Journal of Plant Pathology
https://doi.org/10.1007/s42161-024-01709-w

DISEASE NOTE

First report of cherry green ring mottle virus in sweet cherries in Slovenia

A. Beber[1] · J. Lamovšek[1] · B. Grubar[1] · I. Mavrič Pleško[1]

Received: 8 April 2024 / Accepted: 16 July 2024

Keywords CGRMV · Robigovirus · Sweet cherry Slovenia · RT-PCR

Cherry is a commercially important fruit tree worldwide. Although the majority of the production in Slovenia still relies on old extensive plantations, new cherry orchards are planted each year. The genus *Robigovirus* consists of five viruses of which four are known to infect sweet cherries including cherry necrotic rusty mottle virus (CNRMV), cherry green ring mottle virus (CGRMV), cherry rusty mottle-associated virus and cherry twisted leaf-associated virus. To check for the presence of CGRMV in sweet cherries, 69 sweet cherry samples were collected in orchards in different regions of Slovenia between 2019 and 2023. Total RNA was extracted as previously described by Virscek Marn et al. 2021. In 2019 RT-PCR was conducted using the OneStep RT-PCR kit (Qiagen) with primer pair CGRMV1 MVM (5′-CCTCATWCACATAGCTTAGGTTT-3′; adapted from Li and Mock 2005)/rob re2 MVM (Virscek Marn et al. 2021) to amplify part of the coat protein gene region. Directly sequenced 792 bp amplicon confirmed the presence of CGRMV in one sample from central Slovenia (MT321352). From 2020 to 2023 four additional samples were found infected with CGRMV using primer pair CGRMV1 MVM/rob re 1 MVM (Virscek Marn et al. 2021) located on the same genome region. Only three sequences were deposited in the NCBI (OM451235, PP421047, PP421048) because two sequences obtained in 2020 were identical (OM451235). Additionally, CGRMV specific primer pair 401 h/401c (Zhang et al. 1998) amplifying part of replicase and triple gene block region was used to confirm CGRMV infection in selected samples and amplicons of expected size were obtained. Slovenian sequences represent two groups based on nucleotide sequence identities of the coat protein gene regions. The nucleotide sequence identities within groups were over 98% and 93.9–94% between groups. The first group consisted of two isolates from an unknown cultivar in different locations in central Slovenia with the first isolate (MT321352) showing 98.9% identity with Bulgarian isolate PV021-54S2 (OP921093) and the second isolate (PP421047) showing 98.6% identity with Polish isolate HI28 (JX468875). Sequences from southwestern (OM451235) and southeastern Slovenia (PP421048) formed another group with 99.2% and 98.9% identitiy with American isolate F (AF533150), respectively. The incidence of CGRMV was relatively low (7%, 5 out of 60 samples). This is the second robigovirus detected in sweet cherry trees in Slovenia after the discovery of CNRMV in 2019 (Virscek Marn et al. 2021).

Acknowledgements This study was founded by The Administration of the Republic of Slovenia for Food Safety, Veterinary and Plant Protection and Slovenian Research Agency (grant No. P4-0072 and P4-0431).

Data availability Additional data concerning the work presented are available on request.

Declarations

Ethical approval Research presented did not involve human participants and/or animals.

Conflict of interest The authors have no relevant financial or non-financial interests to disclose and no conflicts of interest that are relevant to the content of this article.

✉ A. Beber
aljosa.beber@kis.si

[1] Plant Protection Department, Agricultural Institute of Slovenia, Hacquetova ulica 17, Ljubljana 1000, Slovenia

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