

Expression Analysis of MicroRNAs in Cotton

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MicroRNAs are a class of newly identified non-protein-coding small RNAs. MicroRNA posttranscriptionally regulates the expression of more than 30% of genes, which control many biological and metabolic progresses, including plant growth and development and response to environmental stress. However, no studies have been performed on microRNA expression in cotton, one of the most important fiber and economic crops. In this study, we employed quantitative real-time PCR (qRT-PCR) technology to monitor and compare microRNA expression in 8 different tissues at different developmental times. Our results showed that microRNAs have a unique expression patterns in different tissues at different developmental times. The microRNA, miRNA 172, was highly expressed in floral tissues compared with other tissues, whereas miRNA 156 had a highly expressed pattern in almost all tissues tested. The results will allow us to better understand the function of microRNAs in cotton growth and development and design new biotechnological strategies for improving cotton yield and quality.