

Performance of Source Nursery of Pollen Parent and Cms Lines of *Brassica napus* L.

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Abstract

The study was conducted with the objective to know the performance of floral and yield characteristics of pollen and CMS parent. Significant variation was observed for flowering and yield contributing characteristics among two CMS lines (Z_1 and Z_2) and 21 pollen parents. The pollen parent Nap2019 was found as early flowering whereas the parent Nap2013 was the late for first flowering. The highest length of anther was found in Nap9907 and short anther in Nap9905. Slender anther was produced by the genotype Nap2037 and bold anther was produced by the genotype Nap9907. Length of filament was the highest in Nap2012 and the lowest in Nap0130. For yield contributing characteristics, the genotype Nap9906 matured earlier than all other genotypes while the maximum duration took by Nap2013. The longest inflorescence was found in the genotype Nap2001 and the smallest in Nap9906. The highest number of siliqua per plant was counted in Nap2066 and it was the lowest in

Nap9906. Wide variability in respect of number of seeds per silique was exhibited among the genotypes and it was the lowest in Nap9901 and the highest in Nap94006. In case of 1000-seed weight, the genotype Nap2022 produced larger seeds and the genotype Nap9907 produced smaller seeds. The highest seed yield per plant was recorded in the genotype Nap2066 and the lowest in Nap9905. In case of CMSZ₁ and CMSZ₂, 50% plants were flowered within 45 days after sowing. The CMS plant produced small, slender anther with shorter filament compare to pollen parents. The out crossing rate of CMSZ₁ and CMSZ₂ was 40.31% and 47.96%, respectively. Time required for days to 80% maturity of CMSZ₁ and CMSZ₂ were about 106 days. The number of silique per plant was found the highest in CMSZ₁ and the lowest in CMSZ₂. The average number of seeds per silique and seed yield per plant was recorded the highest in CMSZ₁ and the lowest in CMSZ₂. The pollen parent with desirable performance and CMS parents CMSZ₂ having higher out crossing rate can be used for future *Brassica napus* hybrid breeding program.

Keywords: Rapeseed (*Brassica napus* L), Pollen parent, CMS line, Floral characteristics, Seed yield

1. Introduction

Rapeseed (*B. napus* L) play a vital role in human diet but the consumption rate of oil in Bangladesh is far below than that of balanced diet (6 g oil per day per capita). The seeds of mustard and rapeseed contain 42% oil and 25% protein (Khaleque, 1985). Recent data indicated that oil crops produces 0.16 million tons of edible oil in every year as against the total requirements of 0.5 million tons for a population of 130 million in Bangladesh (Anon., 1999 and Mondal *et al.*, 2001). The shortage of edible oil has become a chronic problem for the nation. To fulfil the requirement, the country has to import edible oils at the cost of bigger amount of foreign exchange. The share of rapeseed and mustard was 253 640 tons, which comes to 52 percent of the total edible oil production (Anon., 2007). 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 high yielding or hybrid varieties. The present seed yield per hectare of mustard in Bangladesh is far below the level attained in the developed countries of the world (BBS, 2008). Commercial F₁ hybrid cultivars become increasingly important for oilseed crops. For commercial exploitation of hybrid technology in mustard, a cytoplasmic male sterile line (A), a maintainer line (B) and a restorer line (R) are required. Before using in hybrid seed production, these CMS lines and pollen parents need to be evaluated thoroughly for different morphological, floral and agronomic traits.

Investigations leading to the development of new CMS (Cytoplasmic Male Sterile) lines and identification of maintainer lines from the germplasm have brightened the prospects of development of commercial hybrids in *Brassica* (Ogura, 1968). Morph-physiological, floral and yield traits of pollen as well as CMS parent can helps to identify suitable genotypes for commercial hybrids. Extent of outcrossing on a male sterile line is influenced by its floral traits, stigma size, exertion rate, length of filament of the flower in *Brassica napus* (Barrett and Eckert, 1990; Dudley *et al.*, 2007; Goodwillie *et al.*, 2009). Therefore, the present investigation was undertaken with the objective to evaluate pollen parent and CMS lines for different morphological, floral and agronomic traits.

