MOLECULAR ANALYSIS OF CYTOPLASMIC MALE STERILITY IN COTTON

Fei Wang
Mary O'Connell
Department of Plant and Environmental Sciences, New Mexico State University
Las Cruces, NM
James Mac Stewart
CSES University of Arkansas
University of Arkansas
Fayetteville, AR
Jinfa Zhang
Department of Plant and Environmental Sciences, New Mexico State University
Las Cruces, NM

Abstract

Cytoplasmic male sterility (CMS) is a maternally inherited trait in which CMS plants do not produce viable pollen. The genes associated with CMS are located on the mitochondrial genome involving sequence rearrangement of functional mitochondrial genes or of unidentified sequences. Fertility of CMS plants can be recovered by nuclear fertility restorer genes. In this study, the CMS-D8 and restoration (Rf2) system was used. Three new random amplified polymorphism DNA (RAPD) markers were identified for Rf2, one of which was converted to a cleaved amplified polymorphism (CAP) marker. In addition, two amplified fragment length polymorphic (AFLP) markers and one simple sequence repeat (SSR) marker were identified to be linked to the fertility restorer gene (*Rf2*). PPR motif primers were designed based on the conserved pentatricopeptide repeat (PPR) protein genes and used in combination with AFLP primers to test the mapping population and one PPR-AFLP marker was identified. A linkage map was constructed with nine flanking markers including one from a previous study. Restricted fragment length polymorphism (RFLP) of mitochondrial DNA was analyzed among the CMS-D8 cytoplasm, CMS-D2 cytoplasm, and AD1 cytoplasm. Two probes including cotton *atp1* and maize *atp6* detected polymorphism among the different cytoplasmic lines. Fragments involving the *atp1* and/or *atp6* genes could be the candidate genes for CMS-associated gene(s) in mitochondrial genome for the cotton CMS systems.