

UTILIZATION OF NEW CMS SOURCES IN SUNFLOWER BREEDING

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ABSTRACT

Two new CMS sources - CMS PF and CMS-I derived from H. petiolaris ssp fallax and H. annuus ssp lenticularis respectively were studied for their utilization in breeding. Maintainer and restorer behaviour of these two sources were investigated.

One hundred and four lines including maintainers and restorers relating to CMS F were crossed to CMS PF and CMS I. The presence or absence of pollen in Fls were recorded in the field whereas pollen fertility was confirmed in the laboratory by acetocarmine test. For CMS PF, all the tested lines turned out to be maintainers except nine viz., HA-207, HA-232, HA-335, RHA-6D-1, RHA-334, M-106, M-111, IB-19-2R, IB-49. In the background of CMS-I, fertility restoration was observed only in five crosses involving the lines HA-291, RHA-84-SR1, RHA-801, M-134, BLC-166. It was interesting to note that several restorers of CMS F were non-restorers in the cytoplasm background of CMS PF and CMS I.

About fifteen lines showing maintainer behaviour have been converted into male sterile lines in the background of new CMS sources for utilization in breeding. These lines have been stable across the seasons. The converted lines include HA-851, HA-852, HA-853, HA-400, HA-607 and RHA-587.

INTRODUCTION

The discovery of cytoplasmic male sterility in sunflower (Helianthus annuus L) by Leclercq, (1969) and subsequent identification of genes for fertility restoration (Kinman, 1970; Enns et al., 1970; Leclercq, 1971; Vranceanu and Stoenescu, 1971) have resulted in the development of hybrids for commercial cultivation using cytoplasmic male sterility system since 1972. However, almost all sunflower hybrids grown have a single source of cytoplasmic male sterility - CMS F discovered by Leclercq. Diversification of CMS sources is inevitable in any heterosis breeding programme as the use of single CMS source involves a potential risk if it becomes susceptible to a new strain of disease. Fortunately, in sunflower several new sources of cytoplasmic male sterility have been reported (Anaschenko et al., 1974; Heiser, 1982; Leclercq, 1980; Serieys, 1987;

Whelan and Dedio, 1980). In the present investigation, two new CMS sources - CMS PF and CMS-I derived respectively from H. petiolaris ssp fallax and H. annuus ssp. lenticularis were studied with the twin objectives - 1) Establishing distinctness of the CMS sources and 2) to identify maintainers and restorers for the new CMS sources for their subsequent use in the breeding programme.

MATERIALS AND METHODS

One hundred and four lines comprising newly developed inbred lines and maintainers and restorers relating to CMS F were crossed to CMS PF and CMS I during the rainy season of 1993. In summer 1994 F₁ seeds from the crosses were planted. Each hybrid was grown in a single row of 3.6 m length with plant space at 30 cm apart. Each row consisted of about twelve plants. The row to row distance was maintained at 60 cm. The plants were classified as male fertile or male sterile at growth stage of 5.3 (Schneiter and Miller, 1981) based on anther exertion and pollen shedding at anthesis. Pollen fertility was confirmed in the laboratory using 1% Acetocarmine (Chowdhary et al., 1981). If no pollen was visible at this stage plants were classified as sterile. If segregation for fertility was noted, the number of plants in fertile or sterile class were counted and recorded. Based upon this data, the B and R lines could be classified as restorers and maintainers for the new CMS sources.

RESULTS AND DISCUSSION

The reaction of maintainer and restorer lines relating to CMS F as well as other inbred lines in the background of new CMS sources CMS PF and CMS I is presented in table 1 and 2, respectively. The line-wise behaviour of the inbred lines is given in table 3. Out of 104 lines tested including two wild species in the cytoplasmic background of CMS PF, 85 turned out to be maintainers and 11 restorers whereas segregation was observed in 8 crosses. The crosses involving both the wild species (H. petiolaris ssp. petiolaris and H. praecox) were completely fertile indicating presence of restorer genes in the wild species. It is interesting to note that many of the maintainers (51 out of 61 tested) and restorers (34 out of 41 tested) turned out to be maintainer in the background of CMS PF. Only 11 lines including two wild species were observed to be restorers.

For CMS I, out of 104 lines tested 7 were restorers and 67 were non-restorers whereas segregation was observed in 30 crosses. As in case of CMS PF several maintainer and restorers of CMS F were non-restorers in the background CMS I cytoplasm as well. Interestingly both the wild species tested have restorer genes for both the new CMS sources.

From the above results, it is evident that various inbred lines behaved differently in the two CMS background in respect of their maintainer and restorer behaviour thereby indicating that these to new CMS sources are different from one another and that the sources of restoration are rather limited for the new CMS types. The distinctness of these two sources has been established in earlier studies (Virupakshappa *et al.*, 1991 and Virupakshappa *et al.*, 1992). However in the present study, additional maintainer and restorers are reported which enable their utilization in sunflower breeding programme.

