

Global Annotation of Small RNA and MicroRNA Mature Sequences from Developing Ovules of *Gossypium hirsutum* L.

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The involvement of small RNAs in cotton fiber development is under explored. The objective of this work was to directly clone, annotate, and analyze small RNAs of developing ovules to reveal the candidate small interfering RNA/microRNAs (siRNAs/miRNAs) involved in cotton ovule and fiber development. We cloned small RNA sequences from 0~10 days post anthesis (DPA) developing ovules of *Gossypium hirsutum* var. C9082. A total of 6691 individual colonies were sequenced from 11 ovule small RNA libraries that identified 2482 candidate siRNAs, comprising of 583 unique sequences with 12 nt to 39 nt long inserts. Surprisingly, only 6.5% of all cloned small RNAs from 0 to 10 DPA stages displayed overlapping expression in two or more DPA stages, suggesting high specificity of small RNA processing in each DPA stage. We identified a few mirBase-confirmed plant microRNAs, such as miR172, miR390, and ath-miR853-like siRNA, from the small RNA pools of developing ovules that were differentially processed at different DPAs. BLAST analysis identified several cotton genes and EST/cDNA sequences, revealing insights about genes involved in siRNA processing and ovule development. Analysis of putative proteins revealed many important biological processes such as biosynthesis/metabolism, transport, cell growth and organogenesis, gene regulation, photomorphogenesis, response to phytohormones, response to biotic/abiotic stresses and disease resistance, and DNA biogenesis, including many a priori fiber-associated proteins targeted by ovule-derived small RNAs. Our results provide direct molecular evidence of siRNA/miRNA-mediated regulation of fiber development and involvement of photomorphogenesis-related factors in fiber cell initiation and elongation along with other known genetic factors.