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**Research Article**

# Identification of maintainers and restorers for WA and Kalinga sources of CMS lines in rice (*Oryza sativa* L.)

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**Abstract**
The availability of stable cytoplasmic male sterility and fertility restoring system is vital for commercial exploitation of heterosis in rice. This study using three CMS lines *viz.*, APMS 6A, CRMS 32A and PUSA 6A and six testers *viz.*, SR-6-SW-8-1, R 1099-2569-1-1, R-1557-1306-1-568-1, Super rice-7, Super rice-8 and Jitpiti. Based on the pollen fertility (%) and spikelet fertility (%) two genotypes *i.e.* Super rice-8 for APMS 6A and R 1099-2569-1-1 for CRMS 32A were identified as potential restorers and two genotypes *i.e.* SR-6-SW-8-1 for APMS 6A and R-1557-1306-1-568-1 for CRMS 32A were identified as maintainers.

**Key words:** Rice, Pollen fertility, Spikelet fertility, Restorer and Maintainer lines

## Introduction

Rice (*Oryza sativa* L.) is the staple food crop of more than half of world's population and the world population particularly that of the rice consuming countries increasing at a faster rate. By the year 2025, about 785 million tonnes of paddy which is 70 per cent more than the current production will be needed to meet the growing demand (Manomani and Khan, 2003). To meet the demand of increasing population there is need to increase production and productivity. However in spite of tremendous breeding efforts, the yield level has remained static, which warrant exploitation of some innovative approaches. Among different innovative genetic options available for improving the threshold level of rice, exploitation of hybrid vigour is considered to be most feasible and readily practicable. The commercial exploitation of heterosis has been made possible by the use of cytoplasmic genetic male sterility and fertility systems and it can be made possible by identification of maintainers and restorers. Hence, a study was undertaken to identify maintainers with higher adaptability and restorers with higher combining ability.

## Material and Methods

The present investigation was conducted at research farm, Department of Genetics and Plant Breeding, Indira Gandhi Krishi Viswavidyalaya, Raipur, Chhattisgarh during *kharif* 2011.The experimental material comprised of Three CMS lines from two different CMS source *viz.*, APMS 6A, PUSA 6A (Wild Abortive) and CRMS 32A (Kalinga) and six genetically diverse testers- SR-6-SW-8-1, R 1099-2569-1-1, R-1557-1306-1-568-1, Super rice-7, Super rice-8 and Jitpiti with 18 hybrids. The set of 18 hybrids were generated in line ×tester fashion (Kempthrone, 1957). The experiment was laid out in a randomized block design with two replications. The 21 old day seedlings of 18 hybrids and 9 parents were transplanted with a standard spacing of 20×20 cm and ten plants were planted in a single row. Recommended package of practices were followed during crop growth period. Observations were recorded on five randomly selected plants in each treatment for ten traits *viz.*, days to 50 per cent flowering, plant height, tillers per plant, productive tillers per plant, panicle length, pollen fertility, spikelet fertility, thousand grain weight biological yield and grain yield in both the replications. Identification of maintainers and restorers carried out mainly by observing pollen fertility and spikelet fertility percentage. Yield and its component traits of "A" line (CMS line) were recorded on its "B" line.

Pollen fertility of hybrids was assessed at flowering time. For pollen fertility assessment, about two to three spikelets were collected from freshly emerged panicles and examined under microscope with one per cent Iodine-Potassium Iodide (IKI).

$$\text{Pollen fertility (\%)} = \frac{\text{No. of fertile pollen grains}}{\text{Total no. of pollen grains}} \times 100$$

Spikelet fertility of hybrids were assessed at maturity time by taking the count of well filled and chaffy spikelets in each panicle.

$$\text{Spikelet fertility(\%)} = \frac{\text{Total no. of filled spikelets/panicle}}{\text{Total no. of spikelets/panicle}} \times 100$$

Based on the pollen fertility and spikelet fertility percentage in the hybrids, the testers that could produce 0-1 per cent pollen fertility and 0-0.1 per cent spikelet fertility classified as maintainers, 1.1-50 per cent pollen fertility and 0.1-75 per cent spikelet fertility classified as partial maintainers, 50.1-80 per cent pollen fertility and 50.1-75 per cent spikelet fertility classified as partial restorers and >80 per cent pollen fertility and >75 per cent

spikelet fertility classified as potential restorers as per the classification is given by (Virmani *et al.*, 1997).

