

## CHARACTERIZATION OF POLLEN AND CMS PARENTS OF *Brassica napus* GENOTYPES AVAILABLE IN BANGLADESH

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### ABSTRACT

An experiment was conducted at the research field of the Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur during the period from November 2007 to March 2008 to study the morphological characterization of *Brassica napus*. With a view to achieve this goal, twenty two (22) germplasm of *Brassica napus* used as pollen parent and two CMS lines ( $Z_1$  and  $Z_2$ ) used female parent. Results indicated a wide range of variation among the genotypes in respect of flower characters along with yield and yield attributes. Among the pollen parents, the genotypes Nap 9904 and Nap 2022 were found as early flowering, whereas the genotype Nap 9908 was the late for first flowering. Length of anther ranged from as long as 3.60 mm in Nap 2037 to as short as 1.88 mm in Nap 2057. Minimum anther breadth (0.693 mm) was produced by the genotype Nap 2037, while the maximum anther breadth was found in the genotype Nap 248 (0.916 mm). Length of filament varied from 6.22 mm (BARI Sarisha-8) to 8.338 mm (Nap 0130). More than 72% genotypes attained plant height ranged from 95.72 cm to 108.9 cm. The highest number of siliqua per plant was counted in Nap 205 (222.1) and it was the lowest in Nap 179 (63.3). Wide variability in respect of number of seeds per siliqua was exhibited among the genotypes and it was ranged from 16.80 (Nap 2022) to 28.65 (Nap 206). The highest seed yield (11 g) per plant was recorded in the genotype Nap 206 and the lowest in Nap 2057 (2.56 g). Anther and stamen of pollen parents were larger as compared to CMS lines. In CMS $_1$  and CMS $_2$ , the first flower opened at 38.67 and 38.0 days after sowing, respectively.

**Key words:** Characterization. *Brassica napus*, genotypes.

### INTRODUCTION

*Brassica napus* varieties have high seed and oil productivity with bold seeds. They are more tolerant against *Alternaria* leaf blight and aphid attack than the varieties of *B. campestris* and *B. juncea*. High yield potential of *B. napus* is mainly due to elongate flower raceme with moderate number of large siliqua accommodating more number of bold seeds and also due to higher number of plants that can be accommodated per unit area. The yield of rapeseed and mustard is generally low in Bangladesh as compared with the world average. The main problems for this low yield are the use of low yielding local indigenous cultivars, unavailability of locally developed hybrids and low management practices. The present yield of mustard in Bangladesh is 733 kg/ha, which is far below the level attained in the developed countries (1575 kg/ha) of the world (FAO, 2006). With good management and use of hybrid varieties, the present yield level could be increased. Superiority of  $F_1$  hybrid over the better parent is a common phenomenon in both self and cross-pollinated crops. Commercial  $F_1$  hybrid cultivars become increasingly important for oilseed crops. A CMS source within *B. napus* was independently identified by Shiga and Baba (1971, 1973) and Thompson (1972). Although a number of CMS systems are reported in *Brassica*, yet their use in the hybrid seed production is limited. After the discovery of CMS in mustard (Rawat and Anand, 1979), a number of the CMS systems viz., *Ogura muralis*, *Polima* and *napus* were developed and used in hybrid seed production programme. However, *napus* CMS system ( $Z_1$  and  $Z_2$ ) available in the department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University has structural male sterility mechanism, which may open the scope of hybrid variety development in this country. Considering the scope of work in this line, the present investigation was undertaken for the characterization of male and female genotypes of *Brassica napus*.

