Subscribe Free alerts RSS

plant disease

Editor-in-Chief: Alison E. Robertson
Published by The American Phytopathological Society

Posted online on 9 May 2017.

https://doi.org/10.1094/PDIS-03-17-0315-PDN

DISEASE NOTES

First Report of *Maize yellow mosaic virus* Infecting Sugarcane (*Saccharum* spp.) and Itch Grass (*Rottboellia cochinchinensis*) in Nigeria

A. Yahaya, Department of Biological Sciences, Ahmadu Bello University, Zaria, Kaduna State, Nigeria; **M. Al Rwahnih**, Department of Plant Pathology, University of California, Davis; **D. B. Dangora**, Biological Sciences, Ahmadu Bello University, Zaria, Kaduna State, Nigeria; **L. Gregg**, Texas A&M AgriLife Research and Extension Center, Weslaco, TX 78596; **M. D. Alegbejo**, Department of Crop Protection, Ahmadu Bello University, Zaria, Kaduna State, Nigeria; **P. Lava Kumar**, International Institute of Tropical Agriculture (IITA), PMB 5320, Ibadan, Nigeria; and **O. J. Alabi**, Department of Plant Pathology & Microbiology, Texas A&M AgriLife Research and Extension Center, Weslaco, TX 78596.

During routine surveys conducted from February to July 2015 in the northern guinea savannah region of Nigeria, sugarcane and itch grass (*Rottboellia cochinchinensis*) plants showing virus-like mosaic symptoms were encountered in farmers' sugarcane fields in Kaduna State. Symptomatic leaf tissue samples from five randomly selected plants (sugarcane = 4; itch grass = 1) were dried and stored under $CaCl_2$ at room temperature then shipped to Texas A&M AgriLife Research and Extension Center, Weslaco, TX, with USDA-APHIS-PPQ permit (P526P-14-04321) for further analysis. The MagMAX-96 viral RNA isolation kit (Thermo Fisher) was used to isolate total nucleic acid (TNA) from each sample and from a sample subset consisting of pooled leaf tissue materials from both plants. TNA aliquot from the pooled sample was subjected to ribosomal RNA depletion and cDNA library construction using a TruSeq Stranded Total RNA with Ribo-Zero Plant kit (Illumina), then sequenced on the Illumina NextSeq 500 platform. The raw high-throughput sequencing (HTS) reads were analyzed as previously described (Alabi et al. 2015), generating ~43.5 million Illumina reads (76 nucleotides [nt] in length), of which 31,486 de novo assembled

reads mapped to *Maize yellow mosaic virus* (MaYMV; genus *Polerovirus*; family *Luteoviridae*) along with reads mapped to *Sugarcane mosaic virus* (data not shown). Assembly of the sequence reads (CLC Genome Assembler, Qiagen) yielded 5,566 nt long near complete (~99%) genome of MaYMV (KY684356) that was 95 to 97% identical and phylogenetically related to corresponding sequences of MaYMV isolates available in GenBank (KU291099–108). To further confirm the occurrence of this virus in source samples, TNA from individual samples were subjected to two-step reverse transcription (RT)-PCR using the Pol-G-F/Pol-G-R primer pair (Knierim et al. 2010). The expected ~1,100 bp DNA band specific to a region encompassing partial P1-P2 fusion protein and coat protein genes of luteovirids was amplified from three of the five samples (sugarcane = 2; itch grass = 1). The DNA fragment from one sugarcane and the itch grass sample were cloned individually into the pCR2.1 TOPO-TA vector (Life Technologies, Carlsbad, CA) and two independent clones per amplicon sequenced bidirectionally. Pairwise comparisons of sequences from both samples revealed that they shared 99 to 100% nt identity with each other and 97 to 99% identity with the corresponding MaYMV sequences derived by HTS in this study (KY684356), and those retrieved from GenBank (KU291099–108). They also shared 86, 79, and 61% nt identities, respectively, with corresponding sequences of *Barley virus G* (KT962089), *Maize yellow dwarf virus*-RMV (KC921392), and *Sugarcane yellow leaf virus* (AF157029). MaYMV is a recently characterized tentative member of the genus *Polerovirus* reported from maize in China (Chen et al. 2016). Therefore, our results represent, to the best of our knowledge, the first report of MaYMV in sugarcane and itch grass worldwide and the first report of the virus in an African country. The occurrence of MaYMV in these perennial crop and pernicious weed host have implications for disease epidemiology since both plant species could serve as green bridges for virus perpetuation in cereal production systems.

***References*:**

Alabi, O. J., et al. 2015. Plant Dis. 99:1656. [Abstract] [ISI]

Chen, S., et al. 2016. Viruses 8:120. [CrossRef] [ISI]

Knierim, D., et al. 2010. Plant Pathol. 59:991. [CrossRef] [ISI]