

Sugarcane mild mosaic virus recognized as a new ampelovirus species infecting sugarcane

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The complete genome sequence of a previously uncharacterized sugarcane-infecting virus of the genus *Ampelovirus* was obtained by high-throughput sequencing (HTS) and rapid amplification of cDNA ends. This genome consisted of 13,114 nucleotides (nt) and harboured seven open reading frames. Subsequently, 15 additional complete or near-complete genome sequences of this virus were obtained by HTS from different sugarcane varieties originating in Africa, Asia, North and South America. Phylogenetic and pairwise identity analyses with all these sequences revealed that they belonged to a new *Ampelovirus* species, family *Closteroviridae*. The 16 virus isolates were distributed in three phylogenetic groups and potential recombinant events were identified for only one of these isolates. An immunocapture-reverse transcription PCR (IC-RT-PCR) assay was developed with antibodies previously produced against a clostero-like virus that had not yet been recognized by the International Committee on Taxonomy of Viruses but for which the name sugarcane mild mosaic virus (SCMMV) had been proposed. The new ampelovirus was detected by IC-RT-PCR, and Sanger-sequenced amplicons confirmed the identity of the virus based on HTS data. The complete or near-complete sequences reported here represent the first genomic sequences for SCMMV that has a wide geographical distribution. Furthermore, the newly developed RT-PCR diagnostic assay will facilitate the understanding of SCMMV epidemiology and will help improve management and quarantine diagnostic.