

Isolation and Characterization of the Cytoplasmic Male Sterility Associated Gene of Cotton (*Gossypium harknessii*)

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Cytoplasmic male sterility (CMS) is a maternally inherited trait that results in the failure to produce functional pollen. It was identified in many plants, and it is widely used to exploit heterosis. Now, there are some genes associated with the CMS phenomena that have been identified in the mitochondrial genome. For example, specific genes implicated in CMS have been reported in maize, petunia, bean, Brassica, radish, sunflower, rice, carrot, sorghum, pepper, and many others. So, it was generally believed that CMS was frequently associated with dysfunction of mitochondria during pollen development, which could be caused by chimeric open reading frames (ORF), post-transcriptional regulations, or expression of specific proteins. But, we still know little about the CMS associated gene of cotton. So, in this research, *Gossypium harknessii* CMS cotton was used to identify the CMS associated gene. Southern blot analysis was performed using ten mitochondrial gene-specific probes (*cob*, *cox2*, *atp6*, *atp9*, *nad3*, *cox*, *atpA*, *cox1*, *Nad6*, and *Nad9*), which had been reported to be associated to CMS in other higher plants. The results demonstrated that four probes (*cox*, *atpA*, *atp9*, and *Nad6*) revealed RFLPs between male-fertile and CMS cotton lines. Northern blot analysis further indicated that *cox*, *atpA*, and *Nad6* showed polymorphic band of RNA transcripts between male-fertile and CMS cotton lines. These results implied that there must be something different in mitochondria genome, which affected the expression of *cox*, *atpA*, and *Nad6*. Therefore genome walking was performed to analyze these three genes region by using genome walker kits, but no differences were found between fertile and sterile plants for these acquired sequences. Maybe it is because that the first round genome walking did not reach the target regions. So, further genome walking is continuing by using primers designed according to the sequences we obtained. By this research, we hope that we can isolate the CMS associated gene of cotton, and then identify the function of the gene.