RESUMO - AMBIENTAL

EVIDENCES OF MITOVIRUS-DERIVED NON-RETROVIRAL ENDOGENOUS RNA VIRAL ELEMENTS (NERVE) IN PASSIFLORA SPP.

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Mitoviruses consist of a group of ssRNA (+) viruses with a single ORF encoding a deduced viral RNA-dependent RNA Polymerase (RdRp) protein and has no capsid. These viruses belong to the Narnaviridae family and infect mitochondria of phytopathogenic fungi and were recently detected infecting plants. Although a DNA stage in the replication cycle or genome integration is not required, mitovirus-derived sequences can be detected in host mitochondrial and nuclear genomes of plants. In some cases, these mitovirus-derived sequences are capable to be transcribed. Passion fruit (Passiflora spp.) is an economically

important crop for many tropical and sub-tropical countries around the world and the production is affected by many diseases caused by viruses. However, there are no reports of mitoviruses associated with Passiflora spp.. The aim of this study was to identify mitoviruses associated with passion flower plants by molecular techniques. Double-strand RNA (dsRNA) extracted from 22 accessions of Passiflora spp. plants with virus-like symptoms was sequenced using Illumina HiSeq 2500 high-throughput sequencing system. Raw reads were de novo assembled and 23 contigs with high similarity with plant mitoviruses were identified. A 5,5 kb contig (named as Passiflora mitovirus-like PMV) showing a single ORF with mitovirus RdRp motifs was selected for further studies. Oligonucleotides were synthetized for PCR and RT-PCR and used to amplify this mitovirus-derived fragment from both RNA and DNA extracted from passion flower leaves. A 926 nt fragment was amplified from both RNA and DNA from 13 accessions of Passiflora spp. (P. galbana; P. cacao; P. quadrangularis; P. incarnata; P. mucronate; P. malacophylla; P. serratodigitata; P. ferruginea; P. hatschbachii; P. gardneri and P. subrotunda), evidencing a possible endogenization or horizontal gene transfer (HGT). The mitovirus-derived fragments from P. galbana and P. maliformis were cloned and Sanger sequenced. PMV clones share 54% RdRp amino acid identity with chenopodium quinoa mitovirus 1 and phylogenetic analysis of the predicted RdRp with plant and fungi mitoviruses shows that they cluster with other plant mitoviruses. Overall, we present here the first evidence of mitovirus infection in Passiflora spp. as NERVEs and the recovery of mitovirus-derived fragments from RNA samples indicates that PMV is capable to be transcribed.

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