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## NEW DISEASE REPORT

# First report of *Sugarcane bacilliform Guadeloupe A virus* and a novel badnavirus infecting sugarcane (*Saccharum officinarum*) in Côte d'Ivoire

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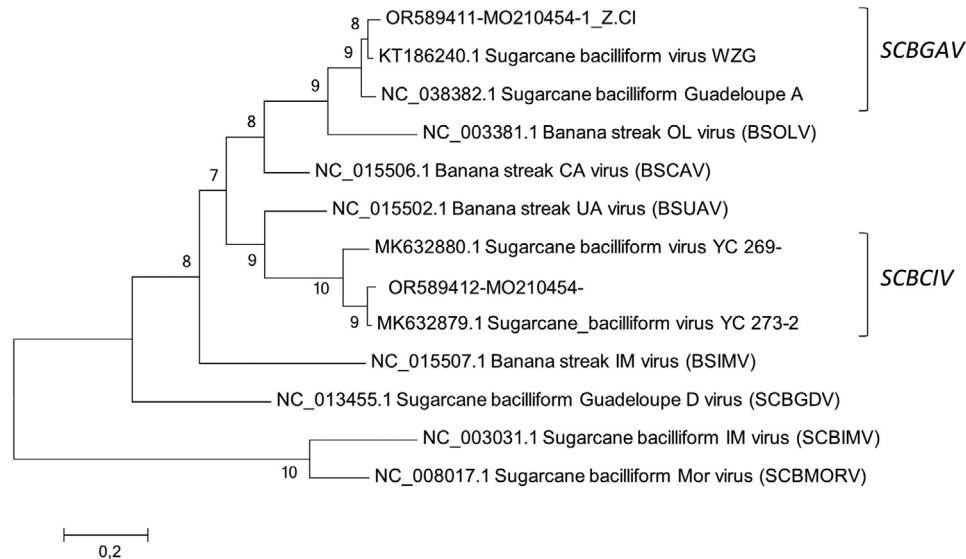
A sugarcane sample presenting typical symptoms of *Sugarcane streak mosaic virus* (SCSMV), was collected in the Zuénoula area, Côte d'Ivoire, in April 2022. After total nucleic acid extraction and ribodepletion, the sample was submitted to Illumina paired-end 2×150 sequencing. After contig assembly and Blastn comparison with GenBank sequences, contigs of SCSMV were obtained, however two other contigs had high identity with badnaviruses. By extension of the initial contigs with Geneious 8.1.9, two complete circular sequences were obtained, presenting typical badnavirus organisation with three putative ORFs. One badnavirus (MO210454-1\_Z.CI, 7445 nt, GenBank Accession No. OR589411), shared 96% nt identity with isolate WZG (KT186240) of *Sugarcane bacilliform Guadeloupe A virus* (SCBGAV) (Muller et al., 2011), the first detection of this virus in Côte d'Ivoire and in Africa. The second isolate (MO210454-2\_Z.CI, 7679 nt, acc. OR589412), shared <75% nt identity in the whole genome with known badnaviruses. The most closely related was *Banana streak UA virus* (NC\_015502, 72% identity).

A criteria for species demarcation in the badnaviruses is >20% nucleotide sequence difference in the polymerase (RT + RNase H) region. In this region, as in the whole genome, MO210454-1\_Z.CI shared 94 to 96% identity with isolates of SCBGAV (KT186240 and NC\_038382). MO210454-2\_Z.CI had 97% and 89% identity, respectively, with the partial sequence of two uncharacterised sugarcane bacilliform virus isolates, YC 273-2 and YC 269-3 (MK632879 and MK632880), collected from sugarcane in China in 2017. It shared less <80% identity with *Banana streak UA virus* (NC\_015502) and the tentative badnavirus *Banana streak CA virus* (NC\_015506), and <75% identity with the other badnaviruses (Figure 1). Thus, MO210454-2\_Z.CI is a tentative novel badnavirus species, also present in China, for which we propose the name *Sugarcane bacilliform Côte d'Ivoire virus* (SCBCIV).

To test the prevalence and diversity of these viruses in Côte d'Ivoire, 106 samples collected in the Zuénoula and Borotou-Koro

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**FIGURE 1** Maximum likelihood tree based on a 579 nt fragment in the RT/RNase H region of two sugarcane badnaviruses from Côte d'Ivoire and 11 from recognised or putative badnavirus species. Sequence alignments were performed with MAFFT (<https://mafft.cbrc.jp/alignments/software/>). Tree reconstruction was performed with MEGA6, using the GTR+G+I substitution model selected with MEGA6. Bootstrap values ( $n = 500$  bootstraps)  $>50\%$  are indicated for each node. Scale bar represents a genetic distance of 0.2.

**TABLE 1** Detection of badnaviruses in sugarcane samples from the Zuenoula and Borotou Koro production areas

Locality	Collection year	Number of samples	Number of positive samples
Zuénoula	2018	15	1
	2020	11	2
	2022	11	4
	2023	23	12
Borotou-Koro	2019	25	0
	2020	11	5
	2022	10	6
TOTAL		106	30

sugarcane production sites between 2018 and 2022 were analysed. Some of these plants had accentuated yellowing on the main vein but this symptom appeared on plants that tested positive and negative for badnavirus subsequently. (Figure 2). Total DNA was extracted as described by Gilbertson et al. (1991). Two primers Badna-F 5'-CCATTTGGTYTGAARAATGCTCC-3' and Badna-R 5'-TCCTCCCATCCNTCCATRCAACC-3', were designed based on Yang et al. (2003) targeting the RT/RNase H region, and 30 samples (28.3%) were positive (Table 1). The 17 samples with strongest PCR amplification were digested with HindIII. Based on the sequences available for MO210454-1\_Z.CI and MO210454-2\_Z.CI, fragments of 370

nt + 190 nt were expected for SCBGAV and 300 nt + 260 nt for SCBCIV. Sixteen samples had profiles of SCBGAV, and one sample had a mixed infection of SCBGAV and SCBCIV. Five samples with a SCBGAV profile were Sanger sequenced (Gensocreen, France). These five isolates shared 93.5–98.8% identity between themselves and with MO210454-1\_Z.CI and other SCBGAV isolates, showing that they were the same species and that the intraspecific diversity of the virus in Côte d'Ivoire is as high as between different countries (data not shown). SCBGAV seems to be more prevalent than SCBCIV in Cote d'Ivoire. Further studies are required to estimate the prevalence and impact of badnaviruses in Côte d'Ivoire.



**FIGURE 2** Symptoms on sugarcane plants which were collected for badnavirus testing

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