

## Genetics of Fertility Restoration in Three CMS Lines of Rice (*Oryza sativa* L.)

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Genetics of fertility restoration in six crosses involving three CMS lines (NMS 4A, IR 58025A and PMS 10A) with their two restorers (NDR 80 and NDR 359) was studied during *Kharif* 2007 at Banaras Hindu University, Varanasi, India. Fertility evaluation of the plants in the  $F_2$  population revealed the presence of two dominant genes with independent segregation in the ratio 9 : 3 : 3 : 1 controlling the fertility restoration. The observed  $x_2$  values in each case were insignificant. The segregation in  $F_2$  and backcross based two dominant genes in all the cases showed good fitness to 9 : 3 : 3 : 1 and 1 : 1 : 1 : 1 segregation, respectively. This indicated that both the restorer lines, NDR 80 and NDR 359 each carried the two independent segregating dominant genes showing additive effects for restoring fertility of the CMS lines.

Key words: Restorer, Hybrid rice, Genetic restorer, CMS Lines

Hybrids offer opportunity to break the yield ceilings of semi dwarf rice varieties. They have already been successfully used in maize, pearl millet and sorghum. The discovery of Cytoplasmic Male Sterility (CMS) in rice (Erickson, 1969; Shinjyo, 1969; Athwal and Virmani, 1972) suggested that breeders could develop a commercially viable F<sub>1</sub> hybrid, but little interest was paid until Chinese scientists reported successful production of F<sub>1</sub> rice hybrids in China (IRRI, 1997). Chinese were the first to release hybrid rice during 1976 for commercial production. Those hybrids yielded 20-30 per cent higher than conventionally bred varieties (Lin and Yuan, 1980).

The most commonly used CMS line in developing hybrids in China, India and else where is IR 58025A, derived from WA cytosterile source due to its stable pollen sterility and availability of restorer genes in rice germplasm (Virmani and Edwards, 1983). In the present study IR 58025A along with two other CMS lines, NMS 4A and PMS 10A were used for identification of new restorer lines. The present paper deals with the genetics of fertility restoration in the three above CMS lines using their two known restorers, NDR 80 and NDR 359.

## **Material and Methods**

Three CMS lines (NMS 4A, IR 58025A and PMS 10A) were crossed with two known restorers (NDR 80 and NDR 359) during *Kharif* 2006 at Banaras Hindu University to study the inheritance of fertility restoration. Half the seeds of 6 F<sub>1</sub>s derived from the crosses were sown during off season, 2006-07 at Central Rice Research Institute, Cuttack, Orissa. Backcrosses to their respective CMS lines were made and F<sub>1</sub>s were also selfed to produce F<sub>2</sub> seeds.

Remaining half seeds of six F<sub>1</sub>s, their F<sub>2</sub>s along with their 12 backcrosses (made during offseason of 2006-07) and parents were sown (space planted) during *Kharif* 2007 at Varanasi under upland rainfed conditions to find out the inheritance of fertility restoration. Standard agronomic practices were followed to raise a good crop.

## **Results and Discussion**

A total of six hybrids involving three CMS lines (NMS 4A, IR 58025A and PMS 10A) and two restorers (NDR 80 and NDR 359) were examined for pollen fertility which ranged from 88 to 92 per cent (Table 1). These six F1s were back crossed with their respective CMS lines and advanced to F<sub>2</sub> generation. Data on pollen fertility in F2 and BC generations (Table 2) showed presence of two dominant genes with independent segregation (9:3:3:1 ratio) controlling the fertility restoration. The observed x2 values in was insignificant. The segregation in F2 and BC based two dominant genes in all the cases showed good fitness to 9:3:3:1 and 1:1:1:1 segregation, respectively. This indicated that both the restorer lines, NDR 80 and NDR 359 carried two independent segregating dominant genes showing additive effects for restoring fertility of the CMS lines.

