IDENTIFICATION OF FIBER-SPECIFIC GENES IN COTTON USING AFLP-cDNA DISPLAY SYSTEM

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Abstract

Improving fiber yield and quality has the highest priority in cotton production. However, molecular basis for the initiation of fiber cells is poorly understood. Fiber cells are developed from the epidermal surface of fertilized ovule or maternal tissue. Conventional approaches are focused on studying genes involved in secondary wall biosyntheses in the late stages of fiber development. The biological process during fiber initiation is unclear, due to lack of proper techniques for study. We have developed an AFLP-cDNA display method to analyze transcription profiles in Arabidopsis polyploids. Using the AFLP-cDNA method, we performed a genome-wide survey of gene expression profiles in fiber initiation stages. By comparing cDNA profiles in leaves, petals, ovules, and young fiber tissues in cotton, we have identified dozens of cDNA fragments present in mature ovules and young fiber cells but absent in leaves and petals. The expression patterns of the candidate genes will be verified in fiber and non-fiber tissues using RT-PCR. We will determine the effects of the genes and maternal and paternal influence on fiber initiation by examining expression patterns of the lintless mutants and cytogenetic lines. Our goal to understand the genetic basis of fiber initiation and improve cotton production by manipulating expression of the genes essential for fiber cell development.