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## MATERIALS AND METHODS

Twenty two pollen lines of *Brassica napus* L. and two CMS lines were grown during November 2006 to March 2007 and assigned randomly to experimental plots at the experimental farm of Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh. Each plot consists of 4 rows of 4 m each with 30 cm space between rows and 15 cm between plants. The experiment was laid out in Randomized Complete Block Design (RCBD) with three replications. Fertilizers were applied at the rate of 270: 170: 100: 150: 5 kg/ha of Urea, TSP, MP, Gypsum and Zinc sulphate, respectively. Cowdung was applied at the rate of 10 M ton/ha. Whole amount of cowdung, TSP, MP, Gypsum, Zinc sulphate and half of Urea were applied at the time of final land preparation. The remaining urea was top dressed at 30 days after seedling emergence. Necessary intercultural operations were taken during cropping period for proper growth and development of the plants. Data were recorded on anther length, filament length, anther breadth, stamen length, days to 50% flowering, days to 80% maturity, number of primary branches per plant, number of secondary branches per plant, length of inflorescence, number of siliqua per plant, length of siliqua, number of seeds per siliqua, 1000-seed weight and seed yield per plant (g). The recorded data for different characters were analyzed statistically using MSTAT, a computer based program to find out the variation among the different genotypes by F-test. Treatment means were separated by Duncan's Multiple Range Test (DMRT).

## RESULTS AND DISCUSSION

The detailed results of the present study have been presented in tables and discussed character wise.

### **Performance of different pollen parents (*B. napus* genotypes)**

#### **Anther length (mm)**

The mean square due to genotypes revealed significant variation existed among the genotypes (Table 1). The genotypes Nap 2037 and Nap 94006 were found to produce the longest (3.600 mm) anther, whereas the shortest (1.880 mm) anther was found in the genotype Nap 2057. It was observed that genotypes Nap 2037 and Nap 94006 was statistically identical to Nap 2066 (3.454 mm) but significantly different from rest of the genotypes.

#### **Anther breadth (mm)**

It was observed from the Table 1 that means square due to genotype was significant for anther breadth. However, minimum anther breadth was produced by the genotype Nap 2037 (0.698 mm) and maximum breadth was produced by Nap 248 (0.916 mm). Anther breadth of more than 68% of the genotypes under study ranged from 0.747 to 0.846 mm. Genotype Nap 2001 (0.909 mm) was statistically similar to Nap 2012, Nap 206 and Nap108 (0.855 mm).

#### **Length of filament (mm)**

The difference in filament length among the genotypes was observed to be statistically significant. The longest filament (8.338 mm) was recorded in Nap 0130 while the shortest (6.220 mm) one was in BARI Sarisha-8 (Table 1). The shortest filament producing genotype was statistically similar with those of Nap 2037, Nap 206, Nap 205, Nap 2022, Nap 179, BARI Sarisha-13 and Nap 2066. The genotype Nap 0130 produced the longest filament was found to be statistically similar to Nap 9901 and Nap 9906 but different from rest of the genotypes. Fifty nine percent of the genotypes under study, which included 13 genotypes produced filament length varying from 6.220 to 7.115 mm.

#### **Length of stamen (mm)**

Stamen length of different genotypes showed significant variation which ranged from 8.580 to 11.265 mm (Table 1). The longest stamen was observed in Nap 94006 (11.265 mm) followed by Nap 0130, Nap 9901, Nap 9906 and Nap 9908. The genotype Nap 179 produced the shortest (8.580 mm) stamen and was statistically similar to the genotype Nap 2022 followed by BARI Sarisha-8, Nap 205, BARI Sarisha-13 and Nap 2057. More than 59% of the genotypes under study had stamen length within range of 9.065 to 9.933 mm.