**Results and Discussion**

The main step in exploitation of hybrid vigour is to identify maintainers and restorers. The results showed that (Table 1) CRMS 32A/ R1557-1306-1-568-1 (0.87% and 0.92%) and APMS 6A/ SR-6-SW-8-1 (0.95% and 1.28%) were identified as maintainers and APMS 6A/ Super rice-8 (86.2% and 77.02%) and CRMS 32A/ R-1099-2569-1-1 (81.4% and 77%) identified as potential restorers. Based on the pollen fertility and spikelet fertility data the results show that $F_1$ hybrids produced by crossing CMS lines with selected rice genotypes behaved differently with regard to pollen fertility. Out of 18 hybrids, two genotypes having restorer reaction, nine genotypes exhibited partial restorer reaction, five genotypes were partial maintainers two genotypes were maintainers (Table 2).

In the present study, the CMS lines APMS 6A (WA) and CRMS 32A (Kalinga) had each one maintainer and restorer. However PUSA 6A had no maintainers and restorers. In some cases the same genotypes behaved as a restorer for the CMS line and as maintainer for the other CMS line. Super rice-8 can be considered as potential restorer for APMS 6A and R-1099-2569-1-1 can be considered as potential restorer for CRMS 32A and these two testers are partial maintainers for the CMS line PUSA 6A. The variations in behaviour of fertility restoration indicateed that their fertility restoring genes are different. Similar results have been reported by Hemareddy *et al.* (2000), Gannamani (2001) and Bisne and Motiramani (2005).

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Among testers, R1557-1306-1-568-1 and SR-6-SW-8-1 were identified as maintainers. The maintainers identified from present investigation will be used to develop locally adapted CMS lines through recurrent backcross programme. The partial maintainers so identified could be multiplied and used in developing new CMS line through repeated back crossing programme. Among testers, R-1099-2569-1-1 and Super rice-8 were identified as potential restorers and these can be utilized to develop rice hybrids with superior yield.

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**Table 1. Pollen fertility and spikelet fertility percentage of different CMS based hybrids in rice**

| Hybrids | Pollen fertility percentage (%) | Spikelet fertility percentage (%) |
|---|---|---|
| APMS 6A/ Super rice-8 | 85.95 | 77.71 |
| APMS 6A/R 1099-2569-1-1 | 67.30 | 64.57 |
| APMS 6A/R 1557-1306-1-568-1 | 3.40 | 3.18 |
| APMS 6A/ SR-6-SW-8-1 | 0.95 | 1.28 |
| APMS 6A/ Jitpiti | 73.10 | 70.55 |
| APMS 6A/Super rice-7 | 52.36 | 49.36 |
| PUSA6A/ Super rice-8 | 50.00 | 45.98 |
| PUSA 6A/R 1099-2569-1-1 | 48.26 | 46.51 |
| PUSA 6A/R 1557-1306-1-568-1 | 11.19 | 9.25 |
| PUSA 6A/ SR-6-SW-8-1 | 54.20 | 50.80 |
| PUSA 6A/Jitpiti | 58.38 | 53.50 |
| PUSA 6A/Super rice-7 | 72.65 | 70.55 |
| CRMS 32A/ Super rice-8 | 74.05 | 73.05 |
| CRMS 32A/R 1099-2569-1-1 | 81.10 | 76.75 |
| CRMS 32A/R 1557-1306-1-568-1 | 0.86 | 0.92 |
| CRMS 32A/ SR-6-SW-8-1 | 46.30 | 43.94 |
| CRMS 32A/Jitpiti | 66.35 | 61.99 |
| CRMS 32A/Super rice-7 | 65.53 | 60.86 |

**Table: 2 Classification of rice genotypes into maintainers, partial maintainers, partial restorers and restorers for WA and Kalinga cytosterile lines**

| Genotypes | Wild Abortive | | Kalinga source |
|---|---|---|---|
| | APMS 6A | PUSA 6A | CRMS 32A |
| SR-6-SW-8-1 | M | PR | PM |
| R 1099-2569-1-1 | PR | PM | R |
| R 1557-1306-1-568-1 | PM | PM | M |
| Super rice-7 | PR | PR | PR |
| Jitpiti | PR | PR | PR |
| Super rice-8 | R | PM | PR |

M: Maintainer; PM: Partial maintainer; PR: Partial restorer; R: Restorer