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Molecular characterization of two papaya ringspot virus isolates that cause devastating symptoms in Norte de Santander, Colombia

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Abstract

Papaya ringspot virus is an RNA virus that belongs to the genus *Potyvirus*, family *Potyviridae* and affects both papaya and cucurbits, causing great economic losses. PRSV isolates are divided into biotypes P and W; both biotypes naturally infect plants in the family *Cucurbitaceae*, whereas the P type also naturally infects papaya (*Carica papaya* L). In the present study, we report the full-length genome sequence of two PRSV-P isolates sampled from the Campo Hermoso (PRSV-CH) and Villa del Rosario (PRSV-VR) localities in Norte de Santander, Colombia. The genomes of these PRSV isolates are 10,326 nt in length and have a predicted ORF of 3344 aa. The identity among Colombian PRSV isolates is 96.9% and 97.3% at the nucleotide and deduced amino acid levels, respectively. PRSV isolates from China had the lowest identity at 78.3% and 89.2% (nucleotide-amino acid), whereas the highest identities were detected in PRSV isolates from Mexico, Venezuela and Hawaii. At the polyprotein level, the amino acid composition surrounding the active polyprotein cleavage sites differ in the Colombian PRSV sequences. The predicted cleavage site in P1/HC-Pro is LEQY/N – LEQY/S instead of MEQY/N. Both of the Colombian PRSV isolates have a putative recombination event in the P1 coding region, which is common in all PRSV isolates from the American continent. The new full-length PRSV sequences from Colombia provide a better understanding of the dynamics of papaya ringspot virus infections in papaya in Colombia and worldwide.

Fig. 1

Fig. 2

Fig. 3

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Ethics declarations

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Conflict of interest

Author Chaves-Bedoya Giovanni declares that he has no conflict of interest. Author Ortiz-Rojas Luz Yineth declares she has not conflict of interest

Ethical approval

This article does not contain any experiments on human participants or animals.

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