

**MOLECULAR IDENTIFICATION  
OF CYTOPLASMIC-SPECIFIC TRANSCRIPTS  
IN COTTON**

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**Abstract**

Cytoplasmic-specific genes have been associated with many economically important traits including male sterility, fertility restorer genes and genes responsible for susceptibility to insects, diseases and environmental stresses in cotton. However, very few cytoplasmic specific functional genes have been reported at the molecular level. The objective of this research was to identify cytoplasmic-specific transcripts using bulked samples from reciprocal crosses involving the maternally-inherited morphological (*cyt-V*) mutant. The *cyt-V* mutant was reciprocally crossed with Pima S-7 (PS-7) and the *virescent* mutant (*v<sub>7</sub>v<sub>7</sub>*), respectively. cDNAs were constructed from bulked samples of the third maternally inherited yellow colored leaves from each of the hybrids using a commercial kit. An automated PCR-based AFLP method was used to screen the differentially expressed genes in the cDNAs. Six *cyt-V* specific transcripts, ranging from 100 bp to 500 bp, were identified indicating the possibility of more than one gene associated with this mutant. Several of these were isolated and sequenced. A BLAST search of the partially sequenced transcripts indicated that four have very little homology with other recorded genes. One of the transcripts has a proline-rich motif while the other has a small core region with strong homology to a 15-amino acid core region with over 75% identity to *leucine aminopeptidase* amino acid sequences from *Arabidopsis thaliana* and other plant species.