

Proteomics Study of Cotton Fiber Cells

LIU Jin-yuan

(Laboratory of Molecular Biology, Department of Biological Sciences and Biotechnology, Tsinghua University, Beijing 100084, China)

A comparative proteomic analysis was applied to explore the mechanism of fiber cell development in cotton. Initially, an efficient protein preparation method was established for proteomic analysis of developing cotton fibers by two-dimensional gel electrophoresis, and a microwave enhanced ink staining technique also was created for fast and sensitive protein quantification in proteomic studies. Using the above approach, the temporal changes of global proteomes of cotton fibers at five representative development stages (5-25 days post-anthesis) were examined. A total of 235 spots were differentially expressed with significant dynamics in elongating fibers, and 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. The results indicated a good correlation between these development-dependent proteins and the biochemical processes of cell elongation of fiber, as well as morphogenesis. Besides, a phospho-proteomic approach, a functional analysis of a cotton glucuronosyl transferase promoter and the transgenic cotton plants with spider dragline silk protein gene, has been extensively studied. The latest progress in our research will be discussed during the meeting.