199

Plant and Invertebrate Virology: PIV

and ZLCV were obtained from the conserved regions of the viruses genomes, allowing the amplification of conserved regions in RT-PCR reaction, from the cDNA obtained. The amplified products were 644 bp (CMV), 535 bp (WMV-2), 398 bp (PRSV-W), 244 bp (ZLCV) and 214pb (ZYMV). In the duplex reactions, by the combinations of oligonucleotides, it was possible to differentiate viruses WMV-2, PRSV-W, ZYMV, CMV and ZLCV. In all reactions, the oligonucleotides used did not show nonspecific amplifications. For triplex reactions, it was obtained only the amplification of 535 bp corresponding to WMV-2 virus, this may be related to the optimization of the PCR reaction and to the competition and/or overlap between the oligonucleotides in the detection of viruses in studies. The multiple detections of viruses developed in this work can reduce the cost and work in the detection and differentiation of viruses. The oligonucleotide designed allows rapid detection and isolated differentiation of PRSV-W, WMV, ZYMV, CMV and ZLCV present in watermelon crops in the state of Tocantins. Financial Support: CNPq.

PIV247 - DIVERSITY OF BEGOMOVIRUSES IN THE WHITEFLY (BEMISIA TABACI)

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Begomoviruses (family *Geminiviridae*) are whitefly-transmitted small circular ssDNA plant pathogens. These viruses cause major losses in horticultural and bean production in Brazil, but their diversity and degree of variability are difficult to assess using traditional sequencing methods. The aim of this study was to evaluate the diversity of begomoviruses in the vector, the whitefly *Bemisia tabaci*, using an Illumina sequencer platform. Adult insects were collected in commercial crops from five different Brazilian states (MG, SP, ES, DF and GO). Following sample maceration and DNase/RNase treatment, viral DNA was extracted and subjected to Rolling Circle Amplification (RCA) in order to enrich the library with circular DNA. Nucleic acids were fragmented, linked to adaptors and then subjected to

Illumina deep sequencing. After sequence trimming and assembly, 19,165 contigs were obtained with 177 hits against the virus RefSeq database. From those, fifteen begomovirus species were identified, with sequences ranging from 38 to 2593 nucleotides and from 83 to 99% identity. Five of them were begomoviruses found in tomato plants, four in sweet potato, two in sida, and one each in euphorbia, beans, soybean, okra and passiflora plants. Due to the high nucleotide identity between the contig sequences and the reference sequences, it is likely that new begomoviruses were not found in this survey. However, the finding of a sweet potato virus that is still not reported in Brazil may suggest that the study of begomoviruses in whiteflies is a powerful surveillance tool to unravel the diversity of this virus group in the country. Financial Support: CNPq, EMBRAPA.

PIV251 - PRELIMINARY EVALUATION OF QUILLAJA SAPONINS EFFECT ON HUMAN ADENOVIRUS 5 REPLICATION CYCLE

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Adenoviruses are important waterborne enteric viruses, have double-stranded DNA genome and belong to the Adenoviridae family. These viruses can infect humans (HAdV) and animals, and are associated mainly with gastroenteritis, respiratory and conjunctivitis infections. Secondary metabolites from plants may interfere in viral infectivity. Saponins, for example, are amphipathic glycosides with surfactants proprieties and able to interact with cholesterol and other sterols. Studies have demonstrated antiviral activity of saponins from the barks of Quillaja saponaria against vaccinia virus, herpes simplex virus type 1, varicella zoster virus, human immunodeficiency viruses 1 and 2, and rotavirus. Thus, the present study aimed to investigate the effects of Quillaja saponins on HAdV-5 replication. The effect of a commercial saponins from Q. saponaria barks (QS) and a crude aqueous extract from *Q. brasiliensis* leaves (QB) on the interaction of HAdV-5 with cell line A549 (human lung cancer cells) was analyzed. The cytotoxicity and the effect on HAdV-5 replication to both samples were assessed by MTT and plaque-forming units (PFU) assays, respectively. Cytotoxicity was not observed in the concentration ranges of 0.98-15.53 µg/mL (QS) and