

枳感染柑橘衰退病毒后的应答基因分析

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Transcriptomic Responses of *Poncirus trifoliata* to *Citrus tristeza virus* (CTV) Infection

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摘要 枳 (*Poncirus trifoliata* L.) 高抗柑橘衰退病毒 (*Citrus tristeza virus*, CTV), 但相关抗性机理仍不为人所知。以嫁接健康枝条的无毒枳作为对照, 用Affymetrix柑橘基因芯片分析了感染CTV后枳叶片中基因的表达变化情况。结果共检测到表达量差异倍数≥ 2的基因295个, 其中216个表达上调, 79个表达下调。

BLAST2GO分析发现, 差异表达的基因中与抗逆反应相关的基因最多, 乙烯、茉莉酸、赤霉素、脱落酸、生长素、水杨酸等植物激素代谢和调节相关基因为数不少, 一些编码细胞壁形成或组分相关蛋白的基因差异表达明显。本研究可为揭示枳抗CTV的机理提供了转录组学线索。

关键词: 枳 柑橘衰退病毒 转录组学变化 CTV侵染

Abstract: Trifoliolate orange (*Poncirus trifoliata* L.) is highly resistant to *Citrus tristeza virus* (CTV), but the underlying mechanism has not yet been known. The transcriptomic patterns in leaves of trifoliolate orange trees infected with CTV were compared with those of uninfected trees by using Affymetrix citrus genome microarray analysis. A total of 295 genes were identified to be differentially regulated by more than 2-fold following CTV infection, among which were 216 up-regulated and 79 down-regulated genes. BLAST2GO gene ontology analysis showed that a large number of the genes are related to responses to biotic and abiotic stimuli and stresses. A significant number of the genes were involved in metabolism and regulation of ethylene, jasmonic acid, gibberellins, abscisic acid, auxins, salicylic acid. Some responsive genes encode either cell wall proteins or those participating in cell wall formation. These results obtained in this study should provide some important transcriptional clues to understanding the mechanism of CTV resistance of trifoliolate orange.

Keywords: trifoliolate orange, *Poncirus trifoliata*, *Citrus tristeza virus* (CTV), transcriptomic changes, CTV-infection

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