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Genetic Divergence in 58 Advanced Lines of *Brassica rapa*

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Abstract: Fifty five advanced line of *Brassica rapa* along with three commercially cultivated varieties as check were evaluated to study the genetic divergence through Mahalanobis D^2 statistics in respect of 10 different morphological characters. As per principal component analysis (PCA), D^2 and cluster analysis, the genotypes were grouped into six different clusters. Relationship was not found between genetic divergence and geographic distribution of the genotypes. Cluster II and cluster III had the maximum (13) and cluster IV had the minimum (6) number of genotypes. The inter cluster distance in most of the cases was larger than the intra cluster distance. The highest inter cluster distance was observed between cluster III and VI (19.52) and that of the lowest between cluster II and IV (3.02). Highest intra-cluster distance was observed in cluster VI (0.67). Plant height, number of secondary branches per plant and seeds per siliqua contributed maximum towards the total divergence. Considering diversity pattern, genetic status and other agronomic performances, line 39 and line 44 from cluster I; line 42 from cluster II; line 2, line 43 and line 45 from cluster V; line 50, line 52, line 54 and line 58 from cluster VI- might be selected as suitable parents in future hybridization program.

Key words: Genetic divergence % Advanced lines % *Brassica rapa*

INTRODUCTION

Brassica is cross pollinated oil crops belonging to the family Brassiceae, have a great economic commercial value and play a major role in feeding the world population. It provides over 16% of the world's edible oil and also gives nutritious vegetables and condiments to animal fodders. In Bangladesh, more than 228 thousand metric ton of mustard and rape seeds are produced among 354.25 thousand hectares of cultivable land of oil crops in the year 2007-2008 [1]. Oil seed production of the country is decreasing and consequently, import cost for edible oil is increasing. The causes of low yield include low yield potential of the varieties, insufficient precipitation when the crops are cultivated under rainfed conditions and the shifting of the crop to the marginal land. Thus to reduce the import of edible oil we need to develop genotypes of high yield potential with more tolerance to biotic and abiotic stress. The improved genotypes should well fit into T. Amon-Mustard-Boro cropping pattern to make it adaptable for the farmer. Genetic diversity is the prerequisite for crop improvement program. In general, use of more diverse parents increase the chances of obtaining higher heterotic F_1 and broad spectrum variability in segregating generations [2]. The quantification of genetic diversity through biometrical procedure made it possible to choose genetically diverse parents for a successful hybridization program. Tomooka [3] reported that evaluation of genetic diversity is important to know the source of genes for a particular trait within the available germplasm. Moreover, genetic diversity among the segregating population also helps to select suitable genotypes for commercial cultivation. So far, in Bangladesh, no intensive work has been reported on the improvement of yield for this crop with particular reference to morpho-physiological traits and genetic divergence. Therefore, the present investigation was carried out to estimate the nature and magnitude of genetic diversity present in a collection of 58 *Brassica rapa* genotypes.

MATERIALS AND METHODS

Altogether fifty eight genotypes including three check varieties (BARI Sarisha-15, SAU Sarisha-1 and Real Tori-7) were used in this study. The experiment was

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carried out in the experimental farm of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University (SAU), Dhaka during November 2007-March 2008. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 13 m × 55 m. A distance of 1 m from block to block, 30 cm from row to row and 10 cm from plant to plant was maintained. Seeds were sown in lines and placed at about 1.5 cm depth in the soil. Data were recorded on ten characters such as days to 50% flowering, days to maturity, plant height, number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of siliquae plant^{-1}, siliqua length, seeds per siliqua, 1000 seed weight and seed yield plant^{-1}. Fertilizers were applied at the rate of 250, 170, 85,150 and 1-1.5 kg ha^{-1} of urea, TSP, MP, Gypsum and boron respectively. Optimum cultural practices were followed to have a healthy crop. Mean data for each character was subjected to multivariate analysis viz., Principal Component Analysis (PCA), Principal Coordinate Analysis (PCO), Cluster Analysis (CA) and Canonical Variate Analysis (CVA) were done by using GENSTAT 513 program [4-6].

