

**IDENTIFICATION OF GENES DIFFERENTIALLY EXPRESSED IN ELONGATING FIBER IN A  
COTTON CHROMOSOME SUBSTITUTION LINE CS-B25**

**S. Bandi**

**D.P. Ma**

**Mississippi State University**

**Mississippi State, MS**

**Abstract**

Recently 17 interspecific chromosome substitution lines (CS-B lines) of upland cotton in *G. hirsutum* TM-1 have been developed and released to the public. These substitution lines have TM1 as background and contain either whole chromosomes or chromosome arms of *G. barbadense* (line 3-79) chromosomes. Among them, the CS-B25 line was reported to have superior fiber properties with increased fiber length, strength, and lower micronaire. CS-B25 has chromosome 25 from *G. barbadense* substituted into TM-1. A comparative analysis of CS-B25 and TM-1 will provide an opportunity to identify and study the genes associated with fiber quality traits. An integrated approach of Affymetrix cotton genome arrays and suppression subtraction hybridization (SSH) was used to identify differentially expressed genes in CS-B25. Poly (A) RNAs from 10-DPA (days post synthesis) fiber were used to perform SSH and microarray analysis. A subtracted cDNA library was constructed with CS-B25 as tester and TM1 as driver. Microarray and SSH analyses showed that 23 genes were up-regulated and 9 down-regulated in CS-B25. The majority of up-regulated genes identified were part of the ethylene signal pathway, ubiquitin-proteasome pathway, and cell wall synthesis.