



Identification of restorers and maintainers from newly developed inbreds in sunflower

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Abstract

Twelve best inbreds for high seed yield and oil content were utilized in crossing with two CMS lines i.e. CMS234 A and ARM243A of *Helianthus petiolaris* Nutt. *sp. petiolaris* background. All the inbreds except DRSI-305 restored fertility in CMS 234A and all the inbreds except DRSI-100 and 305 restored fertility in ARM 243A. Partial restorer reaction was noticed for inbred DRSI-160 in both the CMS lines. In general, most of the inbreds tested behaved as restorers for both the CMS lines. Out of 12 inbreds, DRSI-1, 3, 9, 10, 133, 182 and 256 restored fertility in the two CMS lines and acted as common restorer. Only one inbred DRSI-305 acted as maintainer for CMS 234A while two inbreds DRSI-100 and 305 acted as maintainers, and maintained the sterility in the CMS lines. As the agromorphological performance of the new restorers identified in the present investigation is known, it will help in exploiting new CMS sources in hybrid development.

INTRODUCTION

The ideal method to develop new restorer lines (R line) is by crossing R × R lines from restorer gene pools, which are already identified for fertility restoration in sunflower (Dudhe *et al.*, 2009). In order to identify new restorer lines in sunflower the superior inbred line is crossed with the CMS line and the performance of the male fertility or sterility data of the F₁ plants is checked for restorer/maintainer reaction. The inbred which restores 100% fertility restoration in CMS line is designated as new restorer line for the CMS line. The superior inbred line is produced either through systematic breeding programme or by selection from agronomically superior germplasm and selfing for 6-7 generations. In sunflower PET1 is the original cytoplasmic male sterility discovered by Leclercq (1969) and originated from a cross between *Helianthus petiolaris* Nutt. *ssp. petiolaris* and cultivated sunflower. Several sources of fertility restoration for the PET1 cytoplasm have been identified in wild species of sunflower, most of

which trace to wild annual *Helianthus annuus* L. species (Kinman, 1970; Enns *et al.*, 1970; Leclercq, 1971; Vranceanu and Stoescu, 1971).

Majority of the presently grown commercial sunflower hybrids in the world possess the cytoplasm of *Helianthus petiolaris* (PET-1) (Chandra *et al.*, 2010). In spite of continuous efforts, researchers are unable to identify commercial exploitable CMS sources other than PET-1. Commercial cultivation of sunflower was started in India during 1972 with the introduction of four open pollinated varieties. As the sunflower crop is introduced crop hence, the genetic diversity has narrow genetic base. Hence, in order to broaden the genetic base gene pool lines derived from systematic crossing and selections for several generations have been developed and maintained at IIOR, Hyderabad and designated as gene pool (GP) lines. These gene pools are developed for different traits *viz.*, high yield, high oil, high autogamy, restorer and maintainer gene pool.

Before the actual development of new hybrids the worth of newly developed inbred is assessed by crossing with CMS lines and evaluating the F₁ hybrid for restorer/maintainer reaction. Therefore, sunflower researchers accelerated their effort to develop new diverse sources of CMS and to identify new restorer lines with greater genetic diversity. Keeping this view agronomically superior newly developed inbreds (DRSI lines) were evaluated for their restorer, maintainer behavior, with the objective of identifying diverse maintainers or restorers in sunflower.

MATERIALS AND METHODS

The systematic breeding programme to develop new inbred lines through population improvement programme was initiated during 2004-2009. The newly developed inbreds were continuously selfed and maintained at IOR, Hyderabad from 2010-2016 and designated as GP lines. The important agromorphological characters of 12 best performing newly developed GP inbred lines (GP material) after attainment of genetically homogeneous state the inbred line are designated as DRSI lines and given in table 1. Three rows each of the two cytoplasmic male sterile lines (CMS 234 A and ARM 243 A) and two rows each of the 12 inbreds (DRSI) were planted in the same blocks during *kharif* season 2016, with a spacing of 60 cm between rows and 30 cm between plants. A row length of 4.5 m was maintained. Staggered sowings of male parents, twice at weekly interval, was done to synchronize the flowering and recommended agronomic practices were followed. The heads of male sterile lines and the inbreds were covered with cloth bags at the ray floret stage i.e., just before the commencement of flower opening. The two different CMS sources were crossed to all the 12 inbreds in a line x tester method. Crossing was done by collecting pollen from the inbreds in a petridish with the aid of a small brush which was applied on the disk florets of the corresponding CMS lines between 8 to 11 am and the procedure repeated till the opening of all the disc florets. Precautions were taken to avoid possible contamination. F₁ seeds from each of the 24 crosses were collected separately at maturity for assessing the fertility restoration of the 12 inbreds on the two CMS lines. The identification of inbred behaviour with respect to maintenance and restoration of the cytoplasmic male sterile sources of sunflower involved in the present study was conducted during the *rabi* season of 2016. The F₁ seeds from the 24 crosses were

planted in an unreplicated trial. Each entry was sown in a two rows of 4 m length with a spacing of 60 cm x 30 cm. The fertility restoration behavior of F₁ hybrids was assessed by visual observation after emergence of 50% flowering on all the plants in the two rows.

