

Expression Profiling Identifies Candidate Genes for Fiber Yield and Quality

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Gene expression profiling at early stages (0~2 DPA) of fiber development in *Gossypium hirsutum* identified a number of transcription factors which were down regulated in fiberless mutants relative to wild type controls and which could play a role in controlling early fiber development. Chief among these was *GhMYB25*, a Mixta-like *MYB* gene. Transgenic *GhMYB25*-silenced cotton showed dramatic alterations in fiber initiation and the timing of rapid fiber elongation, reduction in trichomes on other parts of the plant, a delay in lateral root growth, and a reduction in seed production due to reduced fertilization efficiency. Moderate over-expression of *GhMYB25* increased cotton fiber, altered leaf trichome morphology, and increased root branching. High expression increased trichome number but decreased fertility. *GUS* reporter gene constructs introduced into transgenic cotton showed that *GhMYB25* was expressed in the epidermis of ovules, developing initials and fibers, in the trichomes of a number of tissues including leaves, stems and petals, as well as in the anthers, pollen, and the epidermal layers of roots and root initials. Our results provide evidence for a role of *GhMYB25* in regulating cotton fiber development and other specialized outgrowths of epidermal cells and a potential target to improve fiber initiation and hence yield. Gene expression profiles of *G. hirsutum* and *G. barbadense* at different stages of fiber development showed major shifts in transcript functional categories between the fiber elongation and cell wall thickening stages in both species, but little difference between species at the secondary cell wall (SCW) stage. This suggests that earlier developmental stages during primary cell wall (PCW) synthesis may have an impact on the later physical and chemical differences in the fibers of these two species that have significantly different commercial quality attributes. Secondary metabolism genes, particularly in the phenylpropanoid pathway, and pectin synthesis and modification genes were amongst the most statistically different functional categories between the two species during fiber elongation. These pathways determine the chemical composition and rigidity of the non-cellulosic components of the PCW and offer new targets for manipulation to improve fiber quality.