

Identification of Conserved Cotton MicroRNAs and Their Targets

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No study has been performed on identifying microRNAs (miRNAs) and their targets in cotton although cotton is one of the most important fiber and economic crops around the world. In this study, we found 30 potential cotton miRNAs using a comparative genomic approach based on genomic survey sequence analysis and miRNA secondary structure. These cotton miRNAs belong to 22 miRNA families. Expressed sequence tag (EST) analysis indicated that the predicted miRNAs were expressed in cotton plants. Based on the characteristic that miRNAs exhibit perfect or nearly perfect complementarity with their targeted mRNA sequences, a total of 139 potential miRNA targets were identified in cotton genome. A majority of these targets belong to transcriptional factors which regulate cotton growth and development, including leaf, root, stem, flower, and even fiber development. Those miRNAs also may be involved in other cellular and metabolic processes, such as stress response, signal transduction, and secondary wall synthesis and deposition. Some of the newly identified miRNA targets may be unique to cotton species. In this study, we found that at least 3 miRNA families (miR 396, 414, and 782) target callous synthase, fiber protein Fb23, and fiber quinone-oxidoreductase, suggesting that miRNAs play an important role in cotton fiber differentiation and development.