

论文

利用斑茅cDNA芯片研究甘蔗受黑穗病菌侵染后基因差异表达

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摘要:

为了解甘蔗抗黑穗病的分子机制, 利用斑茅干旱胁迫cDNA芯片检测了甘蔗受黑穗病菌胁迫后的基因差异表达。经杂交, 在cDNA芯片的3 860个模板中, 有效差异表达(Ratio值 ≥ 2.0 或 ≤ 0.5)的基因为101个, 其中上调55个, 下调46个。部分基因的定量PCR验证表明, 芯片杂交结果可靠。上调表达基因经测序、冗余序列剔除, 一共获得36个unique ESTs。已知功能的22个上调表达基因, 涉及多条生理代谢途径, 如光合作用、离子转运和核酸代谢途径; 以及多种分子水平的进程, 如基因转录、蛋白质合成与修饰以及细胞信号转导等。另外, 还检测到14个未知功能基因。结果表明, 甘蔗对黑穗病的抗性具有复杂的机制。本研究为解释甘蔗受黑穗病菌胁迫后的基因差异表达及其网络构建奠定了基础, 还可以为今后系统研究甘蔗对生物与非生物胁迫的响应机制提供技术支持。

关键词: 甘蔗 黑穗病菌 斑茅 cDNA芯片 差异表达基因

Application of *E.arundinaceus* cDNA Microarray in the Study of Differentially Expressed Genes Induced by *U.sitaminea*

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Abstract:

RNAs of sugarcane leaves with (treatment) or without (control) the infection of *U. scitaminea* were extracted, subjected to hybridization of cDNA microarray based on *E. arundinaceus* cDNA sequence and further validated by Real-time qPCR. There were about 101 differentially expressed ESTs (with ratio value ≥ 2.0 or ≤ 0.5) among 3 860 genes sets in a microarray plate, with 55 up-regulated, and 46 down-regulated by *U. scitaminea*. After sequencing and redundant sequences elimination, we totally obtained 36 unique ESTs up-regulated after the infection of *U. scitaminea*. Among them, 22 were involved in several metabolism pathways, such as photosynthesis, ion transport and nucleotide metabolism, as well as some genes related to transcription factors, proteins synthesis and modulation, and cellular signal transduction. And the function of the 14 remaining ESTs was unknown. In conclusion, the molecular mechanism of sugarcane smut resistance is complex. This investigation would provide an understanding for differentially expressed genes induced by *U. scitaminea* and set a mode for the systematic research on molecular mechanism of sugarcane responses to biotic and abiotic stress.

Keywords: Sugarcane *Ustilago scitaminea* *E.arundinaceus* cDNA microarray Differentially expressed gene

收稿日期 2008-09-01 修回日期 2008-12-13 网络版发布日期 2009-03-23

DOI: 10.3724/SP.J.1006.2009.00940

基金项目:

本研究由国家高技术研究发展计划(863计划)项目(2007AA100701), 农业部引进国际先进农业科学技术计划(948计划)项目(2006-G37), 国家自然科学基金项目(30170639), 福建省科技厅国家科技项目备案(F2007AA100701)资助。

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