**Table 1. Floral characteristics of 22 pollen parents of *Brassica napus***

Pollen parents	Anther length (mm)	Anther breadth (mm)	Filament length (mm)	Stamen length (mm)
Nap108	2.804	0.855	7.116	9.920
Nap0130	2.503	0.831	8.338	10.841
Nap179	1.977	0.800	6.603	8.580
Nap205	2.745	0.844	6.400	9.145
Nap206	2.927	0.856	6.653	9.580
Nap248	2.712	0.916	6.915	9.627
Nap2001	2.704	0.909	6.966	9.670
Nap2012	3.015	0.857	6.918	9.933
Nap2013	2.470	0.775	7.135	9.605
Nap2022	2.330	0.808	6.570	8.900
Nap2037	3.600	0.698	6.284	9.884
Nap2057	1.880	0.819	7.630	9.510
Nap2066	3.454	0.808	6.727	10.181
Nap9901	2.572	0.793	8.145	10.717
Nap9904	2.850	0.785	7.413	10.263
Nap9905	2.528	0.810	7.115	9.643
Nap9906	2.727	0.846	7.971	10.698
Nap9908	2.952	0.747	7.680	10.632
Nap94006	3.600	0.808	7.665	11.265
BARI Sarisha-7	2.806	0.826	7.093	9.899
BARI Sarisha-8	2.845	0.752	6.220	9.065
BARI Sarisha-13	2.735	0.719	6.635	9.370
F- value	**	**	**	**
LSD (0.05)	0.3757	0.0521	0.4916	0.4543
Mean	2.761	0.812	7.099	9.860
SE ( $\pm$ )	0.1317	0.0183	0.1722	0.1592
CV (%)	8.28	2.90	4.19	2.80

\*\*<sub>1</sub>, P < 0.01

#### Days to 50 percent flowering

Significant variation was observed for days to 50% flowering among the genotypes under investigation (Table 2). The maximum days to 50% flowering was observed in Nap 9908 (45 days) followed by Nap108 (41.67 days), which did not differ significantly from Nap 206. Genotypes Nap 9906, Nap179 and Nap 9904 were significantly different from Nap 9908 and Nap 108. The lowest days to 50% flowering was taken by Nap 0130 (35 days), which was statistically similar to the Nap 2022 and BARI Sarisha-8. About two third of the genotypes produced 50% flowering within 35-38 days after sowing . The differences in days to 50% flowering might be due to the genetical factors of the genotype concerned.

#### Number of primary branches per plant

Marked variation was exhibited in respect of number of primary branches per plant. The maximum number (5.40) of primary branches per plant was produced by the genotype Nap 206 and the minimum (3.0) in BARI Sarisha-7 (Table 2). Fourteen genotypes bearing the primary branches ranged from 3.0 to 3.8.

**Table 2. Mean performance of 22 pollen parents (*B. napus* genotypes) for yield and its contributing characters**

Genotypes	Days to 50% flowering	Days to 80% maturity	No of primary branches	Plant height (cm)	Inflorescence length (cm)	No of siliqua/plant	Siliqua length(cm)	No of seeds/siliqua	1000 seeds weight(gm)	Seed yield/plant (gm)
Nap 108	41.67	107.0	3.5	104.00	73.80	119.1	7.29	23.56	2.70	4.395
Nap 0130	35.00	104.0	3.45	104.20	74.00	152.4	7.27	22.15	3.40	5.215
Nap 179	39.67	107.0	3.3	103.40	62.80	63.30	7.97	23.98	3.15	3.010
Nap 205	38.00	105.0	4.9	116.40	82.95	222.1	6.73	20.72	3.35	7.585
Nap 206	40.67	104.3	5.4	115.50	76.80	178.3	8.87	28.65	2.96	11.00
Nap 248	36.67	103.7	3.2	97.40	61.40	92.90	8.05	21.20	3.25	2.770
Nap 2001	37.00	102.3	3.3	107.60	73.50	132.9	7.14	20.94	3.15	3.435
Nap 2012	36.67	106.3	4.1	104.40	74.70	152.0	7.01	19.36	2.99	4.750
Nap 2013	38.00	103.7	4.2	121.90	86.50	124.8	7.58	22.32	3.28	3.440
Nap 2022	35.67	102.0	3.8	95.90	64.10	117.5	6.86	16.80	2.49	3.495
Nap 2037	38.00	101.0	4.5	99.30	68.30	131.3	7.22	22.72	3.29	6.600
Nap 2057	37.00	104.0	3.5	91.80	65.30	113.1	7.04	19.26	3.10	2.560
Nap 2066	38.00	102.3	3.6	107.50	78.80	140.4	7.37	18.77	3.51	4.085
Nap 9901	38.00	102.3	4.4	112.00	72.30	145.8	7.37	19.76	2.06	5.370
Nap 9904	39.67	103.3	3.6	108.90	69.30	126.9	7.09	25.08	2.95	4.430
Nap 9905	39.67	103.7	3.5	104.60	76.60	116.3	7.63	18.68	2.96	6.450
Nap 9906	40.00	105.0	3.1	112.60	71.70	115.9	8.28	20.68	2.95	4.505
Nap 9908	45.00	105.3	4.1	100.5	67.40	143.6	8.09	22.66	3.01	8.370
Nap 94006	37.67	105.0	4.1	95.70	61.70	139.2	7.81	23.70	3.25	6.295
BS -7	38.67	105.7	3.0	105.9	72.30	136.0	6.30	19.12	3.28	5.005
BS-8	36.00	104.7	3.6	100.8	64.50	135.9	6.76	19.93	3.21	5.865
BS -13	37.67	103.3	3.2	99.50	64.80	106.3	6.98	16.88	2.81	3.130
F value	**	**	**	**	**	**	**	**	**	**
LSD(0.05)	1.184	2.074	0.7781	4.899	5.804	30.87	0.5440	2.457	0.1648	0.2553
Mean	38.38	104.13	3.8	104.99	71.07	132.09	7.39	21.22	3.05	5.080
SE(±)	0.4147	0.7269	0.2726	1.716	2.033	10.82	0.1906	0.8608	0.0577	0.0894
CV(%)	1.87	1.21	12.53	2.83	4.96	14.18	4.47	7.03	3.35	3.08

