Disease Note

Diseases Caused by Viruses

First Report of Melon Chlorotic Spot Virus in Cultivated Sorrel (*Rumex acetosa*) in Belgium

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In 2020, symptoms of putative viral origin were observed on 7% of tomatoes in an organic vegetable farm in Belgium (deformed unevenly ripened fruits, vein clearing, mosaic and purple leaves, and stunted plants). The leaves of 20 symptomatic plants were collected, pooled, and screened for viruses using high-throughput sequencing (HTS) technologies on Illumina NextSeq500 following a virion-associated nucleic acid protocol (Temple et al. 2022, Be_SL1). In total, 3,665,498 reads (PE150) were generated. Bioinformatic analyses (de novo assembly, tblastx search on NCBI, and mapping) using Geneious Prime 2020.1.2 revealed the presence of three viruses known to infect tomatoes: Physostegia chlorotic mottle virus (PhCMoV), 547,142 reads mapped to NC_055466; potato virus Y, 4,056 reads mapped to MW595184; and melon chlorotic spot virus (MeCSV), 55 reads mapped to six out of the eight different MeCSV segments (NC_040448 to NC_040455). Tomato plants have already been artificially inoculated by MeCSV (Lecoq et al. 2019), but this detection (confirmed by independent RT-PCR on the pooled sample) is the first one in natural condition on the farm. The high prevalence of symptoms triggered the research of alternative perennial hosts that can serve as a reservoir during intercropping season. One plant of *Rumex acetosa* showing vein clearing (CT-122) was collected in the same greenhouse the year after. Total RNA was extracted, followed by ribodepletion, and analyzed by Illumina HTS using the protocol described in Temple et al. (2022) for Be_GP1. In total, 4,549,721 PE150 reads were obtained, and bioinformatic analyses confirmed the presence of MeCSV (8,816 reads mapped on the eight RNA segments NC_040448 to NC_040455 with an average 96.52% coverage of the reference sequences) and suggested the presence of an unclassified partitivirus. Consensus sequences were extracted for each segment of MeCSV (OQ818038 to OQ818045) and showed between 83 and 87% nucleotide identity with the reference sequences NC_040448 to NC_040455. RNA1 segment was used to design MeCSV-specific RT-PCR primers for detection (MeCSV-125F 5′-TTTAAG GCCAGATCCAGAGGTTC-3′/MeCSV-498R 5′-TGGATGTGACAACCT GGTAGTAC-3′). Thereafter, in July 2022, 42 *R. acetosa* plants were collected in the same greenhouse. Among them, seven plants showed vein clearing, two showed yellowing with necrosis, two exhibited yellowing and vein clearing, and one showed mosaic. The 42 plants were subjected to RNA extraction and RT-PCR for MeCSV and PhCMoV detection. MeCSV was detected in 13 plants (two asymptomatic plants and all the symptomatic plants except the one exhibiting mosaic where PhCMoV was detected). PhCMoV was also detected in three plants with vein clearing, one with yellowing, and one of the two asymptomatic plants infected by MeCSV. Our results report the first detection of MeCSV in *R. acetosa* and the first detection of MeCSV in Belgium. In addition, according to the hierarchical approach for assessing causal relationships in plant virology (Fox 2020), a preliminary association was observed between symptoms and MeCSV detection (6% prevalence on asymptomatic plants and 92% prevalence on diseased plants [in which seven symptomatic samples were not coinfected by PhCMoV]). Symptom causality should be further investigated, but these results are important for disease management because they suggested that cultivated perennial *R. acetosa* may serve as a reservoir for two emergent plant viruses (PhCMoV and MeCSV) (Lecoq et al. 2019; Temple et al. 2022).

References:

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