Knowledge on genetic control of male fertility restoration is very important in introgression of fertility restoring genes in breeding lines, which is highly desirable to diversify the CMS systems. The genetic control of fertility restoration of CMS system varied with the sources of CMS. Fertility restoration of 'Wild Abortive' cytoplasmic male sterile (CMS) lines in rice, was used in the present investigation, was reported to be dominant monogenic (Huang *et al.*, 1988), dominant digenic and with different types

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No.	Cross	Pollen fertility (%)
1	NMS 4A × NDR 88	88
2	NMS 4A × NDR 358	92
3	IR 58025 A × NDR 88	90
4	IR 58025 A × NDR 358	88
5	PMS 10A × NDR 88	88
5	PMS 10A × NDR 358	92

of gene interactions (Joshi *et al.*, 2003; Anandkumar and Subramaniam, 1992) and two independently segregating dominant genes (Bharaj *et al.*, 1991). In the present investigation, the presence of two dominant genes with independent segregation in F<sub>2</sub> generation was found to control the fertility restoration, which was further confirmed in back crosses (1 : 1 : 1 : 1 segregation) (Table2). However, Anandkumar and Subramaniam (1992) showed fertility restoration was governed by 3 : 1, 9 : 3 : 3 : 1 and 13 : 3 : 1 due to allelic differences and concluded that fertility restoration varied with the CMS systems. Further, Bharaj *et al.*, (1991) reported two dominant genes showing 9 : 3 : 3 : 1 segregation, also anticipated that the two genes appeared to have additive effects; one of them being stronger than the other in imparting fertility restoration. Similarly in the present case also, there appeared to be two

Table 2 Pollen fertility	of plants in F	and Test cross	nonulation of crosses	unland rainfed rice	during 2007
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	Generation -	Number of plants (observed)					Observed X <sub>2</sub> value
Cross		Total	F	PS	PF	CS	9:3:3:1:F <sub>2</sub> 1:1:1:1BC
NMS 4A x NDR 88	F <sub>2</sub>	448	250	89	80	29	0.521
NMS 4A x (NMS 4A x NDR 88)	BC	196	45	50	49	52	0.530
NMS 4A x NDR 358	F <sub>2</sub>	464	266	82	84	32	0.800
NMS 4A x (NMS 4A x NDR 88)	BC	204	50	49	54	51	0.350
IR 58025A x NDR 88	F2	480	276	87	83	34	1.310
IR 58025A x (IR 58025A x NDR 88)	BC	208	57	48	54	49	1.038
IR 58025A x NDR 88	F2	480	280	83	84	33	1.614
IR 58025A x (IR 58025A x NDR 358)	BC	212	59	56	47	50	1.699
PMS 10A x NDR 88	F2	496	284	87	91	34	0.809
PMS 10A x (PMS 10A x NDR 88)	BC	200	53	49	44	54	1.040
PMS 10A x NDR 88	F <sub>2</sub>	512	294	87	102	29	1.625
PMS 10A x (PMS 10A x NDR 88)	BC	224	53	63	50	58	1.750

Pollen sterility: F = fully fertile (>80%), PS = Partially sterile (50 - 79 %), PF = Partially fertile (1-50%), CS = completely sterile (<1%)

dominant genes (R<sub>1</sub> and R<sub>2</sub>). The plant with dominant alleles of the two genes in homozygous (R <sub>1</sub>R<sub>1</sub> R<sub>2</sub> R<sub>2</sub>) or heterozygous condition (R<sub>1</sub>/- R<sub>2</sub>/- ) will be fertile (fertility 80% and above). The plants with dominant alleles of one of the two genes in homozygous or heterozygous condition, but homozygous recessive alleles of the other genes (R<sub>1</sub>/- r<sub>2</sub> r<sub>2</sub> or r<sub>1</sub>r<sub>1</sub> R<sub>2</sub>/-) will behave like partial sterile (fertility from 50-79%) or partial fertile and *vice-versa*. The plants homozygous for the recessive alleles of both the genes (r<sub>1</sub> r<sub>1</sub>r<sub>2</sub> r<sub>2</sub>) will be completely sterile (fertility <1%). The test cross progenies segregated in the expected ratio of 1 (F)

: 1 (PS) : 1 (PF) : 1 (CS), which was expected when two independently segregating dominant genes with additive effects, one of them having stronger effect, control the fertility restorations of WA cytoplasm in CMS lines MNS 4A, IR 58025A and PMS 10A in the present case. The present results and also Bharaj *et al.* (1991) suggested the use of two dominant genes for fertility restoration to develop hybrid rice varieties by using CMS lines of WA origin. Such F<sub>1</sub> hybrids are expected to have high fertility and will consequently result in enhanced yield.

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