## GENE EXPRESSION STUDIES ON FIBERLESS MUTANTS IN COTTON (GOSSYPIUM HIRSUTUM L.) Jinsuk J. Lee, Osama S.S. Hassan, Wenxiang Gao, David M. Stelly, and Z. Jeffrey Chen Department of Soil and Crop Sciences and Intercollegiate Program in Genetics **Texas A&M University College Station, TX** Russell J. Kohel **Crop Germplasm Research Unit USDA-ARS College Station**. TX Xiao-Ya Chen Shanghai Institute of Plant Physiology and Ecology Shanghai Institutes for Biological Sciences **Chinese Academy of Sciences** Shanghai, China Present Address: Agricultural Genetic Engineering Research Institute (AGERI) Agricultural Research Center (ARC), Giza, Egypt

## **Abstract**

Although fiber development is a fundamental biological phenomenon and cotton fiber plays a significant role in textile industry, the molecular basis of fiber initiation and elongation is poorly understood. Fibers are essentially maternally derived seed trichomes. Fiber initiation is a quasi-synchronous process in developing ovules that commences shortly after anthesis. We have examined developmental processes of fiber cell initiation and elongation in three lintless or fiberless mutants, namely, *NIN1, n2n2*, and *LiLi* in the TM-1 isogenic genetic background. Genetic mutations that affect fiber cell elongation also delay the onset of fiber cell initiation and reduce the total number of fiber cells, resulting in short and sparsely distributed lint or "fuzz". *NIN1* and *n2n2* mutants had severe but slightly different effects on the fiber initiation process, whereas *LiLi* had a little or no effect on fiber initiation, although it displayed other morphological defects during growth and development. Changes of gene expression in the mutants were studied by analysis of spotted cotton oligo-gene microarrays that contain ~1,300 70-mer oligos designed from a subset of fiber genes encoding putative chromatin and transcription factors, cell cycle regulation, cell wall biosynthesis, and signal transduction and stress-related pathways. Using a dye-swap experimental design and analysis of variance (ANOVA), we analyzed the microarray data of each experiment consisting of 8 replications. We identified several dozen genes whose expression is down-regulated either in non-fiber tissues or in fibers of the fiberless/lintless mutants. The expression patterns of the candidate genes were verified by RT-PCR analysis. Research is underway to assemble a large set of cotton oligo-gene microarray and determine transcription profiling of fiber initiation in these mutants.