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INHERITANCE OF GENETIC MALE STERILITY IN SAFFLOWER

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ABSTRACT

A few male-sterile plants were identified in the accession CTV-53 and in F_2 population of the cross A-1 x 83-13-3 of safflower. Phenotypically, the male-sterile plants were identical to male-fertile plants except for the nonfunctional pollen grains. The inheritance of male sterility in both cases was found to be monogenic recessive. Crosses among the four male-sterile sources showed allelic identity among MSN-1, MSV-1 and UC-148 male-sterile lines, and all these were nonallelic to the GMS-5 (A) male-sterile strain.

Key words: *Carthamus tinctorius*, male sterility, inheritance, allelism.

Genetic male sterility in safflower (*Carthamus tinctorius* L.) was first reported in 1940 [1] and subsequently by several others [2–7]. The utilization of male sterility in the hybrid seed production is a limiting factor because there is no marker gene available at the early stage of crop development. This hinders the commercial exploitation of the crop. Nevertheless, efforts are being made at various research centers in India to overcome the deficiencies in safflower hybrid seed production. In this context, the present study reports the identification and inheritance of two spontaneous male-sterile mutations in safflower. More diverse the GMS sources, greater the chances of finding male sterility linked marker traits.

MATERIALS AND METHODS

The material for the present study originated from two distinct sources, therefore, each source is described as a separate group.

Group A. During rabi 1991–92, a few male sterile plants were observed in the accession CTV 53 of a breeding nursery raised at the Research Farm of Nimbkar Agricultural Research Institute, Phaltan. Each of these male-sterile plants was maintained by pair-wise sib-mating with fertile plants of the same line to find out the possible heterozygous counterparts. The crossed seeds of each male-sterile plant were sown to raise two rows each of 5 m length in

summer 1992. Ten out of the 14 sib-mated populations segregated for male-sterile and fertile plants, indicating the heterozygous state of their fertile male parents; while the nonsegregating populations showed the homozygous nature of the fertile parents. The male sterility of the segregates was confirmed by selfing five capitula of each plant which did not produce any seed. The male-sterile plants varied for plant height, days to flower and branch angle, with wider and more distinct brush-like capitulum opening. They were selected and maintained by pair-wise sib-mating with the matching fertile plants in the subsequent generations grown in rabi as well as summer seasons of 1992–93 and 1993–94. One of the uniform male-sterile progenies was crossed with the self-pollinated variety Nira during summer 1993. The F_1 generation was raised in a 2-row plot of 5 m length during rabi 1993–94. Two out of the 50 F_1 plants were selfed and two back-crossed with the male sterile plant. The back-cross population was planted in two rows and F_2 population grown in a 12-row plot of 5 m length during summer 1994. The rows were spaced at 45 cm with intrarow spacing of 20 cm. The F_2 and back-cross generations of this cross were observed for sterile and fertile plants. The male sterile derivatives of CTV 53 are designated as MSN.

Group B. A male-sterile plant with slightly pinched capitula of pale yellow flowers was found in F_2 population of the cross A-1 x 83-13-3 during rabi 1992–93. This plant was sib-mated with a male-fertile plant of the same cross having similar flower colour, plant height, days to flower, and shape and size of capitula. The crossed seeds obtained from the male-sterile plant were grown in two rows of 5 m length in summer 1993. The progeny segregated for 50% male-sterile and 50% male-fertile plants at flowering, revealing the heterozygous nature of fertile male parent. The identification of the fertile plants was easy as the anthers filled with yellow pollen were conspicuous in the pale yellow flower background, while the male-sterile plants had white empty anthers. The male-sterile plants which segregated for plant height, days to flower, branch angle, and capitulum size were maintained separately by sib-mating with the fertile plants of similar phenotype to obtain phenotypically diverse male sterile derivatives. However two male-sterile plants were crossed separately with the genotypes Nira and C 2829-5-3. The progenies of the sib-mated male-sterile plants along with F_1 of both the crosses were grown in two 5 m long rows during rabi 1993–94. The male-sterile plants with desirable traits as mentioned above were maintained in each progeny by sib-mating. Two F_1 plants in the cross with var. Nira were selfed, and two were back-crossed with the male-sterile parent. The F_2 and back-cross (BC) populations of the cross with Nira were planted together during summer 1994. The BC population was planted in two rows and the F_2 populations raised in 12 rows of 5 m length. Observations were recorded on the sterile and male-fertile plants in each population. The male-sterile derivatives of this group are designated as MSV. The segregation ratios were tested for the goodness of fit using χ^2 test.

