

# First report of sugarcane white streak virus infecting sugarcane (*Saccharum* spp.) in Côte d'Ivoire

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## KEYWORDS

disease surveys, mastrevirus, nanopore sequencing

Sugarcane (*Saccharum* spp.) is an important interspecific hybrid crop grown for sugar and ethanol production in tropical and subtropical regions around the world. However, its vegetative propagation makes it vulnerable to viral diseases which pose a serious threat to crop yield and quality. Several viruses belonging to species in the genus *Mastrevirus*, family *Geminiviridae* are known to infect sugarcane including maize streak virus, saccharum streak virus, sugarcane chlorotic streak virus, sugarcane streak Egypt virus, sugarcane streak Reunion virus, sugarcane streak virus, sugarcane striate virus and sugarcane white streak virus (SWSV), (Boukari et al., 2020).

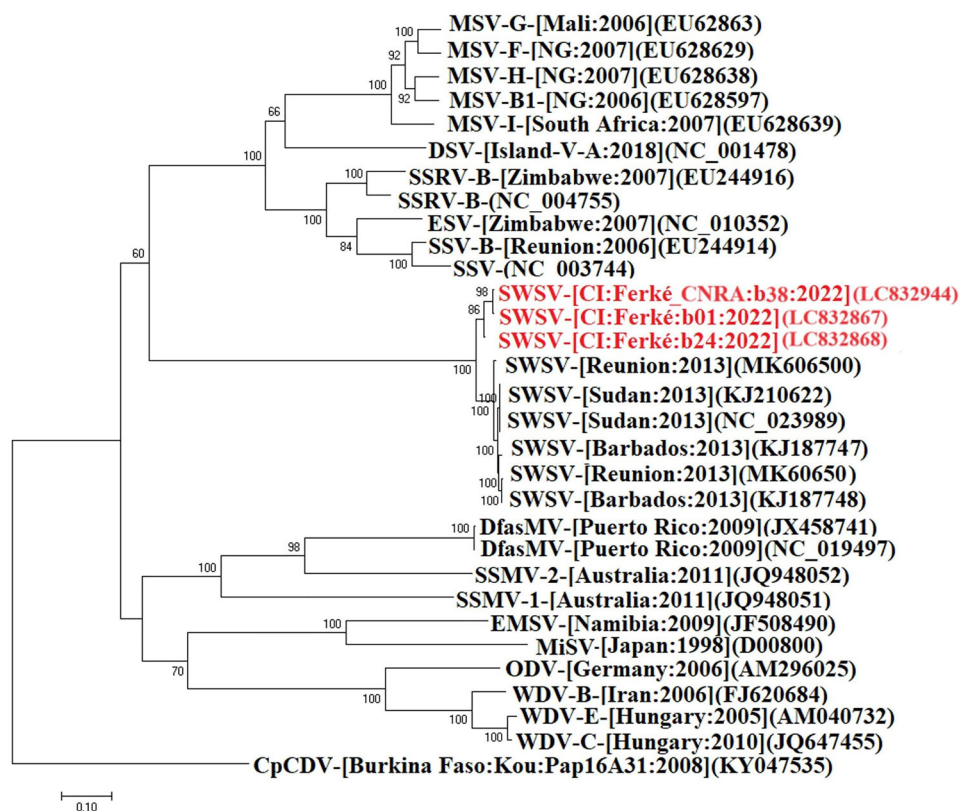
In Côte d'Ivoire, sugarcane streak mosaic virus (SCSMV; genus *Poacevirus*, family *Potyviridae*) is reported as an emerging virus affecting a wide range of sugarcane varieties in the country (Daugrois et al., 2020; Sorho et al., 2020). With the aim of developing a holistic method for controlling its spread on areas cultivated by SUCAF-CI (a sugar company in Côte d'Ivoire), we undertook an inventory of the viruses present on its sites. Twenty-four samples were collected from SUCAF-CI germplasm collections and nurseries, and leaves were analysed by rolling circle amplification with random hexamers followed by nanopore sequencing using a MinION device as described by Ben Chehida et al. (2021). One sugarcane leaf sample (SC\_BC38) with peculiar symptoms (Figure 1) collected in a sugarcane field of the Centre



**FIGURE 1** (A) Mild symptoms associated with the presence of sugarcane white streak virus in sugarcane and (B) severe symptoms observed on cv. Co997 (sample SC\_BC38)

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**FIGURE 2** Maximum-likelihood phylogenetic tree with 1000 bootstraps obtained by alignment of full genomes of sugarcane white streak mosaic virus and other *Mastrevirus* species including Digitaria streak virus (DSV), dragonfly-associated mastrevirus (DfasMV), Eragrostis minor streak virus (EMSV), Eragrostis streak virus (ESV), maize streak virus (MSV), Miscanthus streak virus (MiSV), oat dwarf virus (ODV), Sporobolus striate mosaic virus (SSMV), sugarcane streak reunion virus (SSRV), sugarcane streak virus (SSV), and wheat dwarf virus (WDV). The tree is rooted using chickpea chlorotic dwarf virus (KY047535) as an outgroup. The sequences obtained in this study are in red while those in black were taken from GenBank.

National de Recherche Agronomique of Côte d'Ivoire, located c. 50 kilometers from SUCAF-CI, was also screened.

All 24 samples were positive for SCSMV. Full length SWSV genome sequences were also assembled from samples SC9 (2826 bp, GenBank Accession No. LC832868), SC10 (2828 bp, LC832867) and SC\_BC38 (2828 bp, LC832944). These sequences had the greatest identity, 93.27, 91.90 and 92.23%, respectively, with an SWSV (MK606500) isolate from Réunion Island (Claverie *et al.*, 2023). Nucleotide identities between SC9 and SC10, SC9 and SC\_BC38 and SC10 and SC\_BC38 were 97.9%, 99.3% and 98.1% respectively, indicating their close relationship. In a maximum-likelihood phylogenetic tree constructed with selected *Mastrevirus* genome sequences available in GenBank, the SC9, SC10 and SC\_BC38 isolates formed a distinct clade, separate from isolates from Réunion Island, Sudan and Barbados, supporting their close relationship and implying a common origin (Figure 2).

PCR with SWSV-specific primers SWSV\_561F and SWSV\_1834R (Boukari *et al.*, 2020) followed by Sanger sequencing with the forward primer (Genewiz, Germany) confirmed the presence of SWSV in samples SC9, SC10 and SC\_BC38 and indicated the presence of SWSV in a

fourth sample, SC6. Samples SC6, SC9, SC10 and SC\_BC38 yielded 878 bp, 1079 bp, 929 bp and 930 bp sequences, respectively, and a BLASTn search showed that the sequences of the isolates shared 88.26–98.02% identity with an SWSV isolate from Réunion Island (MK606500) and 87.47–97.44% identity with isolates NC\_023989, KJ187747, KJ210622 and KJ187774 (Candresse *et al.*, 2014).

To our knowledge, this is the first report of SWSV in sugarcane in Côte d'Ivoire and urgent action is required to protect this crop that is so important to the country's economy. Further work is required to determine the contribution of SCSMV and SWSV to disease aetiology and to determine the cause of the peculiar symptoms affecting sample SC\_BC38.

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