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GENETIC DIVERSITY OF RAPESEED (*Brassica napus* L.) GENOTYPES IN BANGLADESH

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Abstract

Genetic diversity in thirty eight traditional rapeseed genotypes was studied under favorable condition through Mahalanobis D^2 statistic for yield and yield contributing characters. The genotypes were grouped into five clusters. The inter-cluster distances were higher than intracluster distances indicating wider genetic diversity among the clusters. The intra-cluster distances were lower in all the cases reflecting homogeneity of the genotypes within the clusters. Among the different cluster the genotypes of the cluster IV, III and I included were taller plant. The genotypes in the cluster III and IV had large size raceme. The genotypes in the cluster IV, III and V exhibited comparatively higher number of siliqua per raceme. Longer siliqua was noticed for the genotypes in the cluster III, IV and I. Higher number of seeds per siliqua noticed in clusters I, II and III. The genotypes of the cluster I and II produced bold size seed. The genotypes in the cluster V and I had high harvest index. The genotypes of the cluster III and I produced high seed yield per plant. Among the different cluster, the cluster III included the genotypes which had high yield, higher number of seeds per siliqua, longer siliqua, siliqua number per raceme and high plant height. Moreover these cluster displayed wide divergence with the genotypes of cluster V. The genotypes of the cluster V had the highest harvest index therefore selection of the parental material for crossing program for improvement of yield in rapeseed is suggested from these two clusters.

Keywords: Rapeseed (*Brassica napus*); genetic diversity; D^2 statistics; cluster analysis

INTRODUCTION

Rapeseed (*Brassica napus*), also known as rape, oilseed rape (and, in the case of one particular group of cultivars, canola), is a bright-yellow flowering member of the family Brassiceae (mustard or cabbage family), cultivated mainly for its oil-rich seed(Wikipedia, 2016).Rapeseed belongs to the family of Cruciferous under genus Brassica are most important oilseed crops, source of vegetable oil, widely grown oilseed crops of Bangladesh occupying 0.532 million ha of land and the production was 0.596 million MT (metric ton) with the yield of 1.12 MT (metric ton)/ ha in 2013-14(Wang& Yin, 2014) It is now ranked first among oilseed crops in Bangladesh as well as the second largest oilseed crop in the world after soybean (FAO ,2015).Domestic production of edible oil in Bangladesh mainly comes from mustard and sesame. Mustard and rapeseed seeds contain 42% oil, 25% protein (Kaul, 2006). In addition, its meal has 38-40% protein that has a complete profile of amino acids including lysine, methionine and cystine.The toxic content in *Brassica napus* are erucic acid and glucosinolate (Rashid, 2013). According to (Mondal *et al*., 2001) oil crops produce 0.16 million tons of edible oil every year as against the total requirements of 0.5 million tons for a population of 130 million in Bangladesh. The shortage of edible oil has become a chronic problem for the nation.

To fulfill the requirement, the country has to import edible oils at the cost of huge amount of foreign exchange. The major activities of plant breeding are building up agene pool of variable germplasm, selection of individual from the gene pool and utilization of selected individual to evolve a superior variety (Zayaet *et al*., 2008). Genetic diversity refers to sum total of genetic variations found in a species or population. It is a prerequisite for the development of improved cultivars with wider adaptability and broad genetic base.

Diversity analysis greatly helps the breeder in identification and proper choice of parents for specific breeding objectives. To realize heterosis, genetically divergent parents are generally considered to be useful. In such crosses more variability could be expected in the resulting segregating progenies (Joseph *et al.,* 1999). Precise information about the extent of genetic divergence on characters used for discrimination among the population is crucial in any crop improvement program, because selection of plants based on genetic divergence has become successful in several crops (Dubey *et al.*, 2006).Genetic diversity is a powerful tool to determine the genetic discrimination among the genotypes which is used to select appropriate parents for hybridization to develop high yielding potential variety (khan2005). With the development of advanced biometrical techniques such as multivariate analysis based on the Mahalanobis (1936) statistics, quantification of divergence among the biological population and assessing the relative contribution of different components to the total divergence at intra and inter-cluster levels have now become possible. Such a study also permits to select the genetically diverse parents to obtain the desirable recombinant in the segregating generations upon crossing.

