

# Fungal RNA viruses: Unexpected complexity affecting more than your breakfast omelet

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Credit: Maria Orlova from Pexels

We've all suffered from viruses, but did you know that they are also a problem for mushrooms and molds? Mycoviruses are viruses that specifically infect fungi and have the potential to impact ecology,

agriculture, food security, and public health. Understanding the nature of these viruses, including their number and evolution, can help us understand their origins and inform our understanding of viruses in general.

Previous research into RNA mycoviruses has relied on their sequence similarity to [viruses](#) that have already been described. However, this approach leaves viruses with different genetic structures or sequences undiscovered. Using an advanced technological approach called Fragmented and Primer Ligated Double Stranded RNA sequencing, or FLDS for short, researchers from the University of Tsukuba were able to identify viral sequences that were previously overlooked.

Summarizing the importance of this work, Professor Hagiwara said: "The current approaches used to identify RNA viruses mean that their genetic diversity has been underestimated. Using FLDS, we were able to study RNA viruses without relying on sequence similarity, which allows us to identify RNA viral sequences that are dissimilar to those previously identified."

Using FLDS, Professors Urayama and Hagiwara, and their colleagues, identified 19 RNA viruses in a fungus called *Aspergillus*. Highlighting the value of this approach, nine of the 19 viruses identified had been undetected using conventional methods of examination. Moreover, 42% of identified viruses had genomes that were segmented, or spread throughout the [host genome](#), and others identified had novel [genome](#) architectures.

RNA-dependent RNA polymerase (RdRp) is an essential gene found in all RNA viruses and allows RNA genome replication from an RNA template. It was commonly understood that all RNA viruses encode RdRp as a single, continuous gene.

"Unexpectedly, we found that viruses within a certain clade of Narnaviridae encode an RdRp gene lacking the catalytic domains," Professor Urayama explains, "but we also found a different open reading frame containing the missing domains." Although some RdRp sequences lacking the catalytic domains have been described previously, those viral genomes also lack the catalytic domains and produce imperfect RdRp proteins. The functional, yet divided, RdRp described by Professors Urayama and Hagiwara, and their colleagues, indicates that researchers should reconsider the structural plasticity of RdRp.

This research shows that FLDS is a powerful approach that should be widely applied to identify high quality viral genomes and is a powerful tool for expanding the current understanding of RNA [virus](#) genome diversity.

**More information:** Yuto Chiba et al. Discovery of divided RdRp sequences and a hitherto unknown genomic complexity in fungal viruses, *Virus Evolution* (2020). [DOI: 10.1093/ve/veaa101](https://doi.org/10.1093/ve/veaa101)

Provided by University of Tsukuba

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