

Identification of Differentially Expressed Genes Associated with Cotton Fiber Development in a Chromosomal Substitution Line (CS-B22sh)

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One of the impediments in the genetic improvement of cotton fiber is the paucity of information about genes associated with fiber development. Availability of chromosome arm substitution line CS-B22sh (chromosome 22 short arm substitution from 3-79, *Gossypium barbadense*, into a TM-1, *Gossypium hirsutum*, background) provides a novel opportunity to study fiber-associated genes because previous studies revealed that this line was associated with some superior fiber quality traits compared to TM-1. We used an integrated approach of suppression subtractive hybridization (SSH), microarray, and real-time reverse transcription-polymerase chain reaction (RT-PCR) technologies to identify the potential genes associated with fiber development. Utilizing mRNAs from 15 days post-anthesis (DPA) fibers, we constructed a SSH cDNA library with chromosome substitution line CS-B22sh as the tester and TM-1 as the driver. The SSH cDNA library was screened using microarrays. Microarray analysis showed that 36 genes were differentially expressed in CS-B22sh 15-DPA fiber compared to TM-1 as confirmed by real time RT-PCR. These genes include two beta-tubulins, an actin, a putative kinesin light chain, a cellulose synthase, glycosyl hydrolase family 3 protein, pyruvate decarboxylase, glycoside hydrolase family 5, GDP-mannose pyrophosphorylase, dynamin-like protein, annexin, and a number of genes involved in signal transduction, and protein, nucleic acid, and lipid metabolisms. To our knowledge, this is the first report on the identification of differentially expressed fiber-associated genes in a cotton chromosomal substitution line.