Besides the above mentioned male-sterile sources, the male-sterile lines UC 148 and GMS-5 (A) governed by single recessive genes, as reported by Heaton and Knowles [5] and

Ramchandram and Sujatha [7], respectively, are also maintained at this center. The four F_1 hybrids of different male sterility source, i.e. MSN- 1 x Nira, MSV-1 x Nira, UC-148 x Bhima, and GMS-5 (A) x II-51-1-10, were crossed in a diallel fashion, excluding reciprocals, to study allelism among the male sterility causing genes of the above GMS sources. The progenies of these crosses were raised during summer 1994. All the progenies were screened for number of sterile and fertile plants.

RESULTS AND DISCUSSION

The three F_1 hybrids, viz. MSN-1 x Nira comprising 50 plants, MSV-1 x Nira with 46 plants, and MSV-1 x C-2829-5-3 with 54 plants grown in rabi 1993–94 were fully fertile, indicating that male sterility in both the new male sterility sources is a recessive trait (Table 1). The F_2 population of the crosses MSN-1 x Nira and MSV-1 x Nira segregated in the ratio of 3 fertile : 1 sterile, confirming that male sterility in each case was caused by a single recessive gene in homozygous state. This was further confirmed by the segregation in the back-crosses. The back-crosses of F_1 to the respective male-sterile parents segregated in 1 fertile : 1 sterile plants. Genetic male sterility in safflower has already been reported to be a monogenic recessive trait [1, 3, 5, 7].

Table 1. Segregation for male-fertile and sterile plants in different generations of safflower

Cross	Observed segregation						χ^2		P	
	F_1		F_2		BC		F_2	BC	F_2	BC
	F : S		F : S		F : S		(3 : 1)	(1 : 1)		
MSN-1 x Nira	50	0	187	67	35	26	0.257	1.327	0.9–0.5	0.5–0.2
MSV-1 x Nira	46	0	165	49	13	19	0.505	1.125	0.5–0.2	0.5–0.2
MSV-1 x C 2829-5-3	54	0	—	—	—	—	—	—	—	—

Note. F—fertile, S—sterile, BC—back-cross.

The allelic relationship among the four genetic male-sterile mutants was studied in four distinct GMS-based hybrids (Table 2). The crosses (MSV-1 x Nira) x (MSN-1 x Nira), (MSV-1 x Nira) x (UC-148 x Bhima), and (MSN-1 x Nira) x (UC-148 x Bhima) segregated into male-sterile and male-fertile plants in their double-cross F_1 generations in the ratio of 3 fertile : 1 sterile, suggesting that all these three male-sterile mutants were induced in the same gene although the three male-sterile mutants had been isolated from unrelated sources. The allele for male sterility in UC-148 is already designated as ms [5]. Due to the allelic relationship among these mutants, the same ms designation is proposed for the male sterility alleles of MSN-1 and MSV-1. However, the crosses (MSV-1 x Nira) x (GMS-5 (A) x II-51-1-10), (MSN-1

Table 2. Frequency of male-fertile and male-sterile plants in crosses involving four different male-sterile mutants of safflower

