Title

Transcriptome analysis of Huanglongbing-infected sweet orange leaves using RNA sequencing and quantitative PCR

Permalink

https://escholarship.org/uc/item/9pz553nz

Authors

Parra, Cynthia C.
Kunta, Madhurababu
da Graça, John V.
et al.

8.2

Transcriptome analysis of Huanglongbing-infected sweet orange leaves using RNA sequencing and quantitative PCR

Parra, C.C., Kunta, M., da Graça, J.V., and Louzada, E.S.

Texas A&M University-Kingsville Citrus Center, 312 N. International Blvd, Weslaco, TX 78596, USA

RNA sequencing (RNA-seq) methods provide a complete description of RNA transcripts including alternative splicing and small RNA characterization. RNA-seq performed in our laboratory on healthy and Huanglongbing (HLB)-infected young leaves revealed that 4,044 transcripts were up-regulated and 2,562 were down-regulated in the diseased trees. Moreover, a number of genes showed alternative splicing events including exon skipping, intron retention, and 5' and 3' alternative splicing. Furthermore, quantitative PCR (qPCR) performed on 20 randomly chosen genes with high differential expression (10 up and 10 down regulated) showed that all were consistent with RNA-seq data. Additionally, variation in levels of gene expression was observed between young and mature leaves. These early host plant response genes due to HLB-infection might be useful in the development of early HLB-detection methods before manifestation of disease symptoms in the infected plants.