

Viruses affecting Ash (*Fraxinus* sp.) in Europe – genome organization and geographic distribution of a putative novel emaravirus

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ABSTRACT

European ash (*Fraxinus excelsior*) populations are not only threatened by the dieback disease which is caused by a fungus. Diseased ash trees are also reported to be affected by several viruses such as *Arabidopsis mosaic virus* (ArMV), *Cherry leaf roll virus* (CLR), *Tomato ringspot virus* (ToRSV), *Tobacco ringspot virus* (TRSV), *Tobacco necrosis virus* (TNV), and *Tobacco mosaic virus* (TMV).

Samples from different ash species exhibiting virus-like symptoms were collected in 2016 and 2017 from different locations in Germany and adjacent countries. Diseased ash trees showed leaf deformation, shoestring, mottle, chlorotic, ringspots, spots and blotching. Some trees had a scattered canopy indicating reduced vigor. The virome of 3 sample pools were determined by next generation sequencing (NGS) prepared from symptomatic leaf samples obtained from Switzerland, Norway and Sweden. Scaffolds were assembled from the resulting NGS datasets indicating the presence of known and novel viruses in the analyzed samples. Interestingly, none of the viruses which have been previously reported from *Fraxinus* sp. were found in the scaffolds. In 2 of the NGS sample pools a putative novel emaravirus could be identified. Further analyses enabled the reconstruction of 5 genome segments of the virus. RT-PCR-based confirmation of identified RNA1-RNA5 in collected plant material provides first insight into the distribution of the putative novel emaravirus and allowed the association with observed symptoms.