

PO13 INVESTIGATIONS INTO THE VIROME OF SUGARCANE IN CUBA

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Knowledge of the sugarcane virome (i.e. all the viruses infecting sugarcane) is critical for the industry and for the movement of sugarcane germplasm using quarantine procedures. Diseases caused by viruses are not always easy to diagnose based on symptoms and sugarcane is often infected by one or several virus species without showing symptoms. In this study, 90 sugarcane samples were collected from sugarcane fields and germplasm collections in Cuba and processed by Virion-Associated Nucleic Acid (VANA) metagenomics and Illumina sequencing. Sequences of four viruses known to cause disease in sugarcane were found in these samples: Sugarcane bacilliform virus (SCBV) in 16 samples, sugarcane mild mosaic virus (SCMMV) in 21 samples, sugarcane yellow leaf virus (SCYLV) in 28 samples, and sugarcane striate virus (SCStV) in two samples. Additionally, RNA extracted from sugarcane cultivar B34104 showing mosaic symptoms was amplified by cDNA-PCR and used for Nanopore sequencing. A total of 4,439 virus reads attributed to three known viruses infecting sugarcane were found among the 430,233 clean reads, namely SCBV, sugarcane mosaic virus (SCMV), and SCYLV. Assembling of the virus reads resulted in a complete consensus genome sequence of SCMV and almost complete genome sequences (>90%) of SCBV and SCYLV. Mapping of the SCMV reads onto the consensus sequence revealed the presence of at least two different genotypes of SCMV in the collected sample. The consensus sequence of SCMV was closest to GenBank accession MT701608.1 (SCMV isolate SC 2086 from Florida) with a 95% nucleotide identity. The genome sequences of SCBV and SCYLV were closest to GenBank accessions NC_038382.1 (SCBV from Guadeloupe) and MF622079.1 (SCYLV strain CUB from Cuba) with 92% and 94% nucleotide identity, respectively. This is the first report of SCMMV and SCStV in Cuba and the first report of a complete genome sequence of SCMV from Cuba.