



陆地棉种子发育过程中microRNA的挖掘与功能研究

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Identification of microRNAs in Upland Cotton

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摘要

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摘要 microRNAs (miRNAs)广泛参与调控植物的生长和发育, 但这类分子是否对棉花胚珠和纤维的生长发育起到重要的作用, 还有待这些小分子的认识, 一般先要从序列信息的获得上开始。应用基因芯片对TM-1 +5 DPA (开花后5 d) 胚珠总RNA进行了miRNA 筛选。结果显示, 含有352 个探针的芯片成功钓取到199 个陆地棉miRNA, 其中绝大多数为首次报道。此外, 对miR399 研究发现, 磷的含量变化相关; miR169 可能与干旱应激反应有关。

关键词: 陆地棉 基因芯片 miRNA 茎环RT-PCR

Abstract: MicroRNAs(miRNAs) are involved in the regulation of plant growth and development, but whether s molecules participate in cotton ovule or fiber growth or development is yet to be verified. Generally, understand these small molecules begins by obtaining sequence information. To clone miRNAs in cotton, an oligonucleotide microarray was used to screen total RNA of +5 days post anthesis TM-1 ovules. The microarray had 352 knowr miRNA probes. Ultimately, 199 miRNAs were probed. In addition, we found that miR399s is related to the phos content of the cotton fiber, and miR169s might play a role under drought stress in cotton.

Keywords: upland cotton microarray miRNA stem loop RT-PCR

Received 2013-06-05;

Fund:

国家“ 十一五” 科技支撑计划项目 (2006BAD13B04), 国家“ 973” 计划项目 (2004CB117301)

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