

S3-O3. Application of High-throughput-sequencing for detection of known and identification of novel plant viruses in broad-leaved forest trees and woody species of urban green space. *Susanne von Barga*¹, Marius Rehanek¹, Thomas Gaskin¹, Max Tischendorf¹, Maria Landgraf¹, Martina Bandte¹, Thierry Candresse², Armelle Marais², Chantal Faure², Thierry Wetzel³, Dag-Ragnar Blystad⁴, Markus Rott^{1,5}, Juliane Langer¹, Jenny Roßbach¹, Artemis Rumbou¹, Michael Kube⁶, Marleen Botermans⁷, Risto Jalkanen⁸, Jean-Sebastien Reynard⁹ and Carmen Büttner¹

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Supported by the COST-DIVAS action FA1407 we successfully incorporated High-throughput sequencing (HTS, NGS) in our diagnostic pipeline to detect known and to identify novel plant viruses in broad-leaved tree species predominating in European forests and urban green space. The viromes of tree species exhibiting suspicious virus-like symptoms of leaves such as chlorotic ringspots, veinbanding and necroses associated with dieback of twigs and parts of the canopy were explored by Illumina RNA-Seq, from total RNA, dsRNA and partially purified virus particles. Bioinformatic analyses of HTS-data identified plant viruses known to affect the investigated tree species such as Apple mosaic virus (ApMV), Cherry leaf roll virus (CLRV), Elm mottle virus (EMoV), or European mountain ash ringspot-associated emaravirus (EMARaV). Further, previously uncharacterized plant viruses could be identified from the generated data. HTS thus contributed to the discovery of unknown viruses belonging to the families Betaflexi-, Caulimo-, Fimo-, and Rhabdoviridae as well as members of unassigned genera. Virus presence in ash, aspen, birch, elm, maple, and oak could be confirmed in diseased trees by virus-specific RT-PCR assays. These results provide first insights into the geographical distribution of known and newly identified viruses as well as on the occurrence of mixed infections.

HTS proved to be an essential diagnostic tool to initiate the determination of current and future impact of plant viruses on important broad-leaved tree species of the forest and urban green spaces. Further studies are required to confirm these plant viruses as the causal agents of the observed diseases and to characterize viruses in more detail the newly identified viruses in order to estimate their epidemiological significance and impact.

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