The promising maintainers identified for the two new sources have been converted into CMS lines (table 4) for their utilization in the sunflower improvement. out of the lines converted HA WG, HA 400, HA 600, HA 850, HA 852 and HA 853 are available in the form of alloplasmic lines having same nucleus but different cytoplasmic background. The converted lines have been found stable across the environments.

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Table 1: Behaviour of maintainer and restorers of CMS F
and other inbred lines in the background of CMS PF

CMS F	Tested genotypes	CMS PF		
		Sterile	Fertile	Segregation
Maintainer	61	51	6	4
Restorer	41	34	3	4
Wild species	2	-	2	-
Total	104	85	11	8

Table 2: Behaviour of maintainer and restorers of CMS F
and other inbred lines in the background of CMS I

CMS F	Tested genotypes	CMS I		
		Sterile	Fertile	Segregation
Maintainer	61	39	3	21
Restorer	41	28	2	9
Wild species	2	-	2	-
Total	104	67	7	30

Table 3: Behaviour of selected maintainer and restorer lines
of CMS F and other inbreds in the background
of new CMS sources CMS PF and CMS I

Genotypes	CMS F	CMS PF	CMS I
HA 86	M	M	M
HA 89	M	M	S
HA 207	M	R	S
HA 232	M	R	S
HA 234	M	M	S
HA 291	M	M	R
HA 300	M	M	M
HA 301	M	M	M
HA 302	M	M	M
HA 303	M	M	M
HA 335	M	R	M
HA 336	M	M	M
HA 338(C)	M	M	M
HA 338(U)	M	M	S

Contd.....

Table 3: (Contd.....)

Genotypes	CMS F	CMS PF	CMS I
HA 339	M	M	S
HA 341	M	M	M
HA 342	M	M	M
HA 343	M	M	M
HA 349	M	M	M
CM 390	M	M	S
HA 400	M	M	M
CM 447	M	M	M
HA 589	M	M	M
HA 604	M	M	M
HA 607	M	M	M
HA 608	M	M	M
HA 821	M	M	M
HA 822	M	M	M
HA 850	M	M	M
HA 851	M	M	S
HA 852	M	M	M
HA 853	M	M	M
HA 392	M	S	M
RHA RR-1	R	M	M
RHA MR-1	R	M	M
RHA 6D-1	R	R	M
RHA 84-SR1	R	M	R
RHA 83R6	R	M	S
RHA 87R1231/1	R	M	M
RHA 87R1228/4	R	M	R
RHA 265	R	M	M
RHA 272	R	M	M
RHA 273	R	M	M
RHA 274	R	M	M
RHA 278	R	M	M
RHA 296	R	M	M
RHA 297	R	S	M
RHA 298	R	M	S
RHA 299	R	M	M
RHA 334	R	R	S
RHA 344	R	M	S
RHA 345	R	M	S
RHA 348	R	M	S
RHA 354	R	M	M
RHA 355	R	S	M
RHA 586	R	M	M
RHA 587	R	M	M
RHA 801	R	M	M
RHA 856	R	M	R
RHA 857	R	M	M
RHA 859	R	M	M

Contd.....

Table 3: (Contd....)

Genotypes	CMS F	CMS PF	CMS I
Acc.No.61	NT	M	M
Acc.No.1431	NT	M	M
Acc.No.1874	NT	S	M
Acc.No.1881	NT	M	M
Acc.No.180	NT	S	S
86LB46	M	M	M
EC 68414	NT	M	M
IB-19-2R	R	R	M
IB-49	R	R	M
M-104	NT	M	M
M-106	NT	R	S
M-107	NT	M	M
M-109	NT	S	M
M-111	NT	R	S
M-114	NT	S	M
M-117	NT	S	S
M-118	NT	M	S
M-124	NT	M	S
M-134	NT	M	R
M-148	NT	M	M
M-164	NT	M	S
BLC-166	NT	M	R
BLC-168	NT	M	S
BLC-171	NT	M	M
BLC-177	NT	M	M
BLC-182	NT	M	M
BLC-188	M	M	M
BLC-192	NT	M	M
BLC-195	NT	M	M
BLC-197	NT	M	S
RLC-200	R	M	M
RLC-201	R	M	S
RLC-209	R	M	M
RLC-210	R	M	M
RLC-212	R	M	S
RLC-214	R	M	M
RLC-215	R	M	S
RLC-221	R	M	M
RLC-222	R	M	M
RLC-230	R	M	M
RLC-233	R	S	M
<u>H.petiolaris</u>			
ssp. <u>petiolaris</u>	R	R	R
<u>H.praecox</u>	R	R	R

M = Maintainer R = Restorer
S = Segregation NT = Not tested

Table 4: Lines converted in to CMS in the two cytoplasmic background.

Lines converted in the background of	
CMS PF	CMS I
HA WG	HA WG
HA 338(c)	HA 400
HA 400	HA 597
HA 607	HA 607
HA 821	HA 850
HA 850	HA 852
HA 852	HA 853
HA 853	RHA 274
RHA MR-1	RHA 265
RHA RR-1	RHA 587
RHA PZ-8R	IB-2
RHA 274	IB-4
RHA 587	IB-24
IB-24	IB-29
	IB-43-1R