

Metagenomic screening of the sugarcane virome in Florida

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Viral metagenomics has revolutionized the way pathologists decipher viral diseases. While the impact of this new approach is still debatable in plant virus diagnostics, viral metagenomics has already produced key advances in viral ecology and has the potential to become a central approach for viral surveillance at the ecosystem scale.

A viral metagenomics study of the sugarcane virome in Florida was carried out in 2013/2014. One hundred and eighty sugarcane leaf samples were collected from different commercial sugarcane (*Saccharum interspecific hybrids*) fields in Florida and from other *Saccharum* and related species taken from two local germplasm collections. Sequence-independent next generation sequencing (NGS) of virion-associated nucleic acids (VANA) was used for detection and identification of viruses present within the collected leaf samples.

All four previously reported sugarcane viruses occurring in Florida were detected: *Sugarcane yellow leaf virus* (149 infected samples out of 180), *Sugarcane mosaic virus* (2/180), *Sugarcane mild mosaic virus* (10/180) and *Sugarcane bacilliform virus* (51/180). Interestingly, this viral metagenomics approach also resulted in the detection of potential new viruses of sugarcane, including Chrysovirus, Mastrevirus, and Umbravirus.

This study provided a snapshot vision of the SCYLV genetic diversity in 2013/2014 in Florida where several genotypes of this virus are present. It also allowed us to assemble the whole genome of at least one new mastrevirus species.

Mots-clés : Metagenomics, sugarcane, virus discovery, deep sequencing, complete genome.