

## Transcriptome and Functional Analysis of Fiber-related Gene Expression in Cotton

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Fiber cell initiation is a complex process involving many pathways, including phytohormones and components for transcriptional and posttranscriptional regulation. Here we report expression analyses of fiber-related genes and small RNAs during fiber development. Using laser-dissected tissues and oligonucleotide microarrays corresponding to 23000 unigenes, we compared transcriptome profiles between the cells in epidermal layers, fibers, and inner integuments of cotton ovules. We found rapid and dynamic changes in gene expression in these different tissue-types. Among the genes that displayed expression changes in fiber and non-fiber tissues, those in the molecular classification of DNA/RNA binding were significantly overrepresented in the fiber cell initials compared to other tissues. Many of these genes encode putative *Myb* transcription factors and DNA binding proteins such as *Gossypium hirsutum Myb25 (GhMyb25)* and *GhRDL1*, homologs, which in *Arabidopsis* are important to leaf trichome development. The transcripts of these transcription factor genes were primarily localized in the epidermal layer of the seed coat. Overexpression of RD22-like 1 (RDL) gene (*GhRDL1*) in *Arabidopsis* induced fiber-like hairs in 5% of the seeds and produced dense trichomes in the leaves. Moreover, many putative phytohormonal and transcription factor genes are targets of microRNAs (miRNAs). Using miRNA microarrays and new sequencing technology, we demonstrated differential accumulation of miRNAs and their targets during cotton fiber development. The data suggest critical roles of transcriptional regulation and RNA-mediated pathways in early stages of fiber development.