#### Days to 80 percent maturity

The analysis of variance for this character showed significant differences among the genotypes (Table 2). The minimum duration (101 days) for 80% maturity was observed in the genotype Nap 2037 followed by Nap 2022 (102 days) and the maximum duration by Nap 108 and Nap 179 (107 days).

#### Plant height at maturity (cm)

Analysis of variance revealed marked variation among the genotypes in respect of plant height (Table 2). Plant height at maturity varied from 91.80 to 121.9 cm. The tallest plant was produced by the genotype Nap 2013 (121.9 cm) followed by the genotypes Nap 205 (116.4 cm) and Nap 206 (115.5 cm). There had no remarkable variation among the genotypes Nap 9904 (108.9 cm), Nap 2001 (107.6 cm), Nap 2066 (107.5 cm), BARI Sarisha-7 (105.9 cm) Nap 9905 (104.6 cm), Nap 2012 (104.4 cm), Nap 108 (104 cm) and Nap 179 (103.4 cm). The height of the plant was found to be minimum in Nap 2057 (91.80 cm) closely followed by Nap 94006 (95.7 cm) and Nap 2022 (95.9 cm). More than 72% genotypes attained plant height within the range between 95.7 and 108.9 cm.

#### Length of inflorescence (cm)

Length of inflorescence showed a wide variation within the genotypes. The longest (86.50 cm) inflorescence was found in the genotype Nap 2013 (Table 2) which was statistically identical to Nap 205 (82.95 cm) but significantly different from rest of the genotypes under studied. The smallest

inflorescence was found in Nap 248 (61.40 cm) followed in increasing order by Nap 94006, Nap 179, Nap 2022, BARI Sarisha-8, BARI Sarisha-13, Nap 2057 and Nap 9908. In respect of length of inflorescence 63.63% of the genotypes under study varied from 62.80 cm to 74.00 cm.

#### **Number of siliqua per plant**

Analysis of variance displayed significant variation regarding the number of siliqua produced per plant and it was varied from 63.30 to 222.1. The highest number of siliqua per plant was produced by Nap 205 (222.1) and the other genotypes were statistically differ from that of the former being placed in the order of Nap 206 (178.3), Nap 0130 (152.4), Nap 2012 (152.0) and Nap 9901 (145.8). The lowest number of siliqua per plant (63.3) was produced in Nap 179 which was statistically similar to the genotype Nap 248 (92.9) but significantly different from rest of the genotypes under studied (Table 2).

