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Inheritance of genetic male sterility and evaluation of newly developed male sterile lines in safflower (*Carthamus tinctorius* L.)

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Abstract
Three genetic male sterile lines HUS-305MS-1, HUS-305MS-2 and HUS-305MS-3 along with check varieties Bhima, A_1, AKS-207, HUS-305 and Phule Kusum were evaluated in 2005 and 2006 to determine the mode of inheritance of newly identified male sterile lines of safflower, to evaluate and characterize the male sterile lines and to identify the most promising genetic male sterile line for utilization in recurrent selection programme. The male sterility was due to single recessive nuclear gene *'ms'*. The GMS line HUS-305MS-1 is significantly superior for seed yield plant^{-1} (83.43 g) over parental variety HUS-305 (62.05 g). However, the performance of other GMS lines HUS-305MS-2 and HUS-305MS-3 was at par with parental variety HUS-305. GMS line HUS-305MS-1 could prove useful in the establishment of random mating population for recurrent selection programme.

Key words: *Carthamus tinctorius* L - genetic male sterility - inheritance

Introduction
Safflower (*Carthamus tinctorius* L) is considered as self-pollinating species. Numerous cases of genetic male sterility system have been reported in safflower (Carapetian and Knowles, 1976; Heaton and Knowles, 1982; Ramchandram and Sujatha, 1991; Singh, 1996; Chitanvis *et al.*, 1999). Majority of steriles have arisen as spontaneous mutants and vast number of male sterility genes (ms) have been reported by Kaul, (1988). In present study, three mutant plants were identified as spontaneous mutants from HUS-305 variety, a national check for high oil content with high yield (Ghorpade, 1999). These mutant plants were maintained by sib mating with parental lines and subsequently homozygous recessive and heterozygote plants were identified and further maintained by sib mating (Ghorpade, 2002). Therefore, the present study was aimed to determine the mode of inheritance of newly identified genetic male sterile lines in safflower, to evaluate and characterize the genetic male sterile lines and to identify the most promising genetic male sterile lines in safflower for development of random mating population for recurrent selection programme.

Materials and Methods
The experimental material comprised of three genetic male sterile lines viz., HUS-305MS-1, HUS-305MS-2, HUS-305MS-3 originated from HUS-305, national check variety for high oil content with high yield. These three GMS lines were evaluated with five elite varieties viz., Bhima, A_1, AKS-207, HUS-305 and Phule Kusum in a randomized complete block design with 3 replications in *rabi* 2005 and 2006 at Shankarnagar Farm, College of Agriculture, Nagpur. Plants were spaced at 45 cm between rows and 30 cm between plants. Border plants were grown on two sides to avoid border effect. The data were recorded on five fertile competitive

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plants for days to 50% flowering, days to maturity, plant height (cm), number of branches plant^{-1}, number of capitula plant^{-1}, number of seeds capitulum^{-1}, 100 seed weight (g), seed yield plant^{-1}, oil content (%). The ten morphological characters were recorded as per the descriptor published by IPGRI, (1983) *viz.,* flower color at three stages; at bud stage, at full bloom, at maturity; leaf color, stamen color, anther color, pollen color, stem color, angle of branching, internode length, leaf shape, leaf margin which are the distinguishing characters for GMS lines which would be useful to maintain genetic purity of GMS lines. Three F_2 populations (msms x Bhima, msms x A_1, msms x AKS-68) and their respective testcrosses were grown in *rabi* 2005. The fertile plants from three F_2's (msms x Bhima, msms x A_1, msms x AKS-68) were grown in *rabi* 2006. The data were analyzed for pooled analysis of variance and segregation ratio was tested by using (χ^2) test.

Results and Discussion

Inheritance of male sterility in segregating F_2 population of safflower crosses involving three genetic male sterile lines HUS-305-MS1, HUS-305MS-2 and HUS-305MS-3 crossed with Bhima, A_1, AKS-68 respectively has been presented in table 1. All segregating F_2 population showed good fit to ratio of 3 male fertile and 1 male sterile confirming the male sterility in each cross was caused by single recessive gene in homozygous state. This allele for male sterility is designated as *'msms'*. The F_2 population of crosses segregates into 3 male fertile and 1 male sterile ratio. This was confirmed in segregation in test crosses which segregates in 1 male fertile and 1 male sterile (Table 1). The frequency of F_3 plants segregating for male sterility from male fertile plants of F_2 families has been presented in table 2. The segregating population of F3 lines of 3 crosses showed a good fit to ratio of 2 male fertile and 1 male sterile. Heaton and Knowles (1982) reported recessive genetic male sterility with single gene *msms* and released two male sterile safflower germplasm lines i.e. UC-148 and UC-149. This male sterile character should prove useful in the establishment of random mating population for recurrent selection programme in safflower.

