

**REGULATION OF GENE EXPRESSION IN THE TRANSITION FROM CELL ELONGATION TO  
SECONDARY WALL FORMATION IN COTTON FIBER****Hee Jin Kim****University of New Orleans****New Orleans, LA****Barbara A. Triplett****USDA-ARS****New Orleans, LA****Abstract**

During the transition from cell expansion to secondary cell wall thickening, the rate of cellulose biosynthesis in cotton fibers rises nearly 100-fold. Although the gene for the cellulose synthase catalytic subunit, *CesA*, was first described from cotton fiber, little is known about how *CesA* expression is regulated. By real-time quantitative PCR (q-PCR) we have identified the group of cotton *CesA* genes that are expressed during cell elongation and another set of *CesA* genes that are expressed during secondary wall thickening. The timing of the transition from elongation to cellulose biosynthesis is well-established for fiber cells produced *in vitro* by cotton ovule cultures. In this study we investigated changes in culture conditions that alter the timing of secondary cell wall *CesA* expression. Relative gene expression levels were monitored by q-PCR using SYBR Green for detection in an Applied Biosystems 7900HT Sequence Detection System. Gene-specific primers were designed with Primer Express ver. 2.0 (Applied Biosystems). Melting curve analyses were conducted to verify primer specificity. Relative transcript levels were determined by a comparative  $C_T$  method using either 18S rRNA or cotton  $\alpha$ -tubulin 4 as normalizers. Twenty-four hour treatment with exogenous indole acetic acid and/or abscisic acid at a time prior to initiation of secondary cell wall synthesis stimulated the premature expression of *CesA1* and *CesA2*, genes responsible for secondary wall synthesis in cotton fiber. Simultaneous treatment with auxin and abscisic acid had an additive effect on relative transcript abundance for *CesA1* and *CesA2*. Similar phytohormone treatments had little effect on the expression of genes predominantly expressed during cell elongation or constitutively expressed throughout fiber development (i.e.  $\alpha$ -tubulin 4,  $\alpha$ -tubulin 5, actin, expansin 1, and ubiquitin conjugating enzyme). Furthermore, addition of exogenous gibberellic acid, an essential phytohormone for fiber elongation down-regulated expression of secondary wall *CesA* genes. Evidence for a similar pattern of phytohormone-mediated gene regulation of a cotton *CesA* promoter in transgenic *Arabidopsis* will be discussed with a model that integrates these results.