2. Materials and Methods

The research work was conducted at the experimental farm, Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University (BSMRAU), Salna, Gazipur, Bangladesh. Among twenty three genotypes, two were CMS (Cytoplasmic Male Sterile) lines (Z1 and Z2: two different cytoplasmic sources) and twenty one male parents or pollen parents (parents from where pollen collected) were used as plant materials. The pollen parent and CMS lines were grown in different row in the experimental field with row spacing of 30 cm between row and plant spacing of 15 cm within the row. The experiment was laid out in a 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 seedlings emergence. Necessary intercultural operation was taken during cropping period for proper growth and development of the plants recommended by Khaleque (1985). Thinning and first weeding was done at 10 days after emergence (DAE). The second weeding was done at 30 DAE followed by application of urea by top dressing. Irrigation was given at regular interval when necessary. For suppression of aphid population Malathion 57 EC was applied three times as foliar spray at an interval of 10-15 days after seedling emergence (Khaleque, 1985). Data were collected from five randomly selected competitive plants of each of the entries on the characters days to 1st flowering, days to 50% flowering, number of primary branches per plant, days to 80% maturity, plant height at maturity (cm), length of inflorescence (cm), number of silique per plant, length of

silique (cm), number of seeds per silique, 1000-seed weight (g), anther length (mm), anther breadth (mm), length of filament (mm), length of stamen (mm), seed yield per plant (g). Out crossing rate (%) was determined for CMS lines using the following formula-

$$\text{Out crossing rate (\%)} = \frac{(\text{Total number of silique per plant})}{(\text{Total number of flowers per plant})} \times 100$$

All data were analyzed using SAS statistical package version 9.01 (2008) to find out the variation among the different genotypes by F-test. Treatment means were separated by Duncan's Multiple Range Test (DMRT) at 5% level of probability for interpretation of the results (Steel and Torrie, 1980).

3. Results and Discussion

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

3.1.1 First flowering

Variation due to genotypes was statistically significant for this character (Table 1). In Nap2019 first flower opened at 30 days after sowing which was statistically similar with Nap9901 (30.33 days), Nap9906 (30.67 days), Nap205 (30.67 days), Nap2012 (31 days) and Nap94006 (31.67 days). The maximum duration (36.33 days) for first opening of flower was required by genotype Nap2013, which was statistically identical to Nap9908 (35 days) but significantly different to the rest of the genotypes. Genotypes having minimum days to flowering are considered good genotypes for earliness. Considering days to flowering, the genotype Nap2013 could be considered as early and quick growing cultivar.

3.1.2 Anther length and breadth

The mean square due to genotypes revealed significant variation existed among the genotypes for anther length and breadth (Table 1). The genotype Nap9907 and Nap9905 were found to produce the longest (2.815) and the shortest (2.075) anther, respectively. On the other hand, maximum anther breadth was observed in Nap9907 (0.918) and minimum in the genotype Nap2037 (0.697). Anther size is directly related to number of pollen grains inside anther. Genotype with larger anther contained more pollen grains which can be produced more seed per plant (Plate 1). The genotype Nap9907 with higher anther length and breadth can be produced more pollen grains inside anther. Several authors (Banga and Labana, 1985; Chen *et al.*, 1993; Sodhi *et al.*, 1993; Hu *et al.*, 1992) found anther development in the pollen parent or maintainer line was normal.

3.1.3 Length of filament

The difference in filament length among the genotypes was observed to be statistically significant. The longest filament (8.41) was recorded in Nap0130 while the shortest (5.41) was in Nap2012 (Table 1). The shortest filament producing genotypes were Nap2001, Nap206, Nap2037, Nap205, Nap2057, Nap012, Nap94006, Nap2066, Nap2019 and Nap9905. The genotype Nap0130 produced the longest filament was found to be statistically different from rest of the twenty genotypes. Filament length can increase the cross pollination rate and improve the seed production. The genotypes with longer filament can be produced more seed compared to the genotypes with shorter filament. Sixty two percent of the genotypes under study which include 13 genotypes produced filament length varying from 6.10 mm to 6.80 mm.

3.1.4 Length of stamen

Stamen length showed significant variation and ranged from 7.913 mm to 10.92 mm (Table 1). The longest stamen was observed in Nap0130 (10.92). The genotype Nap2012 produced the shortest (7.913) stamen and was statistically similar to the genotypes Nap9905, Nap205, Nap206, Nap2057, Nap2037, Nap94006, Nap012, Nap2022 and BARI Sarisha-8. Stamen length could be influenced the pollination and seed production in *Brassica napus*.