Table 1: Inheritance of male sterility in segregating F_2 population of safflower (2005)

F_2 Populations / Test crosses	Observed Plants*		Total number of plants grown	Fit to 3 :1	
	Male Fertile	Male Sterile		χ^2	P
F_2 Populations					
HUS-305MS-1 (msms) Bhima	310	105	420	0.0200	0.90-0.75
HUS-305MS-2 (msms) x A_1	118	43	170	0.250	0.75-0.50
HUS-305MS-3 (msms) x AKS-68	103	34	140	0.0024	0.95-0.90
Total	531	182	730	0.1050	0.75-0.50
Test crosses				Fit to 1 :1	
				χ^2	P
HUS-305MS-1(msms) x F_1(msms x Bhima)	124	110	250	0.828	0. 50-0.25
HUS-305MS-2(msms) x F_1(msms x A_1)	105	120	243	1.000	0.50-0.25
HUS-305MS-3(msms) x F_1(msms x AKS-68)	130	119	255	0.486	0.50-0.25
Total	359	349	748	2.340	0.25-0.10

*- Loss of few plants due to non germination.

Table 2: Frequency of F_3 plants segregating for male sterility from male fertile plants of F_2 families (2006).

F_3 Populations	Observed Plants (F_3)*		Total number of plants grown	Fit to 2 :1	
	Male Fertile	Male Sterile		χ^2	P
HUS-305MS-1 (msms) x Bhima	50	30	97	0.420	0.75-0. 50
HUS-305MS-2 (msms) x A_1	55	20	84	1.500	0.25-0.10
HUS-305MS-3 (msms) x AKS-68	60	27	91	0.206	0.75-0.50
Total	165	77	272	0.249	0.75-0.50

*- Loss of few plants due to non germination.

The ten morphological characters were recorded on three GMS lines (Table 3). The flower color at maturity, stem color, angle of branching and leaf margin are the distinguishing traits for GMS lines which would be useful to maintaining genetic purity of GMS lines. The performance of GMS lines over two years (2005 and 2006) has been presented in table 3. The GMS line HUS-305MS-1 is significantly superior for seed yield plant^{-1} (83.43 g) over parental variety HUS-305 (62.05 g). However, the performance of HUS-305MS-2 and HUS-305MS-3 was at par with parental variety HUS-305. This clearly indicates that agronomic performance of three GMS line was not deviating from original parental line HUS-305. This is in conformity with the findings of Poornima (2003) and Bhakre (2005). Thus the results of this study indicated that GMS line, HUS-305MS-1 could directly be utilized (without conversion) for development of random mating population for development of superior varieties of safflower.

Table 3: Characterization and agronomic performance of male sterile lines of safflower (2005 & 2006)

Genotypes	Flower colour at			Angle of branching	Leaf margin	No. of capitula plant^{-1}	Seed yield plant^{-1} (g)	Oil content (%)
	Bud stage	Full bloom	Maturity					
HUS-305MS-1	Yellow	Yellow	Deep Red	48.2^0	Serrate	55.66	83.43	34.25
HUS-305MS-2	Pale Yellow	Yellow	Light red	47.6^0	Dentate	39.43	62.06	34.70
HUS-305MS-3	Light Orange	Light Orange	Red orange	21.8^0	Serrate	46.56	67.32	33.86
Check varieties								
Bhima	-	-	-	-	-	47.46	97.16	29.56
A_1	-	-	-	-	-	39.63	59.73	30.83
AKS-207	-	-	-	-	-	38.79	67.99	31.58
HUS-305	-	-	-	-	-	42.73	62.05	34.09
Phule Kusum	-	-	-	-	-	46.60	69.03	30.52
SE ±	-	-	-	-	-	2.19	3.48	0.49
C.D. %	-	-	-	-	-	6.34	10.09	1.40

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