## New Disease Reports

## First report of *European mountain ash ringspotassociated virus* in *Karpatiosorbus* × *hybrida* in Finland

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We report the first detection of *European mountain ash ringspot-associated virus* (EMARaV) in *Karpatiosorbus × hybrida* in Finland. The host species varies in morphology, containing primary diploid hybrids of *Sorbus aria* and *Sorbus torminalis* as well as stable apomictic and vegetative propagating forms (Sennikov & Kurtto, 2017). Due to the decorative flowers, berries and leaf colouration in the autumn, the hybrid is planted in urban areas as a woody ornamental in the same way as other *Sorbus* species.

We sampled leaf material from six trees of *Karpatiosorbus*  $\times$  *hybrida* cultivated in a public park in the city of Helsinki, Finland, showing chlorotic ringspots, mottle, line patterns, sometimes accompanied by leaf deformation and decline (Figs. 1-4, Table 1). The observed disease resembled symptoms caused by EMARaV in *Sorbus* spp. (von Bargen *et al.*, 2019) and related hybrid species (Grimová *et al.*, 2015). Additionally, we collected samples from a rowan tree (*S. aucuparia*) with chlorotic ringspots on leaves growing adjacently. The rowan was infested by the pear blister gall mite, *Phytoptus pyri*, which is considered to be the vector of EMARaV.

To confirm the presence of EMARaV, we performed RT-PCR from extracted total RNA. We could demonstrate that six Karpatiosorbus × hybrida and the S. aucuparia were affected by an emaravirus by amplification of a 360 bp fragment from the sampled leaf material using generic primers targeting RNA1 (Elbeaino et al., 2013). Additionally, EMARaV-specific RT-PCRs (von Bargen et al., 2019) detected all tested genome segments (RNA2-RNA4 and RNA6) of the virus in the corresponding samples, while none of the genome segments were detectable in a sample taken from a tree of Karpatiosorbus × hybrida without leaf symptoms. By sequencing PCR products amplified from viral RNA1 and RNA4 we could confirm that all seven sampled trees with leaf symptoms were infected by EMARaV. We compared the nucleotide sequences of the partial RNA1 (348 bp) and the complete coding region of RNA4 (699 bp) with reference sequences from GenBank (Table 1). The minimum nucleotide identity was 97.4% (RNA1) and 98.1% (RNA4), respectively, (Table 1) confirming the virus as EMARaV according to the current species demarcation criteria for the genus (Elbeaino et al., 2018). Sequences have been deposited in the European Nucleotide Archive (ENA) and are available under the accession numbers LR811990-LR812003.

This is the first record of EMARaV affecting *Karpatiosorbus* × *hybrida* in Finland. The rowan tree growing adjacently was infected by the virus, with the putative vector *P. pyri* also being found on the tree. Kallinen *et al.* (2009) confirmed the virus to be widespread in rowan in Finland and Grimová *et al.* (2015) demonstrated that EMARaV is graft-transmissible within species of the *Rosaceae*. It is therefore possible that the virus was

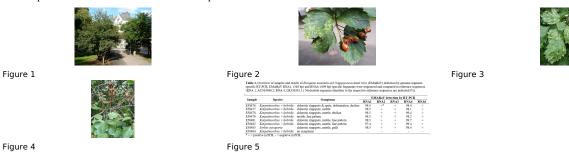
transmitted from the rowan to the *Karpatiosorbus*  $\times$  *hybrida* population by root grafting. However, how the trees in the park in Helsinki acquired the virus remains unknown as their origin and history could not be determined.

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