Exploring the diversity of mycoviruses in grapevine associated fungi

Núria Fontdevila Pareta*, Mia Messaadi*, Nicole Lecoultre, Katia Gindro, Olivier Schumpp
Agroscope, Plant Protection Department 1260, Nyon, Switzerland
*Co-first authors

Mycoviruses in grapevine cultivation

Fungal pathogens represent a significant challenge to grapevine cultivation, causing considerable economic losses worldwide. To mitigate reliance on synthetic fungicides, the development of alternative control strategies is crucial. Mycoviruses offer a promising approach for the biological control of fungal pathogens. By inducing hypovirulence in specific fungal species, they effectively reduce disease severity and present a sustainable solution for vineyard management.

Objectives

- Identify viruses within endophytic fungal communities [1] and assess their prevalence, focusing on both RNA-based genomes and the less common DNA viruses, which exhibit a higher potential for horizontal transmission.
- Analyze the dynamic fungal collection curated at Agroscope Changins (www.mycoscope.ch) to uncover novel or previously characterized mycoviruses.

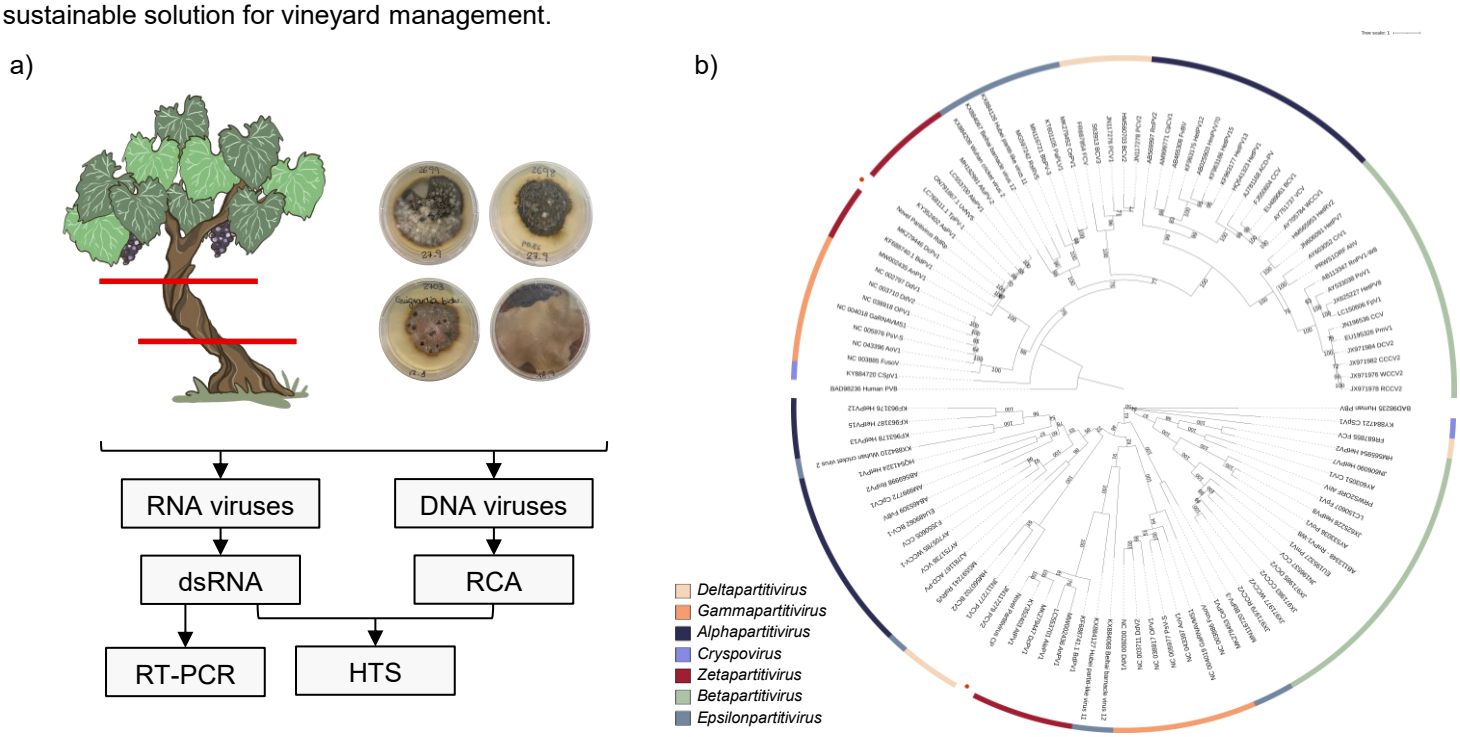

Figure 1. a) Screening strategy implemented to study the diversity of DNA and RNA mycoviruses from a collection of fungal strains kept Agroscope Changins and from endophytic fungal communities. RNA mycoviruses were detected by extracting dsRNA from fungal strains and visualizing the dsRNA profiles on a 0.7% agarose gel. The selected dsRNA profiles were then purified and analyzed by high-throughput sequencing (HTS). Moreover, prevalence of known RNA mycoviruses was studied by RT-PCR. On the other hand, DNA mycoviruses were targeted by amplifying circular DNA from total nucleic acid extracts by rolling circle amplification (RCA) followed by HTS. **b)** Maximum likelihood (ML) phylogenetic tree (rtREV+F+R5 substitution model, MAFFT alignment, 1000 bootstraps) based on the alignments of the RdRp (above) and CP (below) amino acid (aa) sequences of members of the *Partitiviridae* family including the putative novel virus (highlighted with a red dot). The phylogenetic analyses were performed using the Galaxy server and visualized with the iTOL v7 tool. Sequences of Human picobirnavirus were used as outgroups to root the tree. Bootstrap values are shown for each branch, and colored labels represent the genus assigned to each sequence as shown in the legend on the left.

Results and conclusions

- The prevalence of polymycoviruses, including Cladosporium ramotenellum polymycovirus 1 (CrPMV1) (1/27, 3.7%) and Cladosporium cladosporioides polymycovirus 2 (CcPMV2) (2/27, 7.4%), was found to be low in the tested endophytic fungal strains.
- A putative novel viral species was identified through HTS in *Alternaria destruens*. Phylogenetic analysis of the reconstructed genome suggests its classification within the newly proposed genus *Zetapartitivirus* (Figure 1b). According to the proposed demarcation criteria for this genus [2], the reconstructed genome represents a novel zetapartitivirus, closely related to Alternaria alternata partitivirus 1 (AtPV1).
- Additionally, Alternaria alternata chrysovirus 1 (AaCV1) and Sclerotinia sclerotiorum mitovirus 4 (SsMV4) were detected by HTS in *Alternaria destruens*. Notably, this marks the first report of SsMV4 in this host.
- No DNA mycoviruses were detected in *Botrytis cinerea* (0/81) and *Phyllosticta ampelicida* (Engelm.) (0/10) from the fungal collection, highlighting the very limited prevalence of such viruses in the environment.

References

1.Jaccard, A., et al., *New viruses of Cladosporium sp. expand considerably the taxonomic structure of Gammapartitivirus genus.* Journal of General Virology, 2023. **104**(8).
2.Gilbert, K.B., et al., *Hiding in plain sight: New virus genomes discovered via a systematic analysis of fungal public transcriptomes.* PLOS ONE, 2019. **14**(7): p. e0219207.

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