RESULTS AND DISCUSSION

The search for new CMS sources in sunflower and many other crops is a continuous process. Many sunflower investigations have been undertaken to study the causes for the occurrence of CMS and the function of the system CMS - fertility restoration (Christov, 1999). In the present study twelve best inbreds for high seed yield and oil content were utilized in crossing with two CMS lines i.e. CMS234 A and ARM243A of *Helianthus petiolaris* background. All the inbred lines yield more than 30 g of seed yield/plant with nearly 35% of oil content. Morphological characterization of the inbred lines would help to identify the line (Table 1). In all the inbred lines branching is absent while white strips are present on the seed coat. Earlier Dudhe *et al.*, (2018) characterized 3126 sunflower accessions based on 24 DUS descriptors and identified promising accessions which can be utilized based on morphological marker. The two CMS lines are already being used as parents in the development of high yielding hybrids in India and proved as good combiners in development of new hybrids. The CMS 234 A is used as parental line (female line) in the development and release of hybrids *viz.*, BSH-1, KBSH-1, PSFH-67, TCSH-1, KBSH-41, NDSH-1, SCH-35, PSH-569 while ARM 243A is used as female line in the development and release of DRSH-1 hybrid in India. Hence, these two CMS lines proved as best combiners for the development of high yielding hybrids.

The 24 F₁ crosses were studied by visual observation to identify the maintainer, restorer reaction. The performance of inbred lines and maintainer/ restorer reaction is given in table 2. All the inbreds except DRSI-305 restored fertility in CMS 234A and all the inbreds except DRSI-100 and 305 restored fertility in ARM 243A. Partial restorer reaction was identified for inbred DRSI-160 in both the CMS lines. In general, most of the inbreds tested behaved as restorers for both the CMS lines. Out of 12 inbreds, DRSI-1, 3, 9, 10, 133, 182 and 256 restored fertility in all the two CMS lines and acted as common restorer, this indicated for these CMS lines, the fertility restoring genes could be same.

Table 1: Agro-morphological characterization of newly developed inbreds

Name	Pdedigree	DM	HD	SW	DF	LS	LC	PH	PB	WSS
DRSI-1	GP ₉ -8C-2(M)	104.0	14.3	6.7	Early	Medium	Green	Tall	Absent	Present
DRSI-3	GP ₉ -30-5-1	88.0	15.6	4.0	Early	Medium	Green	Medium	Absent	Present
DRSI-9	GP ₉ -38C-2-2	88.0	19.4	3.2	Early	Medium	Green	Very Tall	Absent	Present
DRSI-10	GP ₉ -40-2-2	90.0	16.0	3.0	Early	Medium	Green	Medium	Absent	Present
DRSI-100	GP ₉ -217-4-3	91.0	14.0	5.1	Early	Medium	Green	Tall	Absent	Present
DRSI-133	GP ₉ -279-7-2	90.0	15.6	3.2	Medium	Coarse	Green	Tall	Absent	Present
DRSI-144	GP ₉ -290-1-2	93.0	14.0	5.3	Medium	Medium	Green	Tall	Absent	Present
DRSI-160	GP ₉ -472-1-4	90.0	16.5	4.7	Early	Medium	Green	Medium	Absent	Present
DRSI-182	GP ₉ -682-1-3	91.0	14.4	5.7	Medium	Medium	Green	Tall	Absent	Present
DRSI-224	GP ₉ -839-2-1	90.0	16.7	5.8	Early	Medium	Green	Tall	Absent	Present
DRSI-256	GP ₉ -1032-1-2	91.0	15.0	7.1	Early	Medium	Green	Tall	Absent	Present
DRSI-305	GP ₉ -64-5-2	91.0	17.3	6.1	Early	Coarse	Green	Very Tall	Absent	Present

DM: Days to maturity, HD: Head diameter, SW: 100-seed weight, DF: Days to 50% flowering, LS: Leaf serration, LC: Leaf colour, PH: Plant height, PB: Plant branching, WSS: White strips on seed

Table 2: Maintainer/restorer reaction of different inbred lines in the background of two CMS lines

Inbred	Seed yield/plant (g)	Oil content (%)	CMS234A			ARM243A		
			R	M	PR	R	M	PR
DRSI-1	35	36	R			R		
DRSI-3	30	37	R			R		
DRSI-9	34	37	R			R		
DRSI-10	31	37	R			R		
DRSI-100	38	37	R				M	
DRSI-133	32	36	R			R		
DRSI-144	32	36	R			R		
DRSI-160	34	36			PR			PR
DRSI-182	36	35	R			R		
DRSI-224	30	35	R					
DRSI-256	39	35	R			R		
DRSI-305	34	35		M			M	

R= Restorer; M=Maintainer; PR=Partial Restorer

The inbred lines restoring fertility to different forms of CMS sources were found to be most useful in practical breeding programmes (Chandra *et al.*, 2009). All these inbreds can be tried with other CMS lines with different CMS backgrounds to

confirm its restoration behavior. Only one inbred DRSI-305 acted as maintainer for CMS 234A while two inbrds DRSI-100 and 305 acted as maintainers, and maintained the sterility in the studied CMS lines.

The identified maintainers after testing for their combining ability and agronomic performance over multilocations can be converted into new cytoplasmic male sterile lines. The newly identified inbreds have practical importance for development of diverse hybrids with better heterosis and resistance to diseases and insect pests. DRSI-100 behaved as restorer for one CMS 234 A while it behaved as maintainer for ARM 243A and *vice-versa*, reconciling the diversity among CMS lines of the same source. Kukosh (1981) reported that inbreds were found to carry *Rf* genes and can restore fertility with CMS lines developed with diverse cytoplasmic background.

It is evident from the present investigation that few inbreds behaved differently with the two cytoplasmic backgrounds in respect of maintainer and restorer behaviour suggesting the presence of modifying genes influencing the fertility restoration, resulting in partial fertility (Rukmini Devi *et al.*, 2006; Dudhe *et al.*, 2009). As the agromorphological performance of the new restorers identified in the present investigation is known, it will help in exploiting new CMS sources in hybrid development for better heterosis and diversity of cytoplasm in sunflower.

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