Cross	Male fertile	Male sterile	χ^2 (3 : 1)	P
(MSV-1 x Nira) x (MSN-1 x Nira)	6	2	0.000	0.99–0.95
(MSV-1 x Nira) x (UC-148 x Bhima)	7	1	0.666	0.50–0.20
(MSV-1 x Nira) x (GMS-5(A) x II-51-1-10)	10	0	—	—
(MSN-1 x Nira) x (UC-148 x Bhima)	9	5	0.857	0.50–0.20
(MSN-1 x Nira) x (GMS-5(A) x II-51-1-10)	16	0	—	—
(UC-148 x Bhima) x (GMS-5(A) x II-51-1-10)	4	0	—	—
Pooled (segregating crosses)	22	8	0.044	0.90–0.50

x Nira) x (GMS-5 (A) x II-51-1-10), and (UC-148 x Bhima) x (GMS-5 (A) x II- 51-1-10) produced only male-fertile plants. These observations confirm that the male sterility gene in GMS-5 (A) is different from the ms gene in MSV-1, MSN-1 and UC-148. The male sterility allele of the male-sterile line GMS-5 (A) is proposed to be designated as ms_1.

Preliminary observations on seed yield of the male-sterile and male-fertile plants of the newly developed male-sterile lines under open pollination revealed that seed yield of

Table 3. Seed yield and other characteristics of male sterile lines of safflower under open pollination

Progeny	Seed yield (g/plant)		MS yield to MF (%)	Plant height (cm)	No. of capitula per plant	Capitulum diameter (cm)	Days to maturity
	MS	MF					
MSN-2-1-1	9.30	19.44	47.84	90.4	12.0	2.35	142
MSN-2-1-2	9.24	10.88	84.93	70.8	12.6	2.31	137
MSN-3-1-4	8.48	24.36	34.81	99.8	14.8	2.02	140
MSN-3-2-1	9.70	10.40	93.26	61.0	9.6	2.32	142
MSN-6-1	3.08	3.58	86.03	65.2	7.4	2.40	138
MSN-6-2	8.38	11.78	71.13	78.0	9.2	2.59	145
MSV-1-3	7.32	13.86	52.81	58.8	16.6	1.79	134
MSV-1-4	9.10	12.96	70.21	71.2	25.4	1.93	142
MSV-3-2	11.00	14.30	76.90	64.6	26.0	1.77	136
MSV-10-1	7.62	14.24	53.00	67.2	13.6	2.01	135

Note. Observations were recorded on 5 randomly selected plants.

MS—male-sterile, MF—male-fertile.

male-sterile plants of male-sterile lines ranged from 35–93% of the corresponding male-fertile plants, indicating their usefulness in hybrid development programme (Table 3). The selected male-sterile lines differ from each other for plant height, capitulum number, capitulum diameter and days to maturity, but are uniform within the line for these traits. The variation among the male-sterile lines may have resulted due to recombination of genes of the sterile and fertile plants during initial sib-mating. The recombination of genes was expressed in the form of segregation for these traits in the sib-mating progenies. Subsequently, the male sterile plants which were phenotypically diverse for these traits, were selected and maintained separately in each subsequent generation by sib-mating with fertile plants of similar characteristics. Consequently, the male sterile lines with diverse phenotypes, but uniform within, were selected and are being maintained for further use in breeding programme.

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REFERENCES

1. R. B. Deshpande. 1940. A sterile mutant in safflower (*Carthamus tinctorius* L.). Curr. Sci., **9**: 370–371.

2. R. H. Richaria. 1941. Progress Report of Oilseeds Research Scheme Central Provinces, 1940–41. W.C.P. Govt. Press (quoted by R. H. Richaria (1957): Plant Breeding and Genetics in India. Scientific Book Co., Patna: 130–133).

3. W. W. Ebert and P. F. Knowles. 1966. Inheritance of pericarp types, sterility and dwarfness in several safflower crosses. Crop Sci., **6**: 579–582.

4. J. Carapetian and P. F. Knowles. 1976. Inheritance of genetic sterility in cultivated safflower. Crop Sci., **16**: 395–399.

5. T. C. Heaton and P. F. Knowles. 1980. Registration of UC-148 and UC-149 male sterile safflower germplasm. Crop Sci., **20**: 554.

6. B. M. Joshi, Y. S. Nerkar and N. D. Jambhale. 1983. Induced male sterility in safflower. J. Maharashtra Agric. Univ., **8**: 194–196.

7. M. Ramchandram and M. Sujatha. 1991. Development of genetic male sterile lines in safflower. Indian J. Genet., **51**: 268–269.