

Viruses associated with declining deciduous tree species

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ABSTRACT

Until today virus diseases of trees are not well investigated and research focusing on occurrence and impact is underrepresented compared to other diseases of broad-leaved perennials (Büttner *et al.* 2013). High-throughput sequencing technologies enable the characterization of virus communities affecting important diseased broad-leaved tree species. 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 habitats.

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 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 new, previously unidentified plant viruses could be retrieved from the generated data. NGS contributed to the discovery of six previously unknown viruses belonging to the genera *Badna*-, *Carla*-, and *Emaravirus*, respectively, infecting important tree species of European forests and urban stands. Virus-incidence in birch, elm, maple, poplar, and oak could be confirmed by virus-specific RT-PCR in diseased trees providing first insights into geographical distribution, impact of known and newly identified viruses as well as the occurrence of mixed infections.

References

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