

<https://doi.org/10.1038/s44298-025-00131-y>

A deep dive into giant viruses

Check for updates

Giant viruses are a complex and diverse group infecting organisms from unicellular eukaryotes to animals. From the characterization of novel viruses to the development of advanced bioinformatic tools for taxonomy and classification, these collection of papers highlights the dynamic nature of giant virus research, uncovering new aspects of their diversity, environmental roles, and evolutionary complexity.

Giant viruses represent a complex and heterogeneous group of viruses capable of infecting organisms ranging from unicellular eukaryotes to animals. These viruses belong to the phylum *Nucleocytoviricota* and share a set of genes related to structural and replication modules. Some nucleocytoviruses have historical significance, such as the variola virus, the causative agent of smallpox, which led to hundreds of millions of human deaths and was eradicated in 1980. However, although some nucleocytoviruses like the smallpox virus have been extensively studied throughout the history of virology, the group gained significant attention following the discovery of mimiviruses in 2003—the largest viruses described up to that point. Able to infect amoebas, mimiviruses exhibit unprecedented structural and genomic complexity, and their discovery sparked tremendous interest in the broader scientific community. Since then, several research groups have described other protist-infecting viruses, each larger and more intriguing than the last. In this context, structural, evolutionary, and especially metagenomic studies have expanded our understanding of giant viruses across a wide range of Earth's environments. In this collection of articles, the beauty, complexity, and fascination with giant viruses are renewed, showing that even 20 years after the discovery of the mimivirus, the study of giant viruses remains a dynamic field, still full of major discoveries.

Among the research groups that have been consistently contributing to the discovery and characterisation of giant amoeba-infecting viruses, the group led by Chantal Abergel and Jean-Michel Claverie stands out for the depth and

excellence of their work. In an article published in this collection, their team offers readers a beautiful and comprehensive review highlighting the general and historical aspects of giant viruses over the past 20 years¹.

While efforts to isolate giant viruses remain essential for structural and virus-host interaction analyses, metagenomics applied to the study of giant viruses has revolutionised our understanding of this group's diversity. In this context, Minch and Moniruzzaman present an impressive set of 230 new high-quality giant virus genomes detected via metagenomics from nine different datasets across the global oceans. Using elegant and sophisticated methodologies, they investigated several aspects of these metagenome-assembled genomes, including biogeography, phylogeny, and the presence of key genes relevant to understanding the lifestyle of these viruses².

Other contributions related to the evolution and genomic content of giant viruses were also highlights of this collection of papers. Henriques et al.³ offer an in-depth genomic analysis of 24 newly isolated chloroviruses infecting *Chlorella heliozoae*, including the first giant virus recovered from Greenland³. Their work reveals remarkable genomic diversity within the proposed subgenus *Gammachlorovirus*, defining ten distinct species with high synteny and a shared core of genes. The presence of an open pan-genome with a large fraction of uncharacterised genes highlights the untapped evolutionary potential of this group. This study reinforces the importance of global sampling efforts to uncover the ecological and evolutionary complexity of algal giant viruses. Lamb et al.⁴ reveal the widespread presence of cytochrome b5 genes among *Megaviricetes* viruses from diverse environments, including oceanic, freshwater, terrestrial, and even human-associated samples⁴. Their expression analysis confirms that these viral proteins are functional, with some featuring a unique transmembrane domain. The low similarity between viral and host cytochrome b5 sequences suggests an unresolved evolutionary origin. This work opens intriguing questions about the acquisition and diversification of haemoproteins in giant viruses. Thomy et al.⁵ report the groundbreaking discovery of the first ribosomal protein gene (eL40) encoded by a eukaryotic virus, found in the giant virus FloV-SA2⁵. This gene is also expressed in other uncultivated marine giant viruses,

challenging previous assumptions about viral limits in translation-related functions. Additionally, FloV-SA2 encodes a group II viral rhodopsin, a light-activated protein of unknown role, previously only seen in metagenomic data. These findings position FloV-SA2 as a key model for exploring novel viral strategies to modulate host metabolism.