3.1.5 50% flowering

Significant variation was observed for days to 50% flowering among the pollen parents under investigation. The maximum days to 50% flowering was observed in Nap2013 (43.33) followed by Nap2057(39.33) which did not differ significantly from Nap206, Nap9907, Nap108, Nap205, Nap2001, Nap2066, Nap94006, Nap2022, Nap9908, Nap9905, Nap2037 and Nap9904. The lowest days to 50% flowering was taken by Nap2019 (34.33) which was statistically similar to the Nap9906, Nap2012 and Nap0130. About two third of the genotypes produced 50% flowering within 37-39 days after sowing (Table 2). The differences in days to 50% flowering might be due to the genetical factors of the genotype concerned. The genotype Nap2019 can be selected as parent during the development of short duration *Brassica napus* variety.

3.1.6 Primary branches per plant

Marked variation was exhibited in respect of number of primary branches per plant. The maximum number (4.17) of primary branches per plant was produced by the genotype Nap9908 and the minimum (2.67) in Nap0130 (Table 2). Seventeen genotypes bearing the primary branches ranged from 3.0 to 3.8. Ghosh and Chatterjee (1988) found that the productivity of mustard per unit of area significantly affected by number of primary branches per plant in 8 different elite varieties of Indian mustard.

3.1.7 80% maturity

The analysis of variance for this character showed significant differences among the genotypes (Table 2). The minimum duration (95.67 days) for 80% maturity was required by the genotype Nap9906 followed by BARI Sarisha-8 (96.33 days) and the maximum duration by Nap2013 (109.7days). As maturity days concerned, two genotypes were taken less than 100 days for 80% maturity, exhibiting earliness.

3.1.8 Plant height at maturity

Analysis of variance revealed marked variation among the genotypes in respect of plant height (Table 2). Plant height at maturity varied from 81.67 to 114.7cm. The tallest plant was produced by the genotype Nap2022 (114.7cm) followed by the genotypes Nap9908 (105.3cm) and Nap9907 (101.2cm). The height of the plant was found to be minimum in Nap2057 (81.67cm) closely followed by Nap 9906 (84.34cm). More than 75% genotypes attained height of plant within the range between 82.50 and 98.67cm. For plant height at maturity, 13 genotypes were of short stature with plant height ranged from 81.67 to 98.67cm and remaining eight genotypes with long stature with plant height ranged from 100.00cm to 114.7cm. The variation in plant height of different varieties of canola may be attributed to their genetic potential (Sana et al., 2003).

3.1.9 Length of inflorescence

Length of inflorescence showed a wide range of variation among the genotypes evaluated in this study. The longest (70.0) inflorescence was found in the genotype Nap2001 (Table 2) which was statistically identical with Nap2022, Nap2012, Nap9904, Nap108, BARI Sarisha-8, Nap2037, and Nap9905. The smallest inflorescence was found in Nap9906 (48.67) followed in increasing order by Nap94006, Nap9901, Nap2066, Nap205, Nap2057 and Nap012. In respect of length of inflorescence 61.9% of the genotypes under study varied from 59.17cm to 67.50 cm. The yield increase in brassica could be attributed to increased inflorescence length as it can be accommodate more number of siliqua.

3.1.10 Siliqua per plant

The significant variation was observed for number of siliqua produced per plant and it was varied from 121.5 to 285.8. The highest number of siliqua per plant was produced by Nap2066 (285.8) and the other genotypes were statistically identical with that of the former being placed in the order of Nap9907 (279.1), Nap2001 (273.2), Nap108 (264.0), Nap9908 (259.8), Nap206 (201.3), Nap2037 (199.3), Nap2057 (191.5) and Nap012 (188.0). The lowest number of siliqua per plant (121.5) was produced in Nap9906 which was statistically similar to all the genotypes except Nap2066, Nap9907, Nap2001, Nap108 and Nap9908 (Table 2).

3.1.11 Length of siliqua

The difference in siliqua length among the genotypes was observed to be statistically significant. The longest siliqua (6.58) was produced by the genotype Nap9906 followed by Nap2037 (6.47) while the shortest by Nap0130 (5.26) followed by Nap9905 (5.27) (Table 2). The smallest siliqua producing genotype was statistically identical with those of Nap9905, Nap2001, Nap9901, Nap012, Nap2022 and BARI Sarisha-8. The longest siliqua producing genotypes was statistically similar with those of the Nap2037, Nap94006, Nap206, Nap108, Nap2057, Nap2066, Nap2019, Nap9908 and Nap9904. Wide variability in respect of siliqua length was exhibited among the genotypes.

