

RESUMO - VEGETAL E INVERTEBRADOS

EVOLUTIONARY RECONSTRUCTION OF CITRUS LEPROSIS VIRUS C POPULATION SUGGESTS ITS DIVERSIFICATION INTO THREE LINEAGES BEFORE THE INTRODUCTION OF CITRUS SPP. IN AMERICA.

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Citrus leprosis virus C [CiLV-C; genus Cilevirus, family Kitaviridae; ss(+)RNA genome] is the prevalent virus causing citrus leprosis disease (CL) in Brazilian citrus orchards. Restricted to Latin America, the population of CiLV-C comprises the lineage CRD, widespread from Mexico to Argentina, and the lineage SJP, first detected in areas of the citrus belt São Paulo – Minas Gerais. To delve into the study of the molecular epidemiology and evolution of the CiLV-C population, we obtained the viral nucleotide sequences from 425 symptomatic Citrus spp. samples collected between 1932-2019. Besides, the concatenated sequences of the p29 and mp genes were analyzed to calculate the time of the most recent common ancestor (tMRCA) of these isolates. The growth history of the CiLV-C population was assessed by the Bayesian Markov Chain Monte Carlo method using the BEAST software version 1.10.04, and the following parameters and conditions: substitution model TN93+G, Bayesian skygrid tree model, and time

of last transition point = 87. The maximum clade credibility tree was created by discarding the initial 10% of the chains and summarized in TreeAnnotator and viewed using IcyTree software. Phylogenetic studies indicated the existence of a third lineage, called ASU, represented by only one isolate recovered from a herborized sample collected in Asunción, Paraguay, in 1937. The current distribution and circulation of members of this clade, if any, are still unknown. The genome of CiLV-C_ASU shares ~ 85% nucleotide identity with those from the type members of the clades CRD and SJP and shows signs of inter-clade recombination processes. Members of the CRD lineage were detected in samples from all over Latin American since 1932, but those of the clade SJP were detected only in samples from the citrus belt São Paulo – Minas Gerais, collected after 2015. tMRCA of the three lineages of CiLV-C was estimated at approximately 500 A.D., while diversification of the lineages CRD and SJP was dated after 1870 A.D. Since Citrus spp., were introduced in America after 1520, our analysis suggests that ancestors of viruses of the clades CRD, SJP, and ASU most likely originated in contact with native vegetation in a wild ecosystem of South America.

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