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Impact of genetic diversity on diagnosis of sugarcane yellow leaf virus

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Yellow leaf of sugarcane, also known as yellow leaf syndrome or YLS, was first reported in Brazil and Hawaii in the late 1980s. The causal agent of this disease was identified only a decade later and named sugarcane yellow leaf virus (SCYLV). Since then, this virus was found in an increasing number of sugarcane growing locations where it can induce significant yield losses. We used the genome coding sequence (5561-5612 nt) of 109 virus isolates from 19 geographical locations to investigate the genetic diversity of SCYLV. Sixty-five sequences were newly obtained by high throughput sequencing and 45 were retrieved from GenBank. The 109 virus isolates were distributed in three major phylogenetic lineages (BRA, CUB, and REU), with the exception of one isolate from Guatemala. Twenty-two recombination events were identified among the 109 isolates of SCYLV but no temporal signal was found in the genomic sequence data set. RT-PCR is the most used assay for detection and diagnosis of SCYLV in infected plants. Among the 27 RT-PCR primers reported in the literature, none matched 100% with all the 109 SCYLV sequences. This suggested that the use of some primer pairs may not result in the detection of all virus isolates. Primers YLS111/YLS462 were the first primer pair used by numerous research organizations to detect the virus by RT-PCR and these primers failed to detect isolates belonging to the CUB lineage. In contrast, SCYLV isolates from all three lineages were detected with primer pair ScYLVf1/ScYLVr1. Continuous pursuit of knowledge of SCYLV genetic variability is therefore critical for effective diagnosis of yellow leaf, especially in virus-infected and mainly asymptomatic sugarcane plants. A web-based, interactive visualization of the 109 SCYLV genomes investigated in this study has been created and is available in Nextstrain (https://nextstrain.org/community/grunwaldlab/scylv).