



First report of cassava brown streak disease and associated *Ugandan cassava brown streak virus* in Mayotte Island

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In November 2013, symptoms of yellowing on leaves and brown necrotic rot on tuberous roots (Fig. 1) were observed on different cassava landraces (*Manihot esculenta*) in Dembeni on Mayotte Island, a French Overseas Department in the southwest Indian Ocean. The symptoms, similar to the cassava brown streak disease described in East Africa, suggested the possible involvement of cassava brown streak viruses (Mbanzibwa *et al.*, 2011). The expanding cassava brown streak disease epidemic in East Africa is caused by two ipomoviruses, *Cassava brown streak virus* (CBSV; Monger *et al.*, 2010) and *Ugandan cassava brown streak virus* (UCBSV; Winter *et al.*, 2010). To verify the identity of the causal agent, symptom-bearing leaf samples of 17 affected plants were collected in March and June 2014.

Total RNA was extracted from these samples using the RNeasy Plant Mini Kit (Qiagen, France). For the detection of cassava brown streak viruses, a two-step RT-PCR using CBSDDF2 and CBSDDR primers was used (Mbanzibwa *et al.*, 2011). These primers were designed for simultaneous virus-specific detection of CBSV and UCBSV (amplicons of 344 bp and 440 bp, respectively). RT-PCR products of the expected size for UCBSV were obtained for 11 samples. To confirm the diagnosis, the RT-PCR products were directly and bi-directionally sequenced and contigs assembled using DNABaser (Heracle BioSoft, Romania). Sequences of 376 bp from eight of the 11 samples were obtained which had 99-100% nucleotide identity (MEGA6; Tamura *et al.*, 2013) (EMBL Accession Nos. LN611671 to LN611678; Table 1). The sequences showed the highest nucleotide identity (86%) with isolates of UCBSV from Uganda and Malawi (FN434109; FN433932) and 85% with an isolate of CBSV from Mozambique (FN434436). A phylogenetic reconstruction with publicly available complete genome sequences of cassava brown streak viruses confirmed that the Mayotte isolates are genetically more related to UCBSV isolates than to CBSV isolates from East Africa, and represent a separate lineage that appears to be almost intermediate between current isolates of CBSV and UCBSV (MEGA6; Fig. 2). This is the first report of cassava brown streak disease in Mayotte. Given that cassava is a 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.

Acknowledgements

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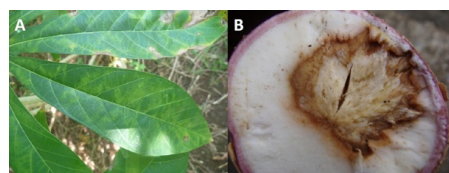


Figure 1

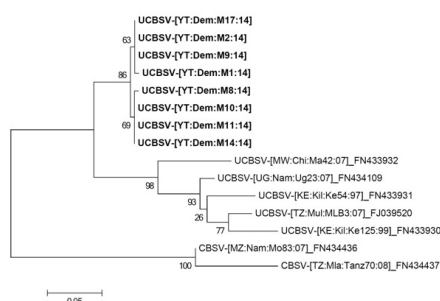


Figure 2

Table 1. Geographical origin of cassava samples presenting cassava brown streak symptoms and description of the Ugandan cassava brown streak virus (UCBSV) isolates.

Sample ID	Date of sampling (dd/mm/yyyy)	Island	Locality	GPS coordinates Latitude Longitude	UCBSV isolates Accession	EMBL accession N°
M1	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M1:14]	LN611671
M2	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M2:14]	LN611672
M8	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M8:14]	LN611673
M9	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M9:14]	LN611674
M10	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M10:14]	LN611675
M11	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M11:14]	LN611676
M14	18/06/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M14:14]	LN611677
M17	13/03/2014	Mayotte	Dembeni	-12.842800 45.181932	[YT-Dem-M17:14]	LN611678

*each sample correspond to a distinct leaf from a different plant

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