## Title

Identification of differentially expressed genes in Citrus sinensis leaves and branches in response to Candidatus Liberibacter asiaticus and Ca. L. americanus



## Journal

Journal of Citrus Pathology, 1(1)

## Authors

Breton, M. C.
Camargo, S. S.
Kishi, L. T.
et al.

## Publication Date

2014

## DOI

10.5070/C411025267

**10.8**

## Identification of differentially expressed genes in *Citrus sinensis* leaves and branches in response to *Candidatus* Liberibacter asiaticus and *Ca.* L. americanus

Breton, M.C.[1], Camargo, S.S.[2], Kishi, L.T.[3], Machado, M.A.[1], and Freitas-Astúa, J.[1,4]

[1]Centro APTA Citros Sylvio Moreira – IAC, Cordeirópolis-SP, Brazil
[2]Universidade Federal do Pampa, Bagé-RS, Brazil
[3]Universidade Federal de São Carlos, São Carlos-SP, Brazil
[4]Embrapa Cassava and Fruits, Cruz das Almas-BA, Brazil

Several studies have addressed transcriptional changes in *Citrus sinensis* samples in response to *Candidatus* Liberibacter asiaticus (CaLas) with the objective to reveal the mechanisms underlying the development of *Huanglongbing* (HLB) and identify possible strategies to manage the disease. The aim of this work was to provide data using NGS technology (RNAseq) for a comprehensive analysis of differential expression changes in *C. sinensis* leaves and branches induced by HLB, caused either by CaLas or CaLam. Four treatments were evaluated; each of them consisted of RNA bulks extracted from five *C. sinensis* HLB symptomatic leaves or branches inoculated with CaLam or CaLas. The samples were subjected to RNAseq sequencing and the differential expression analyses were performed with Cuffdiff. In parallel, we performed a simple parametric test based on the mean and standard deviation to select statistically significant differentially expressed genes (DEG), named RSDA (Relative standard deviation analysis). For this approach, we considered standard deviation values of <0.7, and p-value = 0.01. Several genes associated with disease response, transcription factors involved in the activation of pathways such as the jasmonic acid, salicylic acid and ethylene, as well as genes involved in oxidative stress proved to be differentially expressed in our analyses. In leaves, we identified genes belonging to the WRKY transcription factors, ankyrin repeat family, NB-ARC domain-containing disease resistance, ethylene-forming enzymes and chaperones. In branches, we found many cytochromes, as well as genes involved in callose deposition, AP2/B3 transcriptional factor family and LEA proteins as being differentially expressed. Validation by RT-qPCR was performed for ten DEG.
Financial support: Embrapa-Monsanto agreement; NIST-Citrus (CNPq and Fapesp)