3.1.12 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 17.33 to 23.86. The maximum number (23.86) of seeds per siliqua was recorded in the genotype Nap94006 followed by the genotypes Nap9906 (23.74) and Nap205 (23.67). The minimum number (17.33) of seeds per siliqua was found in the genotypes Nap9901 and other six genotypes were statistically identical with that of minimum seed producing genotype being placed in the order of Nap2001, Nap012, Nap0130, Nap108, Nap9905 and Nap2012.

3.1.13 1000-seed weight

The genotypes differ significantly in respect of 1000-seed weight (Table 2). It was observed that the genotype Nap2022 (4.64) was superior but statistically similar to the genotypes Nap2057 (4.58), BARI Sarisha-8 (4.38), and Nap108 (4.18). The minimum weight of 1000-seed were obtained in the genotype Nap9907 (3.05) which was statistically identical with Nap012 (3.20), Nap205 (3.23), Nap2013 (3.41) and Nap9905 (3.52). More than 50% of the genotypes varied from 3.62g to 4.11g in respect of 1000-seed weight but they were statistically similar. Several investigators (Hashem et al., 1998; Om et al., 1998 & Sana, et al., 2003) found significant differences for 1000-seed weight among different brassica varieties.

3.1.14 Seed yield per plant

The genotypes showed significant differences for seed yield per plant. The highest seed yield (19.43 g) per plant was recorded in the genotype Nap2066 followed by Nap9907 (15.48 g) that was statistically similar. Thus higher seed yield potential of these genotypes can be attributed to this parameter. The lowest seed yield per plant was produced in the genotype Nap9905 (5.90 g) that was statistically identical with all the genotypes under studied except Nap2066, Nap9907, Nap9908, Nap108 and Nap2057. Chen *et al.* (1995) recorded 7.2 g seed yield per plant in *B. napus*. Reddy and Reddy (1998) and Khoshnazar et al. (2000) have also been reported significant differences in seed yield in different varieties of brassica species.

3.2 Performance of CMS lines

From the Table 3 it was found that the first flower opened at 36.67 days after sowing in CMSZ₁ and 50% plants of this line were flowered within 45 days after sowing. In case of CMSZ₂ first flower opened at 32.33 days and 50% flower opened within 44.33 days after sowing. The anther length of CMSZ₁ and CMSZ₂ were 1.792 mm and 1.751 mm, respectively. The anther breadth of CMSZ₁ was 0.710 mm and CMSZ₂ was 0.628 mm. Chen *et al.* (1993, 1995) observed two type of stamen in CMS *B. juncea* var. *tumida*, stamens without an anther, and stamens with thin and degenerate anthers. The length of filament was 1.728 mm in CMSZ₁ and 1.820 mm in CMSZ₂. Stamen length of CMSZ₁ and CMSZ₂ were 3.520 mm and 3.571 mm, respectively.

The CMS plants produced small and slender anther and shorter filament in compare to pollen parents (Plate 1c-e). Jones and Clarke (1943) showed male sterility associated with morphological abnormality anther and filament. Chen *et al.* (1993) was also found CMS line with no anthers or had silk-like structure of stamen with few pollen grains which show lowered vigour and lacking normal external structure in tuber mustard. Male sterile plants were identified by several authors (Banga and Labana, 1985; Sodhi *et al.*, 1993; Hu *et al.*, 1992) based on small flower, small filament, lack of anther, silk like stamen with vestigial and indehiscent anthers. Banga and Amandeep (1995) observed variation in flower traits in different nuclear backgrounds of siifolia CMS system. The out crossing rate of CMSZ₁ was 40.31% and CMSZ₂ was 47.96%. Hackenberg and Kohler (1996) assessed variation in parental lines of rapeseed with regard to out crossing. Results showed that the partially out crossing rate was very high. Branching habit is an important character that contributes to seed yield in *B. napus*. Zhu *et al.* (1999) found that the seed production potentiality was similar between male sterile line and their male or pollen parents.

