

UC Riverside

Journal of Citrus Pathology

Title

Comparison of micro RNA (miRNA) Profiles and Some miRNA Target Gene Expression levels in Roots of Non-infected and Huanglongbing-infected Tangerine (*Citrus reticulata* Blanco cv. 'Sanhu') Trees

Permalink

<https://escholarship.org/uc/item/9k8846mf>

Journal

Journal of Citrus Pathology, 1(1)

Authors

Zhong, Yun
Cheng, Chunzhen
Wu, Bo
[et al.](#)

Publication Date

2014

DOI

10.5070/C411025171

Copyright Information

Copyright 2014 by the author(s). This work is made available under the terms of a Creative Commons Attribution License, available at <https://creativecommons.org/licenses/by/4.0/>

8.3

Comparison of micro RNA (miRNA) Profiles and Some miRNA Target Gene Expression levels in Roots of Non-infected and Huanglongbing-infected Tangerine (*Citrus reticulata* Blanco cv. 'Sanhu') Trees

Zhong, Y.¹, Cheng, C.^{1,2*}, Wu, B.^{1,2}, Bei, X.^{1,2}, Jiang, B.¹, Zeng, J.¹, and Zhong, G.^{1,2**}

¹Institution of Fruit Tree Research, Guangdong Academy of Agricultural Sciences, China

²Citrus Research Institute, Southwest University, China (*: equal contributor; **: corresponding author)

Solexa sequencing was used to reveal the changes in small RNAome profile in roots of mock-inoculated (CK) and Huanglongbing bacteria-inoculated (HLB) 'Sanhu' tangerine (*Citrus reticulata* Blanco) trees. Results showed that the number of reads of both unique and total sRNAs decreased apparently in roots following infection with HLB. Distribution in length of sRNAs changed also remarkably, showing an increase in 22 nt and 21 nt small RNAs (sRNAs) and a decrease in 24 nt sRNAs in HLB-infected samples. A total of 42 known micro RNAs (miRNAs) belonging to 27 highly conserved miRNA families were identified. Comparisons showed that 33 known miRNAs exhibited a significant expression difference between CK and HLB-inoculated samples. In addition, 34 novel miRNAs, among which 24 were differentially expressed, were also identified, and their expression levels were analyzed by qRT-PCR. Three hundred and eighty five potential target genes were predicted for most of the 57 differentially expressed miRNAs. GO and KEGG annotation analysis revealed that most miRNA-target genes were those implicated in developmental process, response to stress and stimulus, transcription and protein metabolism. The characterization of the miRNAomes between the healthy and HLB infected Sanhu tangerine roots provided new insight into the involvement of miRNAs in HLB infection of citrus.