

Transcriptome Profiling and Analysis during Cotton Fiber Cell Development

ZHU Yu-xian

(The National Laboratory of Protein Engineering and Plant Genetic Engineering, College of Life Sciences, Peking University, Beijing 100871, China)

In this project, we aim to elucidate the molecular mechanism controlling initiation and elongation of tetraploid *Gossypium hirsutum* fiber cells by setting up a high throughput custom-designed cDNA microarray and a systematic gene expression profiling during cotton fiber development. We first constructed a microarray consisting of more than 28,000 cotton UniESTs that we obtained by deep-sequencing of several cotton ovule cDNA libraries. After probing the microarray with RNA samples from wild-type and a *fuzzless-lintless* mutant at different developmental stages, we identified ca. 1000 genes somewhat involved in fiber initiation and elongation processes. Second, we wanted to study the biological functions of 10 or more cDNAs individually by using Northern blot, ovule culture, quantitative RT-PCR, pathway analysis and RNAi methods to reveal their roles during various growth stages. We will also apply glycome, lipidome, and metabolome techniques to elucidate the importance of different metabolites during the sustained fast elongation period. Third, the functionalities of the characterized cotton genes will be studied by over-expressing in cotton plants driven by fiber-specific promoters. Fourth, after a high-quality transcriptome profiling for cotton fiber growth, we will try to isolate as many as 300 molecular markers and 20 BAC clones linked to important agronomical traits. Finally, through functional and comparative genomic analysis, we expect to significantly improve cotton fiber properties including length, strength and also lint productivity in transgenic cotton plants by using some of the characterized genes.