#### **Length of siliqua (cm)**

The difference in siliqua length among the genotypes was observed to be statistically significant. The longest siliqua (8.971 cm) was produced by the genotype Nap 206 followed by Nap 9906 (8.284 cm) while the shortest by BARI Sarisha-7 (6.303 cm) followed by Nap 205 (6.726 cm), BARI Sarisha-8 (6.756 cm) and Nap 2022 (6.863 cm) (Table 2). The longest siliqua producing genotypes was statistically differs from rest of the genotypes which were used in the experiment. Wide variability in respect of siliqua length was exhibited among the genotypes.

#### **Number of seeds per siliqua**

Statistical difference could be detected from Table 2 regarding the number of seeds per siliqua among the various *B. napus* genotypes. It varied from 16.80 to 28.65. The maximum number (28.65) of seeds per siliqua was recorded in the genotype Nap 206 followed by the genotypes Nap 9904 (25.08) and Nap 179 (23.98). The minimum number (16.80) of seeds per siliqua was found in the genotypes Nap 2022 and other six genotypes were statistically identical with that of minimum seed producing genotype being placed in the order of BARI Sarisha-13, Nap 9905, Nap 012, Nap 2066, BARI Sarisha-7, Nap 2057 and Nap 2012. Fifteen genotypes under study including that producing maximum seeds per siliqua besides the rest seven mentioned earlier had significantly different in respect of the parameter described.

#### **1000-seed weight (g)**

The genotypes differed significantly in respect of 1000-seed weight (Table 2). It was observed that the genotype Nap 2066 (3.505 g) was superior but statistically similar to the genotypes Nap 0130 (3.40 g) and Nap 205 (3.345 g). The minimum weight of 1000-seed were obtained in the genotype Nap 9901 (2.065 g) followed by Nap 2022 (2.49 g), Nap 108 (2.70 g) and BARI Sarisha-13 (2.805 g). More than 60% of the genotypes varied from 2.95g to 3.28g in respect of 1000-seed weight.

#### **Seed yield per plant (g)**

The genotypes showed significant differences for seed yield per plant. Seed yield per plant ranged from 2.56g to 11.00g (Table 2). The highest seed yield (11.0 g) per plant was recorded in the genotype Nap 206 followed by Nap 9908 (8.37 g) that was statistically different. The lowest seed yield per plant was produced in the genotype Nap 2057 (2.56 g) that was statistically different from rest of the genotypes. Chen *et al.* (1995) recorded 7.2 g seed yield per plant in *B. napus*.

#### **Performance of CMS lines**

From the Table 3, it was found that the first flower opened at 38.67 days after sowing in CMSZ<sub>1</sub> and 50% plants of this line flowered within 46.67 days after sowing. In case of CMSZ<sub>2</sub> first flower opened at 38.0 days and 50% flower opened within 45.0 days after sowing. The average anther length of CMSZ<sub>1</sub> and CMSZ<sub>2</sub> were 1.795 mm and 1.748 mm, respectively. The average anther breadth of CMSZ<sub>1</sub> was 0.712 mm and CMSZ<sub>2</sub> was 0.641 mm. The average length of filament was 1.731 mm in CMSZ<sub>1</sub> and 1.816 mm in CMSZ<sub>2</sub>. Average stamen length of CMSZ<sub>1</sub> and CMSZ<sub>2</sub> were 3.526 mm and 3.564 mm, respectively. The CMS plants produced small and slender anther and shorter filament in compared to pollen parents. The out crossing rate of CMSZ<sub>1</sub> was 40.41% and CMSZ<sub>2</sub> was 47.85%. Branching habit is an important character that contributes to seed yield in *B. napus*. In case of CMS plants the number of primary branches per plant was found 4.10 in CMSZ<sub>1</sub> and 3.80 in CMSZ<sub>2</sub>. Time