RESULT AND DISCUSSION

Principal Component Analysis (PCA): Principal Components were computed from the correlation matrix and genotype scores obtained from first components (which had property of accounting for maximum variance) and succeeding components with latent roots greater than the unity [6]. Contributions of the different morphological characters towards divergence were discussed from the latent vectors of the first two principal components. The genotypes were distantly located from each other. The principal component analysis produce eigen value of each principal component axes of co-ordination of genotypes in which the first axes totally accounted for the variation among the genotypes, where as four of these eigen values above unity accounted for 89.71% (Table 1).

The first two principal axes accounted for 68.03% of the total variation among the 10 characters describing 58 *Brassica rapa* genotypes

Cluster Analysis: Using co-variance matrix with the application of non-hierarchical clustering, the 58 *Brassica* genotypes were grouped into six clusters. These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. This suggested the presence of high degree of divergence in the material. However, Compositions of different clusters with their corresponding genotypes in each cluster are presented in Table 2.

Cluster II and III had maximum number of (13) genotypes followed by I, V, VI and IV, which had 11, 8, 7 and 6 genotypes respectively. Mishra *et al.* [7] reported similar number of clustering in 75 soybean genotypes. Srivastav and Singh [8] got six clusters and Rashid [9] got six clusters in rape seed and mustard. The clustering pattern obtained coincided with the apparent grouping patterns performed by PCA.

Canonical Variate Analysis: Canonical variate analysis was done to compute the inter-cluster Mahalanobiss D^2 values. Statistical distances represent the index of genetic diversity among the clusters. The intra and inter-cluster distance (D^2) values are presented in Table 3.

Table 1: Eigen values and percentage of variation in respect of 10 characters in 58 *Brassica rapa* genotypes

Principal component characters	Eigen values	Percentage of total variation accounted for	Cumulative percentage
Days to 50% flowering (Days)	4.464	44.64	44.64
Days to maturity (Days)	2.339	23.39	68.03
Plant height (cm)	1.194	11.94	79.97
No. of primary branch per plant	0.974	9.74	89.71
No. of secondary branch per plant	0.328	3.28	92.99
No. of siliquae per plant	0.291	2.91	95.90
Length of siliqua (cm)	0.167	1.67	97.57
Seed per siliqua	0.116	1.16	98.73
Thousand seed weight (g)	0.086	0.86	99.59
Seed yield per plant (g)	0.041	0.41	100.00

Table 2: Distribution of 58 genotypes of *Brassica rapa* in six clusters

Cluster	Number of genotypes	Name of genotypes
I	11	Line 3, Line 13, Line 29, Line 32, Line 34, Line 39, Line 40, Line 41, Line 44, Line 47, Line 55
II	13	Line 5, Line 16, Line 19, Line 21, Line 23, Line 26, Line 27, Line 28, Line 30, Line 31, Line 38, Line 42, Line 57 (SAU-Sa1)
III	13	Line 6, Line 10, Line 11, Line 12, Line 15, Line 18, Line 20, Line 22, Line 24, Line 25, Line 35, Line 49, Line 56 (BARI- sarisha- 15)
IV	6	Line 4, Line 7, Line 9, Line 14, Line 17, Line 33
V	8	Line 2, Line 8, Line 36, Line 37, Line 43, Line 45, Line 46, Line 53
VI	7	Line 1, Line 48, Line 50, Line 51, Line 52, Line 54, Line 58 (Real Tori-7)

Table 3: Average intra (Diagonal) and inter cluster distances (D^2) for genotypes of *Brassica rapa*

Cluster	I	II	III	IV	V	VI
I	**0.52**					
II	6.14	**0.44**				
III	9.30	3.20	**0.43**			
IV	3.21	3.02	6.22	**0.42**		
V	4.10	10.13	13.22	7.29	**0.50**	
VI	10.32	16.43	19.52	13.53	6.30	**0.67**

