INSIGHT INTO KEY CONTROL POINTS IN COTTON FIBER DEVELOPMENT THROUGH COMPARATIVE TRANSCRIPTOMICS AND METABOLOMICS IN *GOSSYPIUM HIRSUTUM* AND *GOSSYPIUM BARBADENSE*

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Abstract

We analyzed and compared the transcriptome and metabolome of the 10 to 28 days post anthesis (DPA) fiber of *Gossypium hirsutum* cv Deltapine90 and *Gossypium barbadense* cv Phytogen800. The plants were grown in parallel in a greenhouse with moderate temperature that supported good vegetative growth and the expected development of higher quality fiber in *G. barbadense*. The five days of fiber development analyzed (10, 15, 18, 21, and 28 DPA) included the stages of rapid elongation, transitional cell wall remodeling, and secondary wall cellulose synthesis. Illumina sequencing resulted in the collection of >2 billion reads, with 98% of them having homologs in the *G. raimondii* D genome. The reads with RPKM $\geq$ 2 corresponded to 41,566 transcripts, with approximately 38,000 transcripts expressed in each fiber type. The corresponding fiber metabolome included 205 identified metabolites held in common between fiber species, with no unidentified peaks. Analysis of the results within and across species of fiber had several novel implications, including new insights into the transition stage, control of lignin content, and how *G. barbadense* fiber is able to sustain elongation. For example, we were able to: (a) show that the transitional cell wall remodeling is a distinct stable developmental stage; (b) identify the transcription factor that acts as the apparent master controller of cotton fiber secondary wall thickening; (c) provide evidence for the transcriptional repression of lignification; and (d) implicate the biosynthesis and use of ascorbate in scavenging reactive oxygen species as a major factor supporting greater fiber length.

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