POSTER - RNA AND TRANSCRIPTOMICS

BIOINFORMATIC ANALYSES OF CODING AND NON-CODING RNAS IN BREVIPALPUS YOTHERSI TO STUDY THE INTERACTION WITH CITRUS LEPROSIS VIRUS C, ACARICIDE RESPONSE AND VIROME COMPOSITION.

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Brevipalpus mites cause economic losses in a large number of horticultural and ornamental plants through the transmission of viruses. Affected crops include

citrus and coffee, both of relevance for Brazil. In particular, Brevipalpus yothersi is responsible for the transmission of citrus leprosis, a viral disease especially problematic in the state of São Paulo due to the significance of orange crops. Much effort has been done in understanding the plant-virus interaction, but Brevipalpus mites remain less studied at the genetic level. In genome and transcriptome data, protein-coding sequences have been usually the center of the research, but they typically account for a minor percentage of the whole gene space, whereas several studies suggest that the vast majority of a genome is made of structural and regulatory elements essential to study the biology of species, and to address fundamental questions or practical problems in both academic and applied research. Since a large proportion of those non-coding areas are transcribed, they can be characterized by transcriptomic approaches, including long non-coding RNAs and several types of small RNAs. This work includes the scaffolding of the current genome draft of Brevipalpus yothersi, and transcriptome analyses for the annotation of coding and non-coding areas of its genome, as well as to answer questions regarding the virus-mite interaction, pesticide response and gene silencing pathways in mites. Taking advantage of those research deliveries, the proposal also addresses the development of new-generation pesticides based on RNA interference technology, as an alternative to conventional chemical acaricides. Additionally, exploration of the whole set of viruses that these vectors are able to host becomes of relevance to evaluate their potential as a source of emergent pathogens and inter-crop virus spread, due to the polyphagous nature of these organisms. Forty-five Illumina transcriptome libraries corresponding to 6 Brevipalpus species from 9 different countries and several plant species, including field and laboratory populations, were sequenced to study virome composition. More than 1 billion reads have been used for a homology-based comparison at the protein sequence level against public repositories with Kaiju, a focused analysis of citrus leprosis viral species at the nucleotide level by read mapping with Bowtie2, and a de novo transcript assembly with Trinity and subsequent identification of contigs of viral origin with the machine learning classifier Virsorter2. All the software was run under a Linux OS. Preliminary results show that the virome is primarily structured by geographic location rather than by host plant or mite species and that, despite showing high complexity, identified plant viruses other than those traditionally reported for Brevipalpus mites were rare or low abundant, suggesting specificity as vectors.

Palavras-chave: bioinformatics; transcriptomics; genomics; acarology; virology; virome.