Defining the Transition from Cell Elongation to Secondary Cell Wall Biosynthesis: Promoter Analyses, Transcript Profiling, and Genomic Analysis of Near-isogenic Germplasms that Differ in Fiber Strength

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A distinct set of homoeologous cellulose synthase catalytic subunit (CesA) genes are coordinately up-regulated with the onset of secondary wall formation in cotton fiber as shown by quantitative-RT-PCR. We have characterized a cotton CesA gene promoter [GhCesA4] by *in silico* and functional analyses of a promoter deletion series in cotton ovule cultures and Arabidopsis seedlings. In addition to numerous phytohormone response elements in the GhCesA4promoter, a region between -724 nt and -521 nt is responsible for basal expression of CesA4::GUS in Arabidopsis root vascular tissue and fibers. Additional promoters for several CesA genes expressed during secondary wall formation in *Gossypium hirsutum* L. have been isolated from BIBAC libraries and are being characterized. Comparative transcript profiling of a high fiber strength genotype (MD52ne) and its near-isogenic relative (MD90ne) indicates that the timing of the transition from cell elongation to secondary wall synthesis may play an important role in specifying commercially important fiber properties. Furthermore, new genes whose expression is coordinately regulated with the secondary cell wall CesA genes have been identified. Progress in defining genomic regions differing between the two genotypes will be presented.