Hybridization is a common practice for combining the desirable characters of two or more lines or varieties into a single variety. In several cases, the progenies become far superior to the parents in vigor. Inclusion of more diverse parents (within a limit) is believed to increase the chances for obtaining stronger heterosis and gives broad spectrum of variability in segregating generations (Jessek *et al.,* 2013). In addition, crossing in moderately diverse parents also showed maximum heterosis (Kumer, 2009). The necessity of principal component analysis (PCA), principal coordinate analysis (PCO), non-hierarchical clustering and canonical vector analysis (CVA) for measuring the degree of divergence has been established by several investigators in rapeseed and other crops (kakroo *et al.,* 2001). The present study was, therefore undertaken to assess the extent of genetic diversity in 38 traditional Brassica napus L.genotypes. This will help in classifying those into clusters to select genotypes as prospective parents to develop transgressive segregants which will be ultimately used for developing modern variety (Ruksana *et al*,2005).

MATERIALS AND METHODS

The experiment was conducted with 38 genotypes of rapeseed in the experimental farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Five plants were selected randomlyfromeachplotforcollectionofdataforyieldandyieldcontributingcharacters viz. plant height, raceme length, siliqua per raceme, siliqua length, seeds per siliqua, 1000 seed weight, harvesting index and yield/plants. The data were analyzed following principal component analysis (PCA) and Mahalanobis's (1936) generalized distance (D^2) extended by Rao (1952). Intra and inter cluster distances were calculated

by the methods of (Singh,2000). All statistical analyses were carried out using MSTATC.

RESULTS AND DISCUSSION

Genetic divergence among the rapeseed was studied by estimating Mohalnobis'-D^2 statistics which is presented in Table 1. The D^2 analysis grouped the 38 genotypes into five clusters. The cluster included group the genotypes in the different cluster shown in the Table 1. The cluster I included 15 genotypes, which the highest followed by cluster III which contained 9 genotypes. Cluster IV and cluster III contained 7 and 4 genotypes respectively. The rest of three genotypes were included in the cluster (Hussain *et al.* 2008) studied the genetic divergence using Mahalnobis' D^2 statistic in 40 diverse type of rapeseed and indicated that genotypes differed significantly for yield contributing characters.(Singh *et al.* 1997) studied genetic divergence through D^2 statistic with 50 genotypes of *B. napus* growing in 12 environments based on 13 characters. They searched the clustering pattern and their inter and intra cluster distances. On the basis of stability, high yield and divergence among the genotypes, nine crosses were recommended as suitable for use in breeding programme.

Table 1. Distribution of 38 rapeseed genotypes indifferent cluster for various yield and yield contributing characters

Cluster	No. of genotypes	Name of genotypes
I	15	Bina sarisha-14, Safal, Bina sarisha-6, Bari sarisha-7, Nap-0757, Nap-0957, Nap-0751, Nap-0726-2, Nap-0724-2, Nap-0760, Nap-0838, Bari sarisha-12, Agrani, Nap-0741-1
II	4	Bari sarisha-14, Nap-0740-2, Nap-0839, Tori-7
III	9	Nap-0763, Nap-0721-1, Nap-0758-2, Bari sarisha-8, Bina sarisha-3, Nap-0842-2, Nap-0824, Bina sarisha-5, Nap-0529
IV	7	Bari sarisha-10, Bari sarisha-11, Bari sarisha-2, Bari sarisha-5, Nap-206×Nap-248, BC5897×BARI-8 Bari sarisha-13
V	3	Bari sarisha-3, Bari sarisha-6, Bari sarisha-9

Table 2. Average intra and inter cluster distances D^2among 38 genotypes of rapeseed

Cluster	I	II	III	IV	V
I	**380.15**				
II	1214.47	**392.33**			
III	590.93	1222.83	**573.90**		
IV	903.83	2542.81	1074.27	**871.65**	
V	1008.15	1657.10	1602.06	1789.33	**534.12**

The bold and underline figures are intra-cluster distance.

The D^2 values between and within the different clusters are shown in Table 4.5. There was genetic divergence within the different cluster group which ranged the D^2 value 380 to 871. The cluster IV containing seven genotypes exhibited the highest amount of genetic divergence within the group. The inter-cluster distances (D^2) were always higher than the intra-cluster distances. The distances between the cluster IV and V; III and V and II and V and II and IV were comparatively higher than the other inter-cluster

distances. This means that genotypes of these clusters were more diversified for yield and yield contributing characters. Gupta, V.P. (2002) studied genetic divergence using the D^2 statistics and canonical analysis among 25 genotypes of *Brassica napus*. They reported that genetic and geographical divergence was not related the genotypes were grouped into six clusters of which cluster I was the largest accommodating among these genotypes. The cluster VI had large genetic distance from the remaining clusters. The least variation was noticed between genotypes of the cluster I, entry indicating the closeness of the genotypes included in this cluster.

Contribution of the individual character towards divergence was presented in the Table 4.6. Table showed that harvest index contributed maximum to the genetic divergence and this was followed by 1000 seed weight and plant height. These means that these are the major characters which influenced the estimation of the D^2 values. The rest amount of contribution towards the divergence was noticedthrough the characters. Siliqua length followed by siliqua per raceme, raceme length and seed yield per plant. Goswami *et al*., (2005). studied on some 19 genotypes of rapeseed (*B. napus*). They studied yield and yield contributing characters grouped the genotypes into 5 clusters with clusters I comprising these genotypes, clusters II and III 2 each and clusters IV and V one each. Test weight days to maturing and seed yield.

Table 3. Percent contribution of individual characters toward divergence

Characters	% contribution toward divergence
Plant height	17.92
Raceme length	8.68
Siliqua /raceme	2.13
Siliqua length	0.28
Seeds/Siliqua	12.66
1000 seed weight	19.35
Harvest index	31.72
Yield/plant	7.26

The cluster mean of the genotypes were estimated and presented character wise in Table 4. Among the different cluster the genotypes of the cluster IV, III and I included were taller plant. The genotypes in the cluster III and IV had large size raceme. The genotypes in the cluster IV, III and V exhibited comparatively higher number of siliqua per raceme. Longer siliqua was noticed for the genotypes in the cluster III, IV and I.

Table 4. The cluster means for yield and yield contributing characters in rapeseed

Characters	I	II	III	IV	V
Plant height (m)	110.41	83.25	106.52	126.77	98.75
Raceme length	46.21	33.53	51.58	51.46	37.21
Siliqua/raceme	28.98	22.09	31.38	39.62	32.57
Siliqua length	5.96	4.80	6.99	5.35	5.88
Seed/ Siliqua	21.27	18.14	20.74	14.19	16.55
1000 seed weight	3.63	3.60	3.02	3.17	3.06
Harvest index	32.10	18.42	21.98	29.03	49.56
Yield/plant	2.58	1.78	2.59	1.84	1.77

Higher number of seeds per siliqua noticed in clusters I, II and III. The genotypes of the cluster I and II produced bold sizesize seed. The genotypes in the cluster V and I had high harvest index. The genotypes of the cluster III and I produced high seed yield per plant.

CONCLUSION

The present investigation on genetic diversity of rapeseed genotypes indicated a scope for improvement of grain yield through selection (Rameah *et al,* 2003)Genetic diversity in thirty eight traditional rapeseed genotypes was studied under favourable condition to assess the extent of genetic diversity which helps in classifying those into clusters to select genotypes as prospective parents to develop transgressive segregants that will be ultimately used for developing modern variety of rapeseed. (Dubey, R.N. 2006). Higher inter-cluster distances indicating indicating wider genetic diversity among the cluster also lower intra-cluster distances reflecting homogeneity of the genotypes within the clusters. In this study, the genotypes were grouped into five clusters. Among the different cluster the genotypes of the cluster IV (Bari sarisha-10, Bari sarisha-11, Bari sarisha-2, Bari sarisha-5, Nap-206×Nap-248, BC5897×BARI-8 Bari sarisha-13)III (Nap-0763, Nap-0721-1, Nap-0758-2, Bari sarisha-8, Bina sarisha-3, Nap-0842-2, Nap-0824, Bina sarisha-5, Nap-0529)and I (Bina sarisha-14, Safal, Bina sarisha-6, Bari sarisha-7, Nap-0757, 2Nap-0957, Nap-0751, Nap-0726-2, Nap-0724-2, Nap-0760, Nap-0838, Bari sarisha-12, Agrani, Nap-0741-1) included were taller plant. The genotypes in the cluster III and IV had large size raceme. The genotypes in the cluster IV, III and V exhibited comparatively higher number of siliqua per raceme. Longer siliqua was noticed for the genotypes in the cluster III, IV and I. Higher number of seeds per siliqua noticed in clusters I, II and III. The genotypes of the cluster III and I produced high seed yield per plant. Among the different cluster, the cluster III included the genotypes which had high yield, higher number of seeds per siliqua, longer siliqua, siliqua number per raceme and high plant height. The genotypes of the cluster I and II produced bold size seed. The genotypes in the cluster V and I had high harvest index. Moreover these cluster displayed wide divergence with the genotypes of cluster V. The genotypes of the cluster V had the highest harvest index therefore selection of the parental material for crossing program for improvement of yield in rapeseed is suggested from these two clusters.

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