



利用基因芯片技术筛选棉花产量性状相关的基因

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Identification of Genes Related to Cotton Yield Using Affymetrix Gene Chips

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摘要

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摘要 根据皮棉产量数据的重复性测验及显著性分析, 从SG747(*Gossypium hirsutum* L.)和Giza75 (*Gossypium Barbadosense* L.)的回交自交系群体中选取高产组和低产组品系各3个材料, 取这2组材料和其父母本开花后10 d的纤维进行芯片分析。比较芯片数据, 获得了1508个差异表达基因。对这些差异表达基因进行聚类分析, 结果显示高产组品系和低产组品系分别聚类在一起, 符合基于田间数据分组的预期结果。利用Blast2GO软件对1508个差异表达基因进行Blast-Mapping-Annotation-KEGG分析, 结果表明参与细胞质膜发育、过氧化物酶活性、抗逆和营养物质运输等生物学过程的基因最多。进一步利用RT-PCR分析, 得到一系列与纤维品质和产量等性状密切相关的基因。研究结果为棉花高产基因工程和分子育种提供了丰富的基因资源。

关键词: 棉花 产量 基因芯片 *GhMKRP2 GhPOD*

Abstract: Three lines from high yield and low yield groups were selected from a backcross inbred line (BIL) population, which was developed from a cross between upland cotton SG747 (*Gossypium hirsutum*) and egyptian cotton Giza75 (*Gossypium barbadense* L.). Fiber RNA of 10 days post anthesis from the six BIL lines and parents lines were extracted for Affymetrix Cotton GeneChips. Through the transcriptome analysis among these lines, 1508 differentially expressed (DE) genes were identified based on a two-fold difference or greater. Clustering analysis of these DE genes showed that the high yield BIL lines and the low yield BIL lines clustered into two distinct groups. The Blast-Mapping-Annotation-KEGG analysis by Blast2GO software was performed on the DE genes, and revealed that many genes were related to plasma membrane, oxidation reduction, response to stress and transport. 50 DE genes were selected for further analysis by RT-PCR analysis, and many fiber- and yield-related genes were identified, which would make a firm foundation for further genetic engineering and molecular breeding studies.

Keywords: cotton yield gene chip *GhMKRP2 GhPOD*

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