Multi-scale phenotyping of developing cotton fibers

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Abstract

Cotton fibers in the Gossipyum 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. The trichoblast transitions to 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 "multi-omic" systems level analysis to better understand the fiber elongation process from 5 to 24 days post anthesis. An evolutionarily conserved microtubule-cellulose synthase control module is central to the processes of fiber tapering and anisotropic cell elongation. As such, molecular signatures of transcripts and proteins using quantitative proteomics were profiled and integrated across fiber development. Concurrently, a multi-scale image analysis pipeline was developed. Whole organs and fiber growth was measured under a stereomicroscope, fiber geometry and cellulose microfibril anatomy was characterized with confocal microscopy, and wall thickness was measured via TEM. Changes in the microfibril system are being analyzed in the context of the microtubule-CESA-module of gene expression dynamics. Though correlation of the phenotypic and molecular data is ongoing, these analyses are generating models to predict mechanisms of cellular pathway integration and phenotypic control. Finally, the structural information provides a robust dataset to refine finite element models of fiber growth.

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