

RESUMO - VEGETAL E INVERTEBRADOS

MOLECULAR VARIABILITY OF CITRUS LEPROSIS VIRUS C, THE MAIN ETIOLOGICAL AGENT OF CITRUS LEPROSIS DISEASE

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Cytoplasmic type of citrus leprosis disease caused by the cilevirus citrus leprosis virus C [CiLV-C; family Kitaviridae; ss(+)RNA genome] is the most important viral disease affecting the Brazilian citriculture. Diseased plants show chlorotic and necrotic lesions in the fruits, branches, and leaves. A variability study of CiLV-C carried out in 2016 revealed that the virus population is divided into two lineages: CRD and SJP. Members of these lineages share about 85% nucleotide identity and show signs of recombination events in their RNA2. Members of the clade CRD were detected widespread across Latin America, while members of the clade SJP were only found in three regions within the citrus belt of São Paulo-Minas Gerais, Brazil. In this work, to better understand the distribution and genetic variability of CiLV-C lineages we analyzed 424 lesions from 298 symptomatic *Citrus sinensis* samples collected in South America in the period 1932-2019. In sum, 136 sequences of ORF p29 (cp) and 217 partial sequences of the mp gene, were obtained. Nucleotide (p) and haplotype (Hd) diversities, and selection pressure ($\omega=dN/dS$) of the CiLV-C population were assessed for each subpopulation (CRD and SJP) using DnaSP

and Datamonkey programs. Phylogenetic trees using the Maximum Likelihood method (HKY+G model; 10000 bootstraps) based on the p29 and mp sequences confirmed the existence of the previously described clades. Clade CRD consisted of CiLV-C isolates collected from 1932 and were detected in all regions of Latin America. In contrast, clade SJP only comprised isolates collected in the SP-MG citrus belt after 2015. Remarkably, in this region, 62.7% of the lesions were infected with viruses of the clade SJP, 16.2% with those of the clade CRD, and 19.6% exhibited mixed infections involving viruses of the two clades. The CRD and SJP subpopulations are under purifying selection ($\omega \sim 0.148 - 0.475$) and showed a very low genetic diversity ($p \sim 0.0006 - 0.001$), and high haplotype diversity ($H_d > 0.8$). The current study provides a general snapshot of the CiLV-C population in Latin America and, particularly, of the largest and most important citrus-growing areas of Brazil. The relevance of these results on the citrus leprosis diagnosis using RT-PCR tests will be discussed.