

Viruses associated with diseased broad-leaved tree species in Europe

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ABSTRACT

The identification of previously unknown viruses as well as the determination of mixed infections with several different plant viruses is a prerequisite to determine the impact of viruses on long-living forest trees as well as woody species dominating the urban green space (Büttner et al. 2013). High-throughput sequencing technologies enable the characterization of virus communities affecting important diseased broad-leaved tree species.

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 High-throughput sequencing (NGS, RNA-Seq, Illumina). Analyses of NGS-generated sequence contigs identified plant viruses known to affect investigated tree species such as *Cherry leaf roll virus* (CLRv), *Elm mottle virus* (EMoV) and *European mountain ash ringspot-associated virus* (EMARaV). Further, nearly complete genomes of novel plant viruses could be identified in diseased tree species. Thus, NGS contributed to the discovery of previously unknown viruses belonging to the genera *Badna*-, *Carla*-, and *Emaravirus*, respectively, infecting important tree species of European forests and urban stands. Virus-incidence were confirmed by virus-specific RT-PCR in diseased trees of investigated species. Results provide first insights into geographical distribution, impact of known and newly identified viruses as well as the occurrence of mixed infections in ash, aspen, birch, elm, mountain ash, maple, and oak.

Reference

Büttner, C., von Bargaen S., Bandte, M., Mühlbach, H-P. (2013): chapter 3: Forest diseases caused by viruses. In: Infectious forest diseases. Gonthier P., Nicolotti G. (eds), CABI, 50-75.