In case of CMS plants the number of primary branches per plant was found 3.67 in CMSZ₁ and 3.50 CMSZ₂. Time required for days to 80% maturity of CMSZ₁ and CMSZ₂ were 106.67 and 105.33, respectively. The average plant height of CMSZ₁ was 95 cm and CMSZ₂ was 108.34 cm. The length of inflorescence was 63.34 and 65.89 in CMSZ₁ and CMSZ₂, respectively. The number of siliqua per plant was found 465.67 in CMSZ₁ and 269.00 in CMSZ₂. The longer siliqua (6.28 cm) was produced by CMSZ₁ than CMSZ₂ (6.28 cm). The average number of seeds per siliqua was found in 25.94 g and 19.93 g in CMSZ₁ and CMSZ₂, respectively. CMSZ₁ produced the smallest seeds and 1000-seed weight was 2.97 g. but in CMSZ₂ the 1000-seed weight was found in 3.43 g. The seed yield per plant of CMSZ₁ and CMSZ₂ was recorded 17.16 g and 11.89 g, respectively. Seed production capabilities of cytoplasmic male sterile cabbage derived from Ogura CMS radish was observed by Zhu *et al.* (1999). Seed production capabilities in cross and backcross descendants ranged from 4.1 to 20.8 seeds per pod, respectively. But seed production potentiality was similar between male sterile material and their backcross male parents (Plate 1a-b).

The genotype Nap2019 was found early for days to 1st flowering and the genotype Nap9906 for days to 80% maturity. Anther and stamen of pollen parents were longer as compare to CMS line and its test cross progenies. The genotypes Nap9908, Nap2066, Nap94006 and Nap9906 produced the highest number of primary branches/plant, number of siliqua/plant, number of seeds/siliqua and the longest siliqua. The genotype Nap2066 produced the highest seed yield per plant (19.43 g) and it was the lowest in Nap9905 (5.90 g).

In CMS plants (CMSZ₁ and CMSZ₂) produced small and slender anther, short filament and abnormal pollen grain as compare to pollen parent. Out crossing rate was 40.31% and 47.96% in CMSZ₁ and CMSZ₂, respectively. Hackenberg and Kohler (1996) assessed variation in parental lines of rapeseed with regard to out crossing and found similar results.

4. Conclusion

From the present study it can be concluded that pollen parent with desirable performance can be test cross with CMS lines to develop new CMS lines or restorer lines depending on gene presence in their genome. On the basis of yield contributing characters and higher seed yield potential, the genotypes Nap2066, Nap9906, Nap94006 and Nap2022 are recommended for test cross with CMS line develop maintainer or restorer lines. Information on morph-physiological, floral and yield traits of pollen as well as CMS parent can helps to identify suitable genotypes for commercial hybrids. The CMS parents CMSZ₂ having higher out crossing rate can be used for future *Brassica napus* hybrid breeding program.

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Table 1. Flowering characteristics of 'pollen' parents (parents from where pollen was collected)

Pollen plants	Days to 1 st flowering	Anther length (mm)	Anther breadth (mm)	Filament length (mm)	Stamen length (mm)
Nap012	32.67	2.45	0.784	6.00	8.45
Nap108	34.33	2.81	0.854	6.55	9.36
Nap0130	33.00	2.51	0.830	8.41	10.92
Nap205	30.67	2.44	0.843	5.80	8.24
Nap206	32.67	2.59	0.856	5.67	8.26
Nap2001	32.33	2.67	0.905	5.55	8.22
Nap2012	31.00	2.46	0.861	5.45	7.91
Nap2013	36.33	2.52	0.774	6.65	9.17
Nap2019	30.00	2.66	0.879	6.15	8.81
Nap2022	32.33	2.44	0.807	6.20	8.64
Nap2037	34.00	2.59	0.697	5.80	8.39
Nap2057	34.67	2.43	0.818	5.85	8.28
Nap2066	33.33	2.64	0.807	6.10	8.74
Nap9901	30.33	2.47	0.792	6.50	8.97
Nap9904	32.67	2.53	0.784	6.75	9.27
Nap9905	33.33	2.08	0.810	6.15	8.23
Nap9906	30.67	2.72	0.846	6.25	8.97
Nap9907	33.33	2.82	0.918	6.45	9.26
Nap9908	35.00	2.49	0.746	6.80	9.29
Nap94006	31.67	2.33	0.807	6.10	8.43
BARI Sarisa-8	33.00	2.20	0.751	6.45	8.65
F- value	**	**	**	**	**
LSD (0.05)	1.546	0.215	0.074	0.624	0.664
CV (%)	2.86	5.18	5.31	6.03	4.59

