

1693 Direct Cloning and Annotation of Small RNAs From Developing Cotton Ovules of *G. hirsutum* L

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Small RNAs are crucial to the molecular basis of cotton fiber development because of their known role in regulation of complex developmental process in plants. However, these small RNAs have not been studied in cotton. We directly cloned small RNAs from 0-10 dpa developing ovules of *G. hirsutum* var. C9082 using miRCat™ small RNA-cloning kit (IDT, USA). Results reveal that the small RNA pools of 0 to 10 dpa developing ovules are mostly composed of 23-24-mer small RNAs along with small portion of 21-22-mer RNA sequences that are possible candidates to be microRNAs. Based on BLAST analyses, we identified several 24 mers significantly matching with cotton fiber ESTs and known genes such as sucrose synthase, sugar epimerase, wall-associated kinase, alcohol dehydrogenase A, tearoyl-ACP desaturase, and vacuolar H⁺-pumping ATPase. We identified several mirBase-confirmed plant microRNAs and possibly new cotton-specific microRNAs among 22-21-mer RNA sequences. Some of these siRNAs overlap stages but most are specific to each 0 to 10 dpa ovule library. Details of annotation of small RNA pools and possible fiber-specific microRNAs will be presented.