N. 1991. Genetic diversity and landrace differentiation of mungbean (*Vigna radiata*). An evaluation of its wild relatives as breeding materials. Tech. Bull. Trop. centre, Japan No. 28. Ministry of Agroforestry and Fisheries, Japan.

Uddin, M. J. and M. A. Z. Chowdhury. 1994. Genetic divergence in mustard. *Bangladesh J. Genet. Pl. Breed.* **7(2)**: 23-27.

Vivek S., B. Ram and K. Kamlesh. 2007. Genetic diversity in Indian mustard (*Brassica juncea L*). Czern and Coss. *Progressive Agric.* **7(1&2)**: 105- 110.