Significance at 0.01(**) level

Table 2. Mean performance of 21 pollen parents (*B. napus* genotypes) for yield contributing characters

Genotype	Days to 50% flowering	No. of primary branches /plant	Days to 80% maturity	Plant height at maturity (cm)	Length of inflorescence (cm)	No. of siliqua /plant	Length of siliqua (cm)	No. of seeds /siliqua	1000seed weight (g)	Seed yield /plant (g)
Nap012	36.33	3.00	104.67	90.34	56.67	188.00	5.63	19.14	3.20	6.44
Nap108	38.00	3.00	104.00	95.67	65.50	264.00	6.29	19.67	4.18	14.03
Nap0130	36.00	2.67	105.00	89.17	59.17	131.67	5.26	19.33	3.65	6.13
Nap205	37.33	3.50	106.67	88.00	56.67	157.67	6.08	23.67	3.23	7.93
Nap 206	37.33	3.17	104.33	97.34	60.84	201.34	6.34	22.63	4.09	11.15
Nap2001	37.67	3.00	102.00	100.00	70.00	273.17	5.55	17.83	3.87	9.72
Nap 2012	35.33	3.17	101.00	101.17	66.67	177.17	6.05	20.09	3.59	9.70
Nap2013	43.33	3.17	109.67	93.50	59.17	178.33	5.86	23.64	3.41	9.63
Nap2022	39.00	3.34	105.33	114.67	67.50	164.34	5.65	21.67	4.64	8.70
Nap 9906	34.67	2.84	95.67	84.34	48.67	121.50	6.58	23.74	3.62	6.72
Nap 2019	34.33	2.83	103.33	88.34	59.17	182.33	6.17	20.90	3.68	6.58
Nap2037	37.67	3.50	102.67	97.17	63.34	199.34	6.47	21.64	4.04	10.55
Nap2057	39.33	3.67	105.33	81.67	56.67	191.50	6.26	22.84	4.58	12.03
Nap2066	37.67	3.33	101.67	90.84	56.50	285.75	6.24	22.15	4.12	19.43
Nap 9901	36.67	3.00	101.33	98.67	52.83	183.33	5.60	17.33	3.74	6.67
Nap9904	37.33	3.34	105.67	94.17	65.84	182.67	6.10	21.14	3.76	8.43
Nap9905	38.33	3.73	104.33	87.84	63.34	136.67	5.27	19.90	3.52	5.90
Nap9907	38.67	3.83	105.33	102.84	60.00	279.09	5.78	22.55	3.05	15.48
Nap9908	38.67	4.17	105.00	105.34	66.67	259.84	6.14	22.67	3.67	14.10
Nap94006	38.33	3.34	102.67	82.50	49.17	176.84	6.36	23.87	3.80	10.03
BARI Sarisha-8	36.67	3.17	96.33	87.83	64.67	179.00	5.74	22.77	4.38	7.52
F- value	**	*	**	**	**	**	**	**	**	**
LSD (0.05)	1.786	0.719	2.218	15.12	7.687	85.01	0.421	2.742	0.430	4.875
CV (%)	2.88	13.30	1.30	9.76	7.71	26.30	4.25	7.77	6.86	29.99

Significance at 0.05 (*) and 0.01 (**) level

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

Characters	CMSZ ₁	CMSZ ₂
Days to 1 st flowering	36.67	32.33
Days to 50% flowering	45.00	44.33
Anther length (mm)	1.792	1.751
Anther breadth (mm)	0.710	0.638
Length of filament (mm)	1.728	1.820
Length of stamen (mm)	3.520	3.571
Out crossing rate (%)	40.31	47.96
No. of primary branches per plant	3.67	3.50
Days to 80% maturity	106.67	105.33
Plant height at maturity (cm)	95.00	108.34
Length of inflorescence (cm)	63.34	65.83
No. of siliqua per plant	465.67	269.00
Length of siliqua (cm)	6.28	5.91
No. of seeds per siliqua	25.94	19.93
1000-seed weight (g)	2.97	3.43
Seed yield per plant (g)	17.16	11.89



Plate 1. Showing **a)** flowering of pollen parent and CMS plant in the field, **b)** CMS plant with siliqua as a result of out crossing, **c)** pollen parent and CMS plant, **d)** flowers from pollen parent, CMS and F₁ plant **e)** anthers from pollen parent and CMS plant