Diseases Caused by Viruses

First Report of Raspberry Leaf Mottle Virus Infecting Raspberry in Poland

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The author thanks Mrs. Dorota Starzec for technical assistance.

Funding: This work was performed in the frame of the Polish Ministry of Agriculture and Rural Development multiannual program 2015-2020 “Actions to improve the competitiveness and innovation in the horticultural sector with regard to quality and food safety and environmental protection” (task 2.1). Plant Dis. 105:714, 2021; published online as <https://doi.org/10.1094/PDIS-08-20-1767-PDN>. Accepted for publication 8 October 2020.

Raspberry leaf mottle virus (RLMV), the *Closterovirus* species member of the *Closteroviridae* family, has been associated with raspberry mosaic disease and crumbly fruit disease in red raspberry (*Rubus idaeus* L.) (Martin et al. 2013). RLMV has also been reported infecting blackberry (Jones and McGavin 1998). A survey of virus diseases was conducted from 2016 to 2018 in 34 raspberry commercial plantations in central and southeastern Poland. Leaf samples were randomly collected from 146 plants; among them, 17 plants showed chlorotic spots, vein yellows, mosaic patterns, and deformation of leaves and fruits. RT-PCRs were carried out with pairs of primers specific for RLMV (Tzanetakis et al. 2007), Rubus yellow net virus (RYNV; Jones et al. 2002), black raspberry necrosis virus (Halgren et al. 2007), raspberry vein chlorosis virus (McGavin et al. 2011), raspberry leaf blotch virus (McGavin et al. 2012), and raspberry bushy dwarf virus (RBDV; Mavric Plesko et al. 2009). The pairs of primers CPhF and CPhR (Tzanetakis et al. 2007) as well as 1436F and 1437R (McGavin and MacFarlane 2010) were used to amplify a 452-bp fragment of the coat protein homolog (CPh) gene and a 681-bp of the helicase, respectively. RT-PCR products were obtained for 5/146 from cultivars Malling Promise (MPrOK1 and MPrOK2), Canby (CanKop), Polka (PolKop), and Malling Seedling (MSeWa) in three southeastern Poland plantations. Samples

MPrOK1 and MSeWa were coinfecting with RYNV, and the other three samples were mix-infected with RBDV. Each of these five infected plants showed symptoms of chlorotic spots and mosaic of different intensities, leaf deformation, and reduced growth. The RLMV-specific amplicons were directly sequenced at Genomed company, Warsaw, Poland. The obtained sequences were aligned using ClustalW and were used to query the GenBank database using the BLASTn algorithm. The partial CPh sequences of RLMV isolates from Poland were identical and shared 97.7 and 99% nucleotide (nt) identities with corresponding sequences of RLMV isolates “HCRL Glen Clova” from the United States (DQ357218) and “SCRI stock” from the United Kingdom (FN391551), respectively. However, they shared 99.2% partial CPh amino acid (aa) identity with the corresponding sequences of both reference isolates from GenBank. The representative sequence of PolKop isolate was deposited in GenBank under accession number MT241265. In pairwise comparisons, the partial RLMV helicase sequences derived in this study (MT847633 to MT8347637) were 98.5 to 100% and 99.5 to 100% with each other at the nt and aa levels, respectively. They also shared 98% nt and aa identities with the corresponding sequences of “HCRL Glen Clova.” Considering the low incidence of RLMV in the surveyed area, it can be concluded that the virus is not widespread in Poland. However, the European large raspberry aphid (*Amphorophora idaei* [Börner, 1939]), vector of RLMV (Cadman 1951), is present in Poland, hence the risk of the infected plants serving as inoculum sources for further spread. This is the first report of RLMV infecting red raspberry in Poland.

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The author(s) declare no conflict of interest.

Keywords: raspberry, RLMV, RT-PCR, sequence analysis

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