

Multi-scale phenotyping of developing cotton fiber cells

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Cotton fibers in the *Gossypium* genus are the foundation of a multi-billion-dollar textile industry. Fiber development begins as unicellular trichoblasts emerge from the seed coat epidermis. This hemispherical trichoblast subsequently tapers and executes a complex cell elongation program. Following elongation, the trichoblast becomes a cellulose-generating machine as it puts down layers of secondary cell wall before cell death and desiccation. Elucidating the multi-scale interactions and feedback controls among cytoskeletal systems, cell wall properties, and changing cell geometries will provide an abundance of opportunities to engineer more favorable traits during fiber development. To meet this long-term goal, we are conducting a systems level analysis to better understand the fiber elongation process from 5 to 24 days post anthesis (DPA). An evolutionarily conserved microtubule-cellulose synthase control module is central to the processes of fiber tapering and anisotropic cell elongation. As such, we analyzed the protein abundance of cellulose synthesizing enzymes and their corresponding transcript levels through this developmental period. Concurrently, an image analysis pipeline was developed to determine fiber growth rate, measure fiber geometry, and characterize integral cell wall features through time. These results will highlight the cell wall features that dictate fiber growth behaviors and how they are patterned. Though correlation of the phenotypic and molecular data is ongoing, these analyses will help generate models to predict mechanisms of cellular pathway integration and phenotypic control. In addition, the structural information provides a robust dataset to refine finite element models of fiber cell growth.