

Comparative Proteomic Analysis of the Fiber Elongating Process in Cotton

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A comparative proteomic analysis was performed to explore the mechanism of cell elongation in developing cotton fibers. The temporal changes of global proteomes at five representative development stages (5~25 days post-anthesis [DPA]) were examined using 2-D electrophoresis. Among 1800 stained protein spots reproducibly detected on each gel, 235 spots were differentially expressed with significant dynamics in elongating fibers. Furthermore, 106 differentially expressed proteins were identified from mass spectrometry, and the great majority of these are reported at the protein level in cotton fiber for the first time. These proteins involve different cellular and metabolic processes with obvious functional tendencies towards energy/carbohydrate metabolism, protein turnover, cytoskeleton dynamics, cellular responses, and redox homeostasis, which indicate a good correlation between development-dependent proteins and fiber biochemical processes, as well as morphogenesis. Identification of these proteins, combined with their changes in abundance, provides a global view of the development-dependent protein changes in cotton fibers, and it offers a framework for further functional research of target proteins associated with fiber development.