Bold values indicate intra-cluster distances

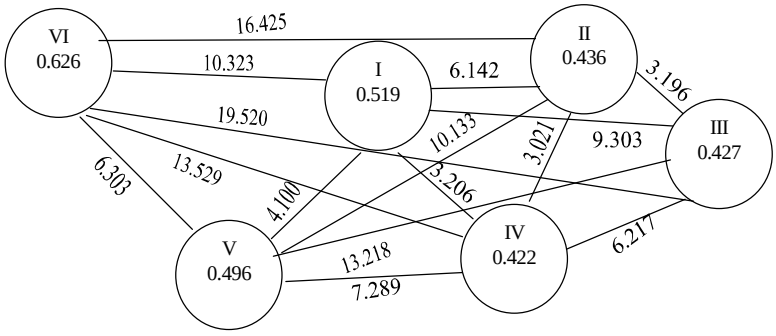

Fig. 1: Diagram showing intra and inter cluster distances of 58 *Brassica rapa* genotypes

Results indicated that the highest inter-cluster distance was observed between cluster III and VI (19.520), followed by between II and VI (16.425), IV and VI (13.529), III and V (13.218), I and VI (10.329), II and V (10.133). The higher inter-cluster distances between these clusters indicate to obtain wide spectrum of segregating population if parents chosen from these distant clusters are used for hybridization program. However, the highest inter-cluster distance was observed between clusters III and VI indicated the genotypes in these clusters were far diverged than those of other clusters. Lowest inter-cluster distance was observed between the cluster II and IV (3.021) followed by I and IV (3.206), II and III (3.196), I and V (4.100) and a similar type of distance was found between I and II (6.142), III and IV (6.210), V and VI (6.303) suggesting a close relationship among the genotypes included within these cluster (Figure 1).

The inter-cluster distances were larger than the intra-cluster distances suggesting wider genetic diversity among the genotypes of different groups (Table 3 and figure 1). Islam [10] obtained longer inter-cluster distances than the intra-cluster distances in a multivariate analysis.

The intra-cluster distance varied from 0.422 to 0.626 while maximum for cluster VI (0.626), which was composed of 7 genotypes and minimum distance was found in cluster IV (0.422) that comprised 6 genotypes.

The clustering pattern of D^2 analysis followed the similar trend of distribution of genotypes in PCA. The D^2 and PCA were found to be alternative methods in yielding information regarding the clustering pattern. Results of different multivariate techniques were superimposed in figure 2. Moreover, the PCA provided information on contribution of the characters towards divergence (Table 3).

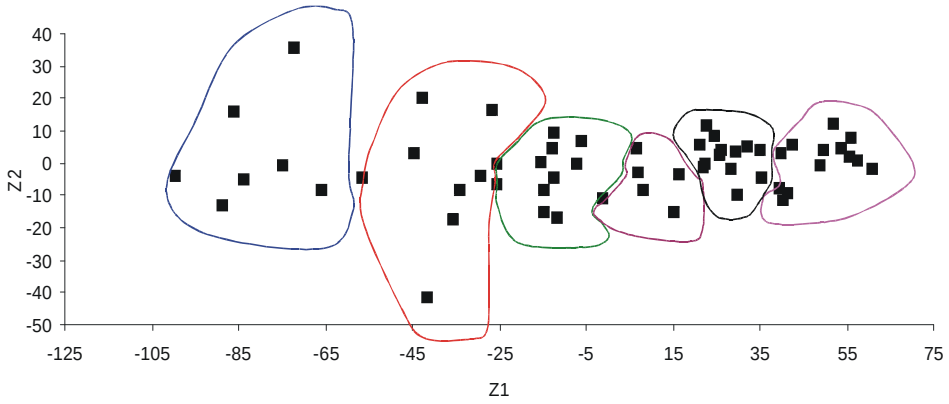

Fig. 2: Scatter distribution of 58 *Brassica rapa* genotypes based on their principal component scores superimposed with clusters.

