

**MOLECULAR ANALYSIS OF CYTOPLASMIC MALE
STERILITY AND RESTORATION OF COTTON**

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Abstract

Cytoplasmic male sterility (CMS) is a maternally inherited trait in which CMS plants do not produce viable pollen. CMS can be obtained from natural populations, crossing, or interspecific cytoplasmic replacement. Previous studies demonstrated that genes associated with CMS are located on the mitochondrial genome involving sequence rearrangement of functional mitochondrial genes or of unidentified sequences. Fertility in CMS plants can be recovered by nuclear fertility restoration genes. Most restorer genes cloned so far are members of the pentatricopeptide repeat (PPR) protein family. In our study, the CMS-D8 and restoration (Rf2) system was used. In a backcrossing population with 112 plants, segregation in male fertility had a ratio of 1 fertile: 1 sterile. Four new DNA markers were identified for Rf2, one of which was converted to a cleaved amplified polymorphism (CAP) marker. Among 36 primer pairs designed from mtDNA genes of Arabidopsis, three primer pairs including two for the cytochrome C biosynthesis gene produced polymorphism among the CMS-D8 line, male fertile maintainer lines with AD1 cytoplasm, and restorer lines. The relationship between these genes and CMS in cotton needs further studies. Primers designed for other genes did not detect polymorphism among the lines, supporting the view that mitochondrial genes are conserved in sequence size in cotton species.