

## Genetics and molecular mapping of fertility restoration genes for CMS-WA system in rice

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### SUMMARY

For feeding the increasing population and enhancing productivity of rice, commercial exploitation of heterosis is essential. The combination of cytoplasmic male sterility (CMS) in one parent and restorer gene (*Rf*) to restore fertility in another are indispensable for the development of hybrid varieties. Searching for restorer genes is a good approach when phenotyping is very time-consuming and requires the determination of spikelet sterility in testcross progeny. The wild abortive (WA) cytoplasm is most widely used for hybrid seed production in rice. There are three major CMS types *i.e.* HL, BT and WA. *Rf3* for CMS-WA is located on chromosome 1, while *Rf1*, *Rf4*, *Rf5* and *Rf6* correspond to CMS-BT, CMS-WA and CMS-HL, located on chromosome 10. Molecular mapping lead to the development of PCR-based markers linked to *Rf* genes and the application of MAS for restorer genes, which would increase the efficiency of selecting putative restorer lines. In addition to use of markers in MAS procedures, these markers can also be used to transfer *Rf* genes into adapted cultivars through a backcrossing programme in an active hybrid rice breeding programme.

**Key Words :** Hybrid rice, Molecular markers, Fertility restoration, Cytoplasmic male sterility

**How to cite this article :** Kayande, N.V. and Kute, N.S. (2012). Genetics and molecular mapping of fertility restoration genes for CMS-WA system in rice : A Review. *Internat. J. Plant Sci.*, 7 (2) : 426-431.

**Article chronicle : Received :** 12.03.2012; **Accepted :** 04.06.2012

Hybrid rice technology offers a potentially viable option for increasing rice yield potential beyond the level of inbred high-yielding varieties by exploiting heterosis, or hybrid vigor, on a commercial scale. Cytoplasmic male sterility (CMS) combined with a fertility restoration system has been found to be the most efficient genetic tool in commercializing this technology in rice (Lin and Yuan, 1980; Virmani and Wan, 1988). The CMS systems have been extensively studied for their cytological, physiological and genetic characteristics. They were usually categorized into Wild Abortive (WA), Bao Tai (BT) and Honglian (HL) based

on the evidence from genetic and cytological studies (Rao, 1988; Li and Yuan, 2000). Among these three, the WA cytoplasm is the most widely used since it is a more stable system with complete pollen sterility (Shinjyo and Omura, 1966). In most of cases it was discovered that fertility restoration is controlled by two independent dominant nuclear genes with one stronger in action than the other (Young and Virmani, 1984; Virmani *et al.*, 1986). Identification of restorers and maintainers from large number of genotypes in the source nursery is the first and foremost step in the hybrid rice breeding. This is done by crossing the available genotypes with CMS lines and evaluating the progenies the test cross nursery for pollen and spikelet fertility. This conventional method of test crossing and evaluating the progenies based on morphological traits is laborious, time consuming and less accurate. Almost one year (two seasons) is required to identify the restorers. Moreover, the method is inefficient as only 15-20 per cent genotypes turn out to be restorers and 80 per cent of efforts in making crosses are wasted. Development of a MAS procedure involving the two main restorer QTLs on chromosomes 1 and 10 would significantly reduce the time

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