Table 4: Relative contribution of the 10 characters to the total divergence of 58 *Brassica*

Characters	Vector-I	Vector-II
Days to 50% flowering *rapa* genotypes	-0.0252	-0.1303
Days to maturity	0.1428	-0.1290
Plant height (cm)	0.0229	0.0965
No. of primary branch per plant	0.1808	-0.2030
No. of secondary branch per plant	0.3748	0.5351
No. of siliqua per plant	-0.1568	-0.0413
Length of siliqua (cm)	-1.1739	-1.7379
Seeds per siliqua	0.3668	0.0736
Thousand seed weight (g)	5.2374	-2.0981
Seed yield per plant (g)	0.0638	-0.0125

The clustering pattern of the genotypes revealed that varieties/lines originating from the same places did not form a single cluster because of direct selection pressure. This indicated that geographic diversity was not related to genetic diversity that might be due to continuous exchange of genetic materials among the countries of the world. Same results have been reported by Murty and Anand [11]; Anand and Rawat [12] in brown mustard; Patel *et al.* [13] in sunflower; Verma [14] in groundnut and soybean.It had been observed that geographic diversity was not always related to genetic diversity and therefore, it was not adequate as an index of genetic diversity. Murty and Arunchalam [15] studied that genetic drift and selection in different environment could cause greater diversity than geographic distance. Furthermore, there was a free exchange of seed material among different region, as a consequence, the characters constellation that might be associated with particular region in nature, lose their individually under human interference and however, in some cases effect of geographic origin influenced clustering that was why geographic distribution was not the sole criterion of genetic diversity.

The free clustering of the genotypes suggested dependence upon the directional selection pressure applied for realizing maximum yield in different regions; the nicely evolved homeostatic devices would favor constancy of the associated characters would thus indiscriminate clustering. This would be suggested that it was not necessary to chose diverse parents for diverse geographic regions for hybridization.

Contribution of Characters Towards Divergence of the Genotypes: Contribution of characters towards divergence is presented in Table 4. The vector-1 (Z1) obtained from PCA, the important characters responsible for genetic divergence in the axis of differentiation were days to maturity (0.1428), plant height (0.0229), Number of primary branches per plant (0.1808), number of secondary branches per plant (0.3748), seeds per siliqua (0.3668), thousand seed weight (5.2374) and seed yield per plant (0.0638). In vector II (Z2), the second axis of differentiation, plant height (0.0965), number of secondary branches per plant (0.5351) and seeds per siliqua (0.0736) were important because all these characters had positive signs. On the other hand days to 50% flowering (-0.0252),

number of siliqua per plant (-0.1568), length of siliqua (-1.1739) in the first axis of differentiation and days to 50% flowering (-0.1303), days to maturity (-0.1290) number of primary branches per plant (-1.7379) thousand seed weight (-2.0981) and seed yield per plant (-0.0125) in the second axis of differentiation had a minor role in the genetic divergence because they had negative signs.

Plant height, number of secondary branches per plant and seeds per siliqua in both the vectors had positive signs, which indicated they were the important component characters having higher contribution to the genetic divergence among the materials studied. The character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization [16].

Selection of Genotypes for Future Hybridization: Selection of genetically diverse parents is an important step for hybridization program. So the genotypes were to be selected on the basis of specific objectives. A higher heterosis could be produced from the crosses between genotypically distant parents [17-20]. Considering the magnitude of genetic distance, contribution of different characters toward the total divergence, magnitude of cluster means for different character and per se performance the following genotypes were considered to perform better if used in hybridization program. From cluster I, line 39 for late flowering and maturity, line 44 for higher value of thousand seed weight could be selected. From cluster II, line 42 could be selected for higher siliqua length and seeds per siliqua. In cluster V, line 45 could be selected for early maturity and lowest plant height, line 43 for early flowering and line 2 selected for higher plant height. From cluster VI, line 52 for higher plant height, early maturity, seeds per siliqua, seed yield per plant; line 50 for highest number of primary branches per plant, Siliqua length and line 54 for higher number of siliquae per plant.

Considering group distance and other agronomic performance the inter genotypic crosses between G 31 and G 58, G 11 and G 58, G 49 and G 58, G 22 and G 58, G 6 and G 58, G 15 and G 58, G 42 and G 58, G 56 and G 58, G 31 and G 54 may be suggested for future hybridization program.

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