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MOLECULAR MAPPING OF RESTORER GENE, RF2 AND RFLP ANALYSIS OF MTDNA IN CMS-D8 COTTON

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Abstract

Cytoplasmic male sterility (CMS) is a maternally inherited trait in which CMS plants do not produce viable pollen. Fertility in CMS plants can be recovered by nuclear restorer genes. Most restorer genes cloned so far are members of a pentatricopeptide repeat (PPR) protein family. In our study, the CMS-D8 and restoration (*Rf2*) system of cotton (*Gossypium hirsutum* L.) was used. In a backcross mapping population (BC1F1) with 112 plants, segregation of male fertility was 1 fertile: 1 sterile ratio. Three new RAPD (random amplified polymorphic DNA) markers were identified for Rf2, one of which was converted to a cleaved amplified polymorphism (CAP) marker. In addition, two AFLP markers and one SSR marker linked to fertility restoration were identified. Primers were designed based on the conserved PPR motifs and these primers in combination with AFLP (amplified fragment length polymorphism) primers were tested on the mapping population for linkage between PPR-AFLP markers and *Rf2*. Several PPR-AFLP markers were identified to be potentially associated with the *Rf2* locus, one of which was confirmed in the mapping population. A linkage map with *Rf2* and nine markers, including one from a previous study, was constructed. Based on MtDNA RFLP analysis, four RFLP markers showed polymorphism between normal cytoplasm and CMS cytoplasm. They are adenosine triphosphatase 1 (ATPase 1), ATPase 6, cytochrome c oxidase 1a (COX1a), and nicotinamide adenine dinucleotide b/c (NAD b/c). However, the relationship between these genes and CMS in cotton needs further studies to establish any causal effects.