STRUCTURAL AND FUNCTIONAL GENOMICS ANALYSES OF TWO NEAR ISOGENIC COTTON (GOSSYPIUM HIRSUTUM L.) LINES DIFFERING IN FIBER MATURITY

Hee Jin Kim David D. Fang USDA-ARS-SRRC Linghe Zeng USDA-ARS-MSA Stoneville, MS Christopher D. Delhom Hong S. Moon USDA-ARS-SRRC New Orleans, LA Yuhong Tang The Samuel Roberts Noble Foundation Ardmore, OK

Abstract

Cotton fiber fineness and maturity are important properties of determining fiber grades in the textile market. To understand the genetic control and molecular mechanisms of fiber fineness and maturity, we studied two near isogenic lines, *Gossypium hirsutum*, Texas Marker-1 wild type (TM-1) and immature fiber (*im*) mutant showing a significant difference in micronaire values. The fibers from *im* mutant plants were finer and less mature with lower micronaire values than those from the recurrent parent, TM-1. A comprehensive fiber property analysis of TM-1 and *im* mutant showed that the lower micronaire of fibers in *im* mutant was due to the lower fiber maturity as compared to the TM-1 fibers. Structural genomics analysis showed that the immature fiber phenotype was controlled by one single recessive *im* gene located on chromosome 3. Transcriptome analysis revealed that the transcriptome data showing the elevated levels of alternative respiration induced in the *im* mutant fibers by stress, biochemical analyses showed that the reactive oxygen species levels of developing fibers from *im* mutant were lower than those from TM-1 fibers. The results provide insight into how the molecular mechanisms involved in the stress responses regulate cotton fiber maturity.