required for days to 80% maturity of CMSZ<sub>1</sub> and CMSZ<sub>2</sub> were 110 and 100, respectively. The average plant height of CMSZ<sub>1</sub> was 140.40 cm and CMSZ<sub>2</sub> was 134.60 cm. The length of inflorescence was 84.50 cm and 82.0 cm in CMSZ<sub>1</sub> and CMSZ<sub>2</sub>, respectively. The number of siliqua per plant was found 396.35 in CMSZ<sub>1</sub> and 242.8 in CMSZ<sub>2</sub>. The longer siliqua (7.064 cm) was produced by CMSZ<sub>1</sub> than CMSZ<sub>2</sub> (6.886 cm). The average number of seeds per siliqua was found 22.74 and 22.46 in CMSZ<sub>1</sub> and CMSZ<sub>2</sub>, respectively. CMSZ<sub>1</sub> produced the smallest seeds and 1000-seed weight was 2.89 g, but in CMSZ<sub>2</sub>, the 1000-seed weight was 2.81 g. The seed yield per plant of CMSZ<sub>1</sub> and CMSZ<sub>2</sub> was recorded 15.95 g and 13.64 g, respectively.

**Table 3. Performance of CMS lines of *Brassica napus* for flower and yield characteristics**

Characters	CMSZ <sub>1</sub>	CMSZ <sub>2</sub>
Days to 1 <sup>st</sup> flowering	38.67	38.0
Days to 50% flowering	46.67	45.0
Anther length (mm)	1.795	1.748
Anther breadth (mm)	0.712	0.641
Length of filament (mm)	1.731	1.816
Length of stamen (mm)	3.526	3.564
Out crossing rate (%)	40.31	47.96
No. of primary branches per plant	4.10	3.80
No. of secondary branches per plant	17.05	14.70
Days to 80% maturity	110.00	108.00
Plant height at maturity (cm)	140.40	134.60
Length of inflorescence (cm)	84.50	82.00
No. of siliqua per plant	396.35	242.80
Length of siliqua (cm)	7.064	6.886
No. of seeds per siliqua	22.74	22.46
1000-seed weight (g)	2.89	2.81
Seed yield per plant (g)	15.95	13.64

The genotypes Nap 9904 and Nap 2022 were found early for days to first flowering and the genotype Nap 2037 for days to 80% maturity. Anther and stamen of pollen parents were longer as compared to CMS lines and its test cross progenies. The genotypes Nap 206 and Nap 205 produced the highest number of primary branches/plant, number of siliqua/plant and number of seeds/siliqua respectively. The genotype Nap 206 produced the highest seed yield per plant (11 g) and it was the lowest in Nap 2057 (2.56 g). The CMS plants (CMSZ<sub>1</sub> and CMSZ<sub>2</sub>) produced small and slender anther, short filament and abnormal pollen grain as compared to pollen parent. Out crossing rate was 40.31% and 47.96% in CMSZ<sub>1</sub> and CMSZ<sub>2</sub>, respectively.

## REFERENCES

- Anonymous, 2006. FAO, Production Year Book. Food and Agricultural Organization of United Nations, Rome 00108, Italy. 57: 115-133
- Chen, Z. J., Zhang, M. F., Wang, B. L., Dong, W. H. and Huang, S.Q. 1995. Study of fertility and agronomic traits in cytoplasmically male sterile lines of Indian mustard. *Acta Horticulturae Sinica*. 22(1): 40-46.
- Rawat, D. S. and Anand, I. J. 1979. Male sterility in Indian mustard. *Indian J. Genet. Pl. Breed.* 39: 412-414.
- Shiga, T. and Baba, S. 1971. Cytoplasmic male sterility in rape plants (*Brassica napus* L.). *Japan J. Breed.* 21 (2): 16-17.
- Shiga, T. and Baba, S. 1973. Cytoplasmic male sterility in oil seed rape (*Brassica napus* L.) and its utilization to Breeding. *Japan J. Breed.* 23: 187-189.
- Thompson, K.F. 1972. Cytoplasmic male sterility in oil seed rape. *Heredity*. 29: 253- 257.