

# Viruses associated with declining broad-leafed tree species in Europe



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## Outline

The virome of several deciduous tree species exhibiting virus-suspicious symptoms such as chlorotic ringspots, veinbanding and necroses of leaves associated with dieback of twigs and parts of the canopy were determined by a high-throughput sequencing (NGS) approach (RNA-Seq, Illumina).

Analyses of generated sequence contigs identified plant viruses known to affect investigated tree species such as Apple mosaic virus (ApMV), Cherry leaf roll virus (CLRv), Elm mottle virus (EMoV) and European mountain ash ringspot-associated virus (EMARaV).

Further, nearly complete genomes of new, previously unidentified plant viruses could be retrieved from the generated data.

Virus-incidence in sets of symptomatic trees were confirmed by RT-PCR (see tables).

## Emaraviruses



Tree species	Location*	Virus (genome segments)	Samples (n)
<i>Sorbus aucuparia</i>	D, DK, FIN, GB, N, S	EMARaV (4)	44
<i>Quercus robur</i>	D, S	New Emaravirus 1 (4)	52
<i>Acer pseudoplatanus</i>	D	New Emaravirus 2 (6)	15
<i>Populus tremula</i>	S, FIN, N	New Emaravirus 3 (5)	15

\* D = Germany, DK = Denmark, FIN = Finland, GB = Great Britain, N = Norway, S = Sweden

Infection of tree species with the respective Emaravirus correlates with observed symptoms.

## Viruses in birch

Virus	<i>Betula</i> sp. (Berlin, D)	<i>B. pubescens</i> (Rovaniemi, FIN)
CLRv	52/73*	3/3
ApMV	4/73	not tested
ArMV	0/73	0/3
New Badnavirus	22/73	3/3
New Carlavirus 2	11/73	0/3

\* virus infected trees per total trees tested

Mixed infections of birch trees in Berlin with Cherry leaf roll virus (CLRv), Badna- and/or Carlaviruses are the rule and not the exception.

Virus	Elm trees (n)	Location*
EMoV	5	B, BB
New Carlavirus 1	65	B, BB, MP
Mixed infection	3	B, BB
Sampled trees	73	Northern Germany

\* B = Berlin, BB = Brandenburg, MP = Mecklenburg-Pomerania

Mottle and chlorotic ringspots previously attributed to an EMoV infection is closer linked with a new Carlavirus.

## Viruses in elm



The study provides insights into geographical distribution, impact of known and newly identified viruses as well as the occurrence of mixed infections.