

Deciphering the complex ecology of plant and mycoviruses in wild grasses by analysing the virome associated with individual plants

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Before the domestication of plants, plant viruses were co-evolving with wild plants growing in mixed species communities, thereby potentially resulting in complex interactions (antagonism, commensalism, mutualism). The development of agriculture deeply modified ecosystems, altering the dynamics of virus-plant pathosystems and accelerating the rate of virus evolution and emergence. High-throughput sequencing technologies have now enabled more comprehensive studies of viromes at different scales, from individual plants to entire ecosystems, offering insights into virus ecology within agro-ecological landscapes.

Recent virome studies revealed diversified and largely unknown viral communities in natural ecosystems, with high rates of co-infection and a high abundance of persistent or cryptic viruses. However, many studies focused on plant pools, showing the viral richness but missing important ecological information such as viral prevalence, co-infection and spatial distribution of virus infection. In this context, we conducted a study in the Natural Park “Burdinale-Mehaigne” (Belgium) to explore virus diversity and ecology in individual plants and pooled samples of two grass species, *Lolium perenne* and *Poa trivialis*, from pastures and high biological value grasslands.

Using a virion-associated nucleic acids (VANA) metagenomic approach on 143 individual plants, the study found for both host species a higher virus prevalence (79%) in pastures, dominated by phytoviruses, whereas grasslands showed lower virus prevalence (48%), with a predominance of mycoviruses. High prevalence of co-infected plants was observed but with low virus accumulation. For yellow dwarf viruses (B/CYDVs), comparison of sequenced genomes within and between plants suggested a high genetic diversity, and a novel BYDV-like species was identified in *Poa trivialis*. Additionally, *Lolium perenne* was identified as a key virus reservoir, hosting up to 25 different virus species compared *Poa trivialis* infected by up to 16 viruses. These findings underscore the significant role of wild plant communities as virus reservoirs, influencing virus ecology across both natural and agricultural landscapes.

Key-words : Virus ecology, wild grasses, virus metagenomics