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DISEASE NOTE

First report of Cucumis melo endornavirus infecting Cucurbitaceae plants in Slovakia

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A symptomatic cantaloupe melon plant (*Cucumis melo* L.) encoded MVU2/21 grown in a garden in Velke Ulany (western Slovakia), showing pronounced chlorotic leaf spots and dwarfed growth was analysed by high-throughput sequencing (HTS). Total RNAs were isolated from apical leaves collected in August 2021. HTS was carried out on an Illumina MiSeq platform and obtained high-quality reads (~26,4 millions, average length 131 nt) were analyzed using CLC Genomics Workbench v.10.1.1 and Geneious v.2020.2.5. BLASTn analysis of *ca*. 24,400 generated contigs revealed a complex viral infection involving watermelon mosaic virus (WMV), zucchini yellow mosaic virus (ZYMV) and Cucumis melo endornavirus (CmEV, family *Endornaviridae*). A 15,075 nt de novo assembled contig (OL957252) corresponded to nearly complete CmEV genome with 97.9% nucleotide identity to NC_029064. Typical genome organisation and CmEV motifs, including three glucosyltransferases (Sabanadzovic et al. 2016), were found in MVU2/21 polyprotein. The MVU2/21 total RNAs were subsequently subjected to RT-PCR using primers reported by Zeng et al. (2020) as well as two newly designed primer pairs: CmE_14443F (5´-TATGCGGTT GACTGGACAGG-3´)/CmE_14931R (5´-TTATGAGCC ACAGCGGTCAC-3´) and CmEV_4145F (5´-CTTGCC TTGAAGGTAGATCG-3´)/ CmEV_4634R (5´-GATTGT CCGCACCGTATAAC-3´). Sanger sequencing of the specific 489, 490 and 710 bp PCR products unambiguously confirmed the HTS data. In order to analyse the potential presence of CmEV in Slovakia, additional leaf samples from melons, cucumbers and squashes from four different localities were tested by RT-PCR using the above primers. Five out of 40 samples collected from different locations and hosts, i.e. melon (MVU1/21), cucumber (UVU1/21, UVU2/21), squash (TPE 2/21) and patison (CPTV6) tested positive for CmEV. Partial genomic sequences of all Slovak isolates amplified using CmEV_4145F/4634R primers (OL957253-OL957257) shared high nucleotide identity to MVU2/21 (97.2–100%). CmEV was previously reported outside Europe (Sabanadzovic et al. 2016; da Costa et al. 2019; Zeng et al. 2020). Our work thus extents data on CmEV geographical distribution and host range.

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Declarations

Research involving human participants and/or animals This article does not contain any studies with human participants or animals performed by any author.

Conflict of interest The authors declare that there is no conflict of interest for this submission.

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