

**NOVEL GENES ASSOCIATED
WITH ABSCISSION IN COTTON**

**Liwei Chen, Narendra K. Singh and Curt M. Peterson
Auburn University
Auburn, AL**

Abstract

Abscission is a process whereby plants shed their organs such as leaves, flowers and fruits. The process of abscission involves a series of physiological and biochemical changes that lead to the breakdown of the middle lamella and primary cell wall of target cells in the abscission zone, then separation of the target cells and abscission. In cotton, flower and boll abscission limit yield potential and delayed abscission of later formed leaves in the upper part of the canopy contributes to increased staining and trash in lint during harvesting. Studying the genes associated with abscission in cotton may permit genetic manipulation of this crop for increased yield and improved lint quality. The objectives of this study are: (1) to isolate and characterize genes associated with abscission in cotton, and (2) determine the temporal and spatial expression of abscission associated genes in abscission zone tissues. CA43, a cDNA clone, was isolated from a cotton abscission cDNA library which was constructed using mRNA extracted from petiole abscission zones 48 h after ethephon treatment. The CA43 cDNA hybridized to an mRNA of about 1.1kb that exhibited its highest level of expression in abscission zones 24 to 48 h after ethephon treatment. Southern blot analysis of CA43 suggests that it is encoded by a single gene in the cotton genome. Translation of the CA43 DNA sequence revealed 140 amino acid residues which likely represents a partial length of gene, because the initiator methionine codon was not found. The predicted amino acid sequence of CA43 cDNA exhibited maximum homology with Tasselseed2 (Ts2), showing 47.14% identity and 18.57% similarity. The predicted CA43 product belongs to a family of short-chain alcohol dehydrogenase having a highly conserved YxxSK motif which is thought to be involved in catalysis or subunit interaction. Clone CA73 was isolated from the abscission cDNA library and was expressed significantly in abscission zone 24 h after ethephon treatment. Comparison of the CA73 nucleotide and protein sequences has not revealed any significant sequence similarity. The roles of these two genes remain to be elucidated