

TRANSCRIPTOME OF THE *Brevipalpus yothersi* AND *CITRUS LEPROSIS VIRUS C* INTERACTION

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Brevipalpus yothersi (Acari: Tenuipalpidae), former synonym of *B. phoenicis* s.l., is recognized as vector of plant viruses that cause diseases of great economic importance, such as citrus leprosis. Considered a peculiar pathosystem, given its non-systemic character, strategies such as functional genomics (transcriptome) can contribute significantly with information for the management of that disease. In order to obtain information on the virus-vector interaction, differential gene expression were evaluated using mRNAseq (Illumina) technology in mites from isolines reared on healthy or CiLV-C infected sweet orange fruits. After high throughput sequencing and quality control (FASTQC), the data were analyzed with R language and Bioconductor software packages. The reads were mapped in the *B. yothersi* genome to identify the differentially expressed genes (DEGs). Functional analyzes were conducted using Blast2Go and the NCBI database, targeting similar proteins in *Tetranychus urticae* mites and others arthropods. We identified 5,690 DEG, with 2,736 up- and 2,954 down-regulated genes. Most of the up-regulated genes were related to xenobiotic detoxification processes, especially those related to resistance to acaricides/insecticides. A set of 30 DEGs were evaluated by RT-qPCR. This set included contigs related to detoxification, antiviral activity and response to stress, immunity, digestion and primary metabolism, and those with potential involvement in the *B. yothersi*/CiLV-C interaction. Twenty-eight of the selected genes were validated, confirming the differential expression under virus-infected and non-virus conditions. Some of the highlighted genes were ABC transporters, GST, chitinases-3, cathepsin-B, legumains, JNK-4, pancreatic lipases, serine proteases, Hsp71kD. These and other DEG, along with biological data, will allow inferences to elaborate a model for the virus-vector interaction.

Keywords: leprosis pathosystem, RNAseq, arthropod, mite vector.

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