In the context of the growing importance of genomics, metagenomics, and taxonomic classification studies for understanding the world of giant viruses, new and sophisticated tools have been essential for handling the impressive amount of data being generated. Ha and Aylward⁶ introduce TIGTOG, a machine learning-based tool designed to predict the taxonomic classification of giant viruses, particularly those derived from incomplete metagenome-assembled genomes⁶. By leveraging protein family profiles and a random forest algorithm, TIGTOG achieves impressive classification accuracy—99.6% at the order level and 97.3% at the family level—across a diverse set of 1531 Nucleocytoviricota genomes. This method reduces reliance on fixed marker genes and offers a fast, reliable way to classify giant viruses, with the potential for adaptation to other viral groups. Pitot et al.⁷ introduce GVClass, a powerful new tool designed to identify and classify giant viruses from sequence data with high accuracy⁷. By leveraging conserved orthologous groups and consensus single-protein phylogenies, GVClass provides reliable taxonomic assignments and estimates of genome completeness and contamination. The tool achieves over 90% accuracy at the genus level and is fully integrated into the IMG/VR database. GVClass represents a major step forward in addressing the complexity of giant virus classification and genomic analysis.

At last, Gajigan et al.⁸ present a detailed analysis of the infection cycle of the giant virus *Oceanusvirus kaneohense* (TetV-1) in the green alga *Tetraselmis*. Through ultrastructural observations and transcriptomic profiling, they identify key infection stages and shifts in gene expression over time. The infection triggers major changes in host transcription, particularly in lipid metabolism and endocytosis-related pathways. Many highly expressed genes from both virus and host remain uncharacterized, highlighting important gaps in our understanding of giant virus–host interactions.

In conclusion, this collection of articles showcases the vibrant and rapidly evolving landscape of giant virus research. From groundbreaking discoveries in virus identification and genomic innovation to the development of advanced bioinformatic tools for classification, the studies highlight the immense complexity and ecological relevance of the *Nucleocytoviricota*. Together, they reinforce that even two decades after the discovery of the mimivirus, the field remains dynamic and full of surprises, with much still to uncover about the biology, evolution, and environmental roles of these fascinating entities.

Jônatas Santos Abrahão ✉

Departamento de Microbiologia, Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.

✉ e-mail: jonatas.abrahao@gmail.com

Published online: 31 May 2025

References

1. Bosmon, T., Abergel, C. & Claverie, J. M. 20 years of research on giant viruses. *npj Viruses* **3**, 9 (2025).
2. Minch, B. & Moniruzzaman, M. Expansion of the genomic and functional diversity of global ocean giant viruses. *npj Viruses* **3**, 32 (2025).
3. Henriques, L. R. et al. Revealing the hidden diversity of *Chlorella heliozoae*-infecting giant viruses. *npj Viruses* **3**, 12 (2025).
4. Lamb, D. C. et al. Cytochrome b5 occurrence in giant and other viruses belonging to the phylum nucleocytoviricota. *npj Viruses* **3**, 8 (2025).
5. Thomy, J., Schvarcz, C. R., McBeain, K. A., Edwards, K. F. & Steward, G. F. Eukaryotic viruses encode the ribosomal protein eL40. *npj Viruses* **2**, 51 (2024).
6. Ha, A. D. & Aylward, F. O. Automated classification of giant virus genomes using a random forest model built on trademark protein families. *npj Viruses* **2**, 9 (2024).
7. Pitot, T. M., Bruna, T. & Schulz, F. Conservative taxonomy and quality assessment of giant virus genomes with GVCClass. *npj Viruses* **2**, 60 (2024).
8. Gajigan, A., Schvarcz, C., Conaco, C., Edwards, K. & Steward, G. Ultrastructural and transcriptional changes during a giant virus infection of a green alga. *npj Viruses* <https://doi.org/10.1038/s44298-025-00128-7> (2025).

Acknowledgements

J.S.A. acknowledges the colleagues who submitted manuscripts to this collection and the team at *npj Viruses* for their assistance in

managing the articles. J.S.A. is supported by CNPq, CAPES, FAPEMIG, and the Pro-Reitoria de Pesquisa e Pós-Graduação of UFMG. J.S.A. is a CNPq researcher.

Author contributions

J.S.A. served as guest editor of this Collection and authored this text.

Competing interests

The author declares no competing interests.

Open Access This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by-nc-nd/4.0/>.

© The Author(s) 2025