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SINGLE INDIVIDUAL WHITEFLY TRANSCRIPTOMES AS A POTENTIAL TOOL FOR PLANT VIRUSES DETECTION[1]/ Transcriptomas de um único inseto de mosca-branca como uma ferramenta em potencial para a detecção de vírus de plantas.

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The whitefly, *Bemisia tabaci*, is a complex of more than 43 cryptic biological species and a major agricultural pest that causes extensive damage to plants directly through phloem-feeding and indirectly through transmission of plant pathogenic viruses, belonging to the genera *Begomovirus, Carlavirus, Crinivirus, Ipomovirus* and *Torradovirus*. There is still a lack of genomic data available among the different whitefly species found in Brazil. Understanding the genetic and transcriptomic composition of these insect pests, the viruses they transmit and the microbiota is crucial to sustainable solutions for farmers to control whiteflies. Illumina sequencing was used to obtain transcriptomes of single individual of whiteflies from six different populations from Brazil including Middle East-Asia Minor 1 (MEAM1), Mediterranean (MED) and New World 2 (NW2) collected in different hosts. Sequenced reads were assembled using CLC Genomics Workbench. Assembled reads were mapped to reference genomes to obtain the complete mitochondrial genome of the whiteflies followed by Bayesian Analysis for species identification. Moreover, BLASTn searches on the non-redundant nucleotide database were performed followed by a analysis using the software BLAST Grabber, which can infer the NCBI taxonomy for the BLAST hits and visualize it, in order to detect the presence of endosymbionts and potential virus particles in the samples. Among the six samples, 62028 contigs were assembled. The BLASTn searches found a total of 108 contigs associated to plant virus particles, including species belonging to the genus *Begomovirus*. We will discuss the utility of the single whitefly transcriptome method and resulting data.

Key words: Mitochondrial; Bemisia tabaci; Endosymbionts

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