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### 棉花纤维发育早期RNA-Seq转录组分析

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### Transcriptome Analysis of Early Developing Cotton Fiber by RNA-Seq

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**摘要** 为了揭示棉花纤维发育早期基因表达变化情况, 本研究以纤维长度存在显著差异的两个陆海回交近交系NMGA-062 (32.58 mm) 和 NMGA-105 (27.06 mm) 为材料, 利用Illumina HiSeq™ 2000对0、3 DPA (Days post anthesis) 的胚珠及10 DPA的纤维进行RNA-Seq测序。六个文库进行拼接, 共得到长度大于200 bp的Unigene 98464个, 总长度约为88.2 Mb。对10 DPA的纤维转录组数据进行差异表达分析, 共筛选到1931个差异表达基因, 1536个Unigene上调, 395个Unigene下调。GO (Gene ontology) 功能显著性富集和Pathway显著性富集分析发现, 差异表达基因富集在脂质转移活性 (Lipid transport activity) 分子功能组和脂质代谢通路 (Lipid metabolism pathway), 由此推测脂类相关基因可能在纤维伸长发育过程中起重要作用。通过对棉纤维发育10 DPA基因转录水平差异比较分析, 为深入开展纤维伸长相关功能基因的克隆和功能验证提供了丰富的资源, 并为揭示棉花纤维伸长的机制打下了坚实的基础。

**关键词:** 棉纤维发育早期 RNA-Seq qRT-PCR

**Abstract:** To obtain global insights into early developing fiber transcriptome characteristics, six sequencing libraries of early developing cotton fiber were constructed and sequenced using Illumina RNA sequencing. These libraries represented initiation (0 d post-anthesis (DPA) and 3 DPA) and elongation (10 DPA) stages from two backcross inbred lines having significant differences in fiber length: NMGA-062 (32.58 mm) and NMGA-105 (27.06 mm). Each sample yielded 4.6 Gb of available transcriptome data, with 98464 unigenes longer than 200 bp obtained by *de novo* assembly. When we compared NMGA-062 with NMGA-105 at 10 DPA, we uncovered 1931 differentially expressed genes (DEGs), of which 1536 were up-regulated and 394 were down-regulated. Gene Ontology functional enrichment and pathway enrichment analyses revealed that the DEGs were primarily associated with lipid transport and metabolism pathways, suggesting that lipid-related genes play an important role in cotton fiber elongation. The large number of DEGs detected by comparative analysis of 10-DPA cotton fiber transcriptome profiles provides a firm foundation for cloning and functional verification of fiber-related genes.

**Keywords:** early developing cotton fiber RNA-Seq qRT-PCR

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