

A complex virome identified in declining birch

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ABSTRACT

The application of bioinformatic tools on NGS data of birch enables to identify new plant viruses continuously in birch samples from different origin. The virome of birch seems to be more complex and heterogenic as compared to other investigated deciduous trees and this is in some way special. The virome includes DNA as well as RNA viruses with their specific characteristics and they consequently influence the host plants diverse. In 2015 and 2016 the incidence of 4 viruses (CLRV, ApMV, Carlavirus and Badnavirus (Rumbou et al. 2017) of the heterogenic virome of birch was investigated in symptomatic leaves in Berlin (Landgraf et al. 2017). Different combinations of viruses in single and mixed infection were detected by RT-PCR. Some viral combinations are more distinct distributed in Berlin birch than others, so that the question of their relevance in birch and the observed “leaf roll disease” poses. The picture of heterogeneity is also known from the leaf symptomatology in virus containing birch leaves. As the correlation of symptoms and viral infection is not shown yet for the mixed infections, it is unknown if the complexity of the virome is causative for the complicated symptomatology. Epidemiology and pathogenicity of the new discovered viruses as well as species specificity, life cycle, mode of transmission, host plant range and phylogeny are totally unknown and have to be investigated within the next years.

References:

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