

# New viruses related to both giant viruses and herpesviruses

April 29 2023

---



Plankton collected during the Tara Expedition. Credit: Christian SARDET / Tara Océans / Plankton Chronicles / CNRS Images

Metagenomic data from