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DISEASE NOTE

First report of maize-associated umbra-like virus in maize in Brazil

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To investigate the virome in maize plants, sixteen maize leaf samples with viral symptoms of yellow stripes from three Brazilian locations (Riacho Fundo/DF, Juazeiro/BA, and Uberlândia/MG) were pooled, and viral particles were semi-purified via differential centrifugation and a 20% sucrose cushion step. Semi-purified virus from gramineous plants showing yellow stripes (eight plants of *Brachiaria* spp. and twelve plants of *Panicum* spp. from Campo Grande, MS, Brazil) was also prepared using the same method aiming to investigate viruses associated with maize plants. Total RNA from two pooled samples was extracted using the Quick-RNA Plant Miniprep Kit (Zymo Research) and sequenced together by high-throughput sequencing (HTS) on the Illumina NovaSeq6000 platform, generating 10 G reads of 150 nt paired-ends for metagenomic analysis. The sequences were analyzed using bioinformatics methods as described by Blawid et al. (2017). A 3,006-nt contig, which had the higher identity with maize-associated umbra-like virus (MaULV) was assembled from 3,695 reads, with a coverage of 182.4x. The genomic sequence of the MaULV isolate (LC851045) showed 97.41% identity with the Mexican isolate (OK018180) and 95.52% with the Ecuadorian isolate (OM937759). The same maize leaf samples showing yellow stripes used for the metagenomic study (16 samples) had been individually stored in an ultrafreezer and tested for MaULV by RT-PCR using the primers, Maize_Umbra_F (CGAAAATACAAGATCCAACCGA) and Maize_Umbra_R (ATCCGTCTGCCTTCAACCTC) targeting the open reading frame 2 of MaULV (593nt long). Total RNA form leaf samples was extracted using the Total RNA Purification kit (Cellco Biotec). cDNA was synthesized with M-MLV RT (Thermo Fisher Scientific) and amplified for PCR (Taq DNA Polymerase, Sinapse Biotecnologia). Two maize samples from Juazeiro (BA) out of 16 were positive by RT-PCR, which were also confirmed by RT-qPCR using the GoTaq® qPCR Master Mix kit (Promega), with the primers Maize_Umbra_qPCR_F (AGCCGTGGAGCAATTGAGTC) and Maize_Umbra_qPCR_R (CATCGACCGACTTCAGCCAA). MaULV was not detected in other gramineous plants used for the metagenomic study. The two MaULV-positive samples were also positive for maize rayado fino virus and maize striate mosaic virus by RT-PCR, showing co-infections. This is the first report of MaULV in Brazil.

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Data availability The genome sequence of MaULV has been deposited in NCBI GenBank database under accession number LC851045.

Declarations

Ethical approval This work does not contain any studies with human participants or animals performed by any of the authors.

Conflict of interest The authors declare that they have no conflict of interest.

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