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 379, 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 56 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 dehydrogenase, 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.