

Genetic diversity analysis in some advanced lines of *Brassica napus*

Firoz Mahmud^a, Md. Golam Rasul^b, Md. Abdur Rahim^{a,*}

^a Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka-1207, Bangladesh

^b Department of Genetics and Plant Breeding, Bangabandhu Sheikh Majibur Rahman Agricultural University, Gazipur, Bangladesh

* Corresponding author, e-mail: rahimgpb@yahoo.com, rahimma11@yahoo.com

Received 12 Aug 2008

Accepted 5 Nov 2008

ABSTRACT: The genetic diversity of 22 rapeseed (*Brassica napus*) advanced genotypes was studied using principal component analysis, non-hierarchical clustering, and canonical vector analysis. The genotypes were grouped into four clusters. Cluster II contained the maximum number of genotypes (9) and cluster III contained the lowest (2). The highest inter-cluster distance was found between cluster I and cluster III and the lowest between cluster I and cluster II. The highest intra-cluster distance was noticed for cluster III and the lowest for cluster II. Cluster I had the highest mean values for siliqua length and thousand seed weight. Cluster III had the lowest cluster mean values for the number of days to 50% flowering and the number of days to maturity with moderate seed yield. Crosses between genotypes belonging to cluster II with those of cluster I and cluster IV might therefore produce high heterosis in yield as well as earliness.

KEYWORDS: genotype cluster, rapeseed

INTRODUCTION

Rapeseed (*Brassica napus* L., 2n=38) is an important oil seed crop belonging to the family Cruciferae. The seeds of mustard and rapeseed contain 42% oil and 25% protein¹. The oil is mainly used in food. Oil and fat are not only a source of energy but also contain fat-soluble vitamins A, D, E, and K. The oil cake contains proteins of high biological value and applicable quantities of calcium and phosphorus, and is used as a very good animal feed as well as fertilizer for various crops.

Rapeseed along with mustard are currently ranked as the world's third most important edible oil crop in terms of area and production after soybean and cotton². Major producing regions include Canada, China, northern Europe, and the Indian sub-continent. The rapeseed and mustard grown in Bangladesh comprise three species viz. *B. campestris*, *B. juncea*, and the newly introduced *B. napus*. These crops have the largest area and production among the oil crops grown in Bangladesh³.

Genetic diversity is essential to develop cultivars with increased yields, wider adaptation, desirable qualities, and pest and disease resistance. Inclusion of more diverse parents (within a limit) in hybridization is supposed to increase the chance of obtaining maximum heterosis and give a broad spectrum of

variability in segregating generations. With this aim, an attempt was made in the present study to analyse genetic diversity among 22 advanced genotypes of *B. napus*.

MATERIALS AND METHODS

Twenty two advanced genotypes of *B. napus* were grown in randomized complete block design with three replications at the experimental farm of Bangabandhu Sheikh Majibur Rahman Agricultural University, Gazipur, Bangladesh during the winter of 2006. The genotypes were collected from the Department of Genetics and Plant Breeding, Bangabandhu Sheikh Majibur Rahman Agricultural University. The plot size was 4 rows of 3 m width. A distance of 1.5 m from block to block, 30 cm from row to row, and 10 cm from plant to plant was maintained. The fertilizers urea, triple super phosphate, muriate of potash, gypsum, and zinc sulphate were applied in quantities of 270, 170, 100, 150, and 5 kg/ha, respectively, along with 10 t/ha of cow dung. With the exception of half of the urea, the cow dung and fertilizers were applied at the time of final land preparation. The remaining urea was top dressed 30 days after seedling emergence. The standard agronomic practices were maintained to raise a healthy crop. Data on 10 randomly selected plants from each plot were recorded on 11 characters viz., days to 50% flowering, days to 80% maturity,

plant height, number of primary branches per plant, number of secondary branches per plant, inflorescence length, siliqua length, number of siliquae per plant, number of seeds per siliqua, thousand seed weight, and grain yield per plant. The data were subjected to principal component analysis and tested with the D^2 -statistic using GENESTAT 5, Release 4.1.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among the genotypes for all the 11 characters under study revealing the presence of notable genetic variability among the genotypes. The 22 genotypes were grouped into four clusters through non-hierarchical clustering (Table 1). Most of the genotypes (9) were grouped into cluster II, followed by 7 and 4 in clusters I and IV, respectively. Two genotypes were grouped into cluster III. Ananda and Rawat⁴ reported 4 clusters in brown mustard. Six clusters were found by Afroz et al⁵.

The average inter- and intra-cluster distances are presented in Table 2. The inter-cluster distances in all cases were larger than the intra-cluster distance indicating the presence of wider diversity among the genotypes of distant groups. Islam and Islam⁶ also obtained larger inter-cluster than intra-cluster distances in a multivariate analysis. The maximum intra-cluster distance occurred in cluster III and the minimum was in cluster II. This suggests that the genotypes in cluster III were more diverse (heterogeneous) than those of other clusters, being relatively homogeneous in cluster II. The maximum inter-cluster distance was found between clusters I and III, followed by II and III, and III and IV, indicating wide genetic diversity between them. Similar reports were also made by Afroz et al⁵. The minimum inter-cluster distance was found between clusters I and II suggesting genotypes

Table 2 Average intra- (bold) and inter-cluster distances (D^2) for advanced genotypes of *B. napus*.

Cluster	I	II	III	IV
I	10.832	272.896	1312.253	745.7335
II		65.754	1408.109	562.3879
III			38.120	2411.655
IV				136.617

in these clusters were genetically close. The clustering pattern of the genotypes revealed that genotypes originating from the same places may not form a single cluster because of direct selection pressure. Instead, geographic diversity is related to genetic diversity that might be due to the continuous exchange of genetic material among the countries of the world. Ananda and Rawat⁴ found similar results in brown mustard.

Table 3 shows that cluster I ranked first for mean values of siliqua length and 1000-seed weight (longer siliquae and larger seeds are found in this cluster) and second for number of seeds per siliqua, and it had also the lowest cluster mean for plant height indicating dwarf plants are included in this cluster. Cluster II had the highest mean number of primary branches per plant, number of secondary branches per plant, inflorescence length, number of siliquae per plant, and grain yield per plant. Cluster II also ranked second for days to 80% maturity, siliqua length, and 1000 seed weight. Cluster III possessed genotypes with the second highest cluster mean for number of primary branches per plant, number of secondary branches per plant, number of siliquae per plant, and grain yield per plant, and the lowest for days to 50% flowering

Table 3 Cluster means for 11 characters of 22 advanced genotypes of *B. napus*.

Characters	Clusters			
	I	II	III	IV
Days to 50% flowering	38.00	39.25	37.95	38.56
Days to 80% maturity	104.75	103.50	103.35	103.44
Plant height (cm)	100.40	115.95	103.79	104.90
No. of primary branches per plant	3.25	5.15	3.82	3.55
No. of secondary branches per plant	8.05	16.12	8.53	7.34
Inflorescence length (cm)	62.10	79.87	70.75	71.51
Siliqua length (cm)	8.01	7.80	7.23	7.35
No. of siliquae per plant	78.10	200.20	140.95	117.49
No. of seeds per siliqua	22.59	24.68	20.91	20.41
Thousand seed weight (g)	3.20	3.15	3.12	2.90
Grain yield per plant (g)	2.89	9.29	5.50	4.05

Table 1 Distribution of 22 advanced genotypes of *B. napus* in four clusters. *N* = number of genotypes.

Cluster	<i>N</i>	Names of genotypes
I	7	G1(Nap 108), G3(Nap 179), G14(Nap 9901), G15(Nap 9904), G16(Nap 9905), G17(Nap 9906), G18(Nap 9808)
II	9	G2(Nap 130), G7(Nap 2001), G8(Nap 2012), G9(Nap 2013), G11(Nap 2037), G13(Nap 2066), G19(Nap 94006), G20(Bari Sharisha 7), G21(Bari Sharisha 8)
III	2	G4(Nap 205), G5(Nap 206)
IV	4	G6(Nap 248), G10(Nap 2022), G12(Nap 2057), G22(Bari Sharisha 13)

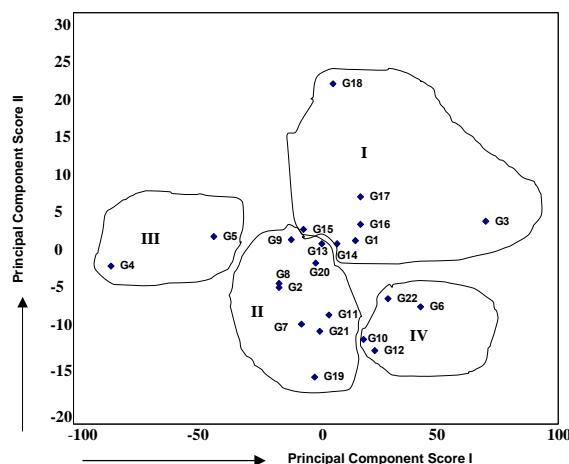


Fig. 1 Scatter diagram of 22 advanced genotypes of *B. napus* based on their principal component scores superimposed with clustering.

and days to maturity, with moderate seed yield. Thus early maturing genotypes were included in this cluster. Cluster IV produced the second highest cluster mean for days to 50% flowering, plant height, and inflorescence length. The maximum range of variability was observed for the number of siliquae per plant (78.10–200.20) among all the characters in the four clusters.

A two-dimensional scatter diagram was constructed using components I and II as the axes (Fig. 1). The genotypes were apparently distributed into four clusters. The genotypes of cluster III were more diverse than those of cluster I.

The canonical variate analysis revealed that the vectors (Vector I and II) for days to 80% maturity and siliqua length were positive across two axes indicating these two characters contributed the most towards divergence (Table 4). The characters contributing the most to the divergence are given greater importance when deciding on the cluster for the purpose of further selection and choice of parents for hybridization⁷.

It is assumed that the maximum amount of heterosis is manifested in cross combinations involving genotypes from the most divergent clusters. Genotypically distant parents are able to produce higher heterosis^{8,9}. However, for a practical plant breeder, the objective is not only high heterosis but also to achieve a high level of production. In the present study, the maximum distance occurred between cluster I and III. Considering this, it appears that the crosses between the genotypes belonging to cluster III with those of clusters I and IV might produce high heterosis in yield as well as earliness.

Table 4 Relative contribution of the 11 characters to the total divergence of genotypes.

Characters	Vector I	Vector II
Days to 50% flowering	-0.0012	0.0616
Days to 80% maturity	0.0074	0.0129
Plant height (cm)	-0.1167	0.7705
No. of primary branches per plant	-0.0138	0.0018
No. of secondary branches per plant	-0.0621	0.0020
Inflorescence length (cm)	-0.1319	0.6061
Siliqua length (cm)	0.0025	0.0169
No. of siliquae per plant	-0.9812	-0.1731
No. of seeds per siliqua	-0.0145	0.0644
Thousand seed weight (g)	-0.00130	0.0003
Grain yield per plant (g)	-0.04471	-0.0239

REFERENCES

- Khaleque MA (1985) A guide book on production of oil crops in Bangladesh. DAE and FAO/UNDP Project BGD/79/034, 'Strengthening the Agricultural Extension Service' Khamarbari, Farmgate, Dhaka, p 3.
- FAO (1999) *FAO Production Year Book*, Vol 53, Food and Agricultural Organization of United Nations, Rome, p 115.
- Anonymous (2001) Statistical Year Book of Bangladesh 2000. Bangladesh Bureau of Statistics, Ministry of Planning, Government of the People's Republic of Bangladesh, Dhaka.
- Ananda IJ, Rawat DS (1984) Genetic diversity, combining ability and heterosis in brown mustard. *Indian J Genet Plant Breed* **44**, 226–34.
- Afroz R, Sharif MSH, Rahman L (2004) Genetic divergence in mustard and rape (*Brassica* spp.). *Bangladesh J Plant Breed Genet* **17**, 37–43.
- Islam MS, Islam MO (2000) Genetic diversity in rape-seed and mustard (*Brassica* sp.). *Bangladesh J Plant Breed Genet* **13**, 25–30.
- Jagadev PN, Samal KM, Lenka L (1991) Genetic divergence in rape mustard. *Indian J Genet Plant Breed* **51**, 465–6.
- Ghaderi A, Shishegar M, Regai A, Ehdai B (1979) Multivariate analysis of genetic diversity for yield and its components in mungbean. *J Am Soc Hort Sci* **104**, 728–32.
- Mian MAK, Bahl PN (1989) Genetic divergence and hybrid performance in chickpea. *Indian J Genet Plant Breed* **49**, 119–29.