



Occurrence of cassava brown streak disease and associated *Cassava brown streak virus* and *Ugandan cassava brown streak virus* in the Comoros Islands

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Cassava brown streak disease (CBSD) has emerged as the most important viral disease of cassava (*Manihot esculenta*) in Africa and is a major threat to food security. The expanding CBSD epidemic in East and Central Africa is caused by two ipomoviruses (family *Potyviridae*), *Cassava brown streak virus* (CBSV; Monger *et al.*, 2010) and *Ugandan cassava brown streak virus* (UCBSV; Winter *et al.*, 2010). In 2014, symptoms of yellowing on leaves and brown necrotic rot on tuberous roots on different cassava landraces on the west coast of Mayotte (Maoré) were associated with CBSD and UCBSV (Roux-Cuvelier *et al.*, 2014). Similar symptoms were observed in April 2015 in the north of Mayotte and in July and September 2016 in the three other islands of the Comoros archipelago: Grande Comore (Ngazidja), Anjouan (Ndzuwani) and Mohéli (Mwali) (Figs. 1). To evaluate the disease epidemic in the south-western Indian Ocean islands and to verify the identity of the causal agents, symptomatic leaf samples of 67 affected plants were collected and tested.

Total RNA was extracted from these samples using the RNeasy Plant Mini Kit (Qiagen, France). For the detection of cassava brown streak viruses, two-step RT-PCR was performed using the CBSDDF2 and CBSDDR primers (Mbanzibwa *et al.*, 2011). These primers were designed for simultaneous specific detection of CBSV and UCBSV (amplicons of 344 and 440 bp, respectively). RT-PCR products of the expected sizes for CBSV and UCBSV were obtained for 31 and 14 samples, respectively (Table 1). To confirm the diagnosis, the RT-PCR products were directly and bi-directionally sequenced and contigs assembled using DNA Baser (Heracle BioSoft, Romania). Thirty-seven nucleotide sequences were obtained from the 45 RT-PCR positive samples (GenBank Accession Nos. MF948187-MF948223; Table 1). Twelve sequences of 374 bp showed the highest nucleotide identity (91-93%) with an isolate of UCBSV from Mayotte (LN611675). The other 25 sequences of 280 bp showed the highest nucleotide identity (96-99%) with isolates of CBSV from Uganda, Kenya and Tanzania (KJ606250, LT560330 and GU563322). A phylogenetic reconstruction with publicly available complete genome sequences of cassava brown streak viruses confirmed that CBSV and UCBSV isolates from Grande Comore, Anjouan, Mohéli and Mayotte are genetically related to isolates from East Africa (MEGA6; Tamara *et al.*, 2013; Fig. 3). Altogether, these results demonstrate that CBSD epidemic has reached the four islands of the Comoros archipelago and as in East and Central Africa the disease is caused by two ipomoviruses, CBSV and UCBSV.

This is the first report of CBSD in Grande Comore, Anjouan and Mohéli which demonstrate the expanding epidemic of CBSD in the south-western Indian Ocean islands. Given that cassava is an important staple food in the Comoros archipelago and Madagascar, this report is of great significance for managing the health of cassava in this region, and warrants urgent attention from regulatory institutions.

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Figure 1



Figure 2



Figure 3



Figure 4

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