

Title:

Candidatus Liberibacter americanus induces significant reprogramming of the transcriptome of the susceptible citrus genotype

Journal Issue:

[Journal of Citrus Pathology, 1\(1\)](#)

Author:

[Mafra, V.](#), Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo
[Martins, P. K.](#), Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo
[Francisco, C. S.](#), Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo
[Ribeiro-Alves, M.](#), Fundação Osvaldo Cruz, Rio de Janeiro
[Freitas-Astúa, J.](#), Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo; EMBRAPA Cassava and Fruits, Cruz das Almas, Bahia, Brazil
[Machado, M. A.](#), Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo

Publication Date:

2014

Permalink:

<https://escholarship.org/uc/item/6hj4m66d>

Local Identifier:

iocv_journalcitruspathology_25266

Abstract:

In Brazil, *Huanglongbing* (HLB) is caused by *Candidatus Liberibacter americanus* (CaLam) and *Ca. L. asiaticus* (CaLas). Both species are vectored by the Asian citrus psyllid and are restricted to the phloem of infected citrus, where they promote a severe imbalance in the translocation of nutrients and other important substances along the plant. Several studies of the transcriptional response of citrus to HLB have been reported, but only for infection caused by CaLas. This study evaluated the transcriptional reprogramming of a susceptible genotype (Pera sweet orange) challenged with CaLam, using a customized 385K microarray chip. The analyses showed that a large number of genes and biological processes were significantly altered upon CaLam infection. Among the changes we highlight induction of zinc transporters, modulation of enzymes related to sugar metabolism, decreased photosynthesis, induction of several defense-related genes and modulation of enzymes regulating ROS production. Several biological processes reported as differentially modulated upon infection with CaLas responded similarly to CaLam. The large number of receptor-like proteins, PR genes, NBS-LRR and transcription factors (such as WRKY and MYB) found showed that even a susceptible citrus genotype is able to actively respond to infection by CaLam, as reported for CaLas. Twenty candidate genes were selected for validation in symptomatic and asymptomatic PCR-positive leaves of Hamlin sweet orange infected with CaLas or CaLam. Finally, using *insilico* approaches, we compared our results with all published studies using CaLas to hypothesize a global feature of the defense/susceptibility mechanisms of citrus in



response to the bacteria. These results have been explored in selection of target genes for genetic engineering to control HLB. Also, further transcriptome (RNAseq) experiments using tolerant and susceptible citrus genotypes infected with CaLam or CaLas using different time points are in progress to investigate the dynamics of expression of these genes during early stages of infection.

Copyright Information:



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



eScholarship
University of California

eScholarship provides open access, scholarly publishing services to the University of California and delivers a dynamic research platform to scholars worldwide.

10.7

***Candidatus* Liberibacter americanus induces significant reprogramming of the transcriptome of the susceptible citrus genotype**

Mafra, V.¹, Martins, P.K.¹, Francisco, C.S.¹, Ribeiro-Alves, M.², Freitas-Astúa, J.^{1,3}, and Machado, M.A.¹

¹Centro de Citricultura Sylvio Moreira, Cordeirópolis, São Paulo

²Fundação Oswaldo Cruz, Rio de Janeiro

³EMBRAPA Cassava and Fruits, Cruz das Almas, Bahia, Brazil

In Brazil, *Huanglongbing* (HLB) is caused by *Candidatus* *Liberibacter americanus* (CaLam) and *Ca. L. asiaticus* (CaLas). Both species are vectored by the Asian citrus psyllid and are restricted to the phloem of infected citrus, where they promote a severe imbalance in the translocation of nutrients and other important substances along the plant. Several studies of the transcriptional response of citrus to HLB have been reported, but only for infection caused by CaLas. This study evaluated the transcriptional reprogramming of a susceptible genotype (Pera sweet orange) challenged with CaLam, using a customized 385K microarray chip. The analyses showed that a large number of genes and biological processes were significantly altered upon CaLam infection. Among the changes we highlight induction of zinc transporters, modulation of enzymes related to sugar metabolism, decreased photosynthesis, induction of several defense-related genes and modulation of enzymes regulating ROS production. Several biological processes reported as differentially modulated upon infection with CaLas responded similarly to CaLam. The large number of receptor-like proteins, PR genes, NBS-LRR and transcription factors (such as WRKY and MYB) found showed that even a susceptible citrus genotype is able to actively respond to infection by CaLam, as reported for CaLas. Twenty candidate genes were selected for validation in symptomatic and asymptomatic PCR-positive leaves of Hamlin sweet orange infected with CaLas or CaLam. Finally, using *in silico* approaches, we compared our results with all published studies using CaLas to hypothesize a global feature of the defense/susceptibility mechanisms of citrus in response to the bacteria. These results have been explored in selection of target genes for genetic engineering to control HLB. Also, further transcriptome (RNAseq) experiments using tolerant and susceptible citrus genotypes infected with CaLam or CaLas using different time points are in progress to investigate the dynamics of expression of these genes during early stages of infection.

(Support: Citrus Research & Development Foundation, and NISC Citrus)