Disease Note

Diseases Caused by Viruses

First Report of Banana Bunchy Top Virus in Banana (*Musa* spp.) and Its Eradication in Togo

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Funding: This research was supported by the CGIAR Research Program on Roots, Tubers and Bananas (CRP-RTB) as part of the grant "The ALLIANCE for Banana Bunchy Top Disease Control in Africa". Plant Dis. 00:00, 2020; published online as https://doi.org/10.1094/PDIS-03-21-0473-PDN. Accepted for publication 23 April 2021.

Banana (including plantain; *Musa* spp.) is a vegetatively propagated semiperennial crop in fields and backyard gardens in Togo. Banana bunchy top disease (BBTD), caused by banana bunchy top virus (BBTV, genus *Babuvirus*), is the most economically important viral disease; infection with it causes severe stunting and production losses of 90 to 100% within two seasons (Kumar et al. 2015). The virus is spread by banana aphid, *Pentalonia nigronervosa*, and through vegetative propagation from infected sources. BBTV occurrence was first reported in West Africa in 2011, with confirmation in the Republic of Benin (Lokossou et al. 2012) and in Nigeria in 2012 (Adegbola et al. 2013). A regional alliance (https://www.bbtvalliance.org/) has been established for BBTV surveillance through frequent surveys in countries neighboring those affected, such as Togo. The surveys conducted in September 2018 in banana growing areas in Togo revealed plants with typical symptoms (severe stunting, bunchy growth with shortened petioles with chlorotic streaks and yellow leaf margins) in three banana fields. Locations were Tsévié, Préfecture de Zio, (6.44°N, 1.21028°E), Lilicope, Préfecture de Zio in Maritime region (6.56583°N, 1.18639°E), and Amoutchou, Préfecture de l'Ogou in Plateaux region (7.3775°N, 1.17472°E). Leaf samples were collected from symptomatic (n = 8) and asymptomatic plants (n = 30) and used for DNA extraction followed by a polymerase chain reaction (PCR) for BBTV detection to amplify a ~240-bp sequence of DNA-R encoding for the core replicase gene (Mansoor et al. 2005). All samples from symptomatic plants (n = 8) tested positive, and asymptomatic plants were negative. To ascertain virus identity, the 240-bp PCR product was purified and sequenced in both directions. A BLAST search of the sequence (NCBI GenBank accession no. MK073116) revealed 99% identity with DNA-R sequences of BBTV isolates from Africa (e.g., JQ437549-Benin, JN290301-Nigeria). Further analysis of the 240-bp nucleotide sequence with maximum-likelihood phylogenetic analysis using MEGA-X software grouped the BBTV isolate with sub-Saharan African subclade of the South Pacific group (Kumar et al. 2015). To further confirm the virus identity, two samples from symptomatic (PCR positive) and asymptomatic (PCR negative) plants from Tsévié were tested by TAS-ELISA using a BBTV ELISA reagent set (cat. no. SRA24700-1000, Agdia, France) following the manufacturer's protocol. Only samples from two symptomatic plants that were positive in PCR reacted positively in TAS-ELISA; asymptomatic plants were negative. BBTV was not observed in any of the 22 locations surveyed as a follow-up in banana producing areas. To our knowledge, this is the first report of BBTV infecting banana in Togo. The plants detected in the three sites were eradicated in the follow-up action implemented by the alliance team together with the Direction de la Protection des Végétaux of Togo. Follow-up surveys were conducted in the same regions in 2019 and 2020 to ensure disease-free status in these sites and other banana producing regions in Togo. Efforts have been made to raise awareness about BBTD recognition, diagnosis, and eradication. To the best of our knowledge this is the first case of rapid detection and eradication of BBTV in a country in sub-Saharan Africa. This study illustrates the importance of regular surveillance for early detection of invasive virus threats and the value of rapid eradication to contain viruses before spread and establishment in a new territory.

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The author(s) declare no conflict of interest.

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Keywords: viruses and viroids, diagnostics, etiology, pathogen detection, pathogen diversity

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