



Occurrence of satellite RNAs associated with *Cucumber mosaic virus* isolated from banana (*Musa* sp.) in Ivory Coast

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Cucumber mosaic virus (CMV; genus *Cucumovirus*, family *Bromoviridae*) was identified in mosaic-diseased banana (*Musa* sp.) in all banana-growing areas including Ivory Coast with an incidence ranging between 5 and 25% (Aka *et al.*, 2009). CMV often encapsidates subviral non-coding RNA molecules known as satellite RNAs (satRNAs) (Feng *et al.*, 2012). From March to July 2010 and June to August 2011, a total of 260 leaf samples showing mosaic symptoms (Fig. 1) were collected in seven major dessert banana (AAA genome) growing areas of Ivory Coast located in Agboville, Azaguié, Grand-Bassam, Tiassalé, Dabou, Abengourou and Aboisso. The presence of CMV was confirmed in symptom-bearing samples by double antibody sandwich (DAS)-ELISA using CMV polyclonal antibodies (CMV-DTL/ToRS, LOEWE Biochemica GmbH, Germany). A total of 248 out of 260 (95.3%) banana leaf samples collected in the seven locations reacted positively to CMV polyclonal antibodies using DAS-ELISA.

CMV-infected samples were further characterised by reverse transcriptase (RT)-PCR with specific primers designed from the coat protein (CP) gene sequence (Sharman *et al.*, 2000). RT-PCR results confirmed the ELISA results with CMV detected in the seven areas surveyed. SatRNAs associated with CMV isolates were also detected using RT-PCR with a degenerate primer pair (Gafny *et al.*, 1996). A satRNA RT-PCR product of approximately 380 bp in size was obtained from 35 out of 248 CMV isolates. SatRNAs were reported in CMV isolates from six of the seven locations screened. RT-PCR products of the partial CP gene and satRNA associated with one CMV isolate (BM26 and sBM26) were purified using a QIAquick PCR purification kit (Qiagen, Benelux) and sequenced in the forward direction (Macrogen Inc., Seoul, South Korea). The nucleotide sequence of CMV-BM26 (GenBank Accession No. KC189911) shared 95-97% identity with other CMV strains of subgroup IA and that of sBM26 (KC713593) shared 93% identity with necrogenic satRNA variants associated with CMV strains FG (X89004), PG (X86426) and F2 (X86426), but only 85% and 88% identity with satRNAs of CMV strains B1 (M16586) and B2 (M16587) causing respectively chlorosis and attenuated disease in tomato.

To our knowledge, this is the first report of the presence of satRNA

associated with CMV in Ivory Coast. SatRNAs can have different effects on CMV replication, pathogenesis, and symptom expression, depending on the host plant and the CMV strain (Feng *et al.*, 2012). Furthermore because CMV is one of the most widespread plant viruses in the world with an extensive host range of about 1200 species (Jacquemon, 2012), more work is needed to assess the effect of satRNAs on the pathogenicity of CMV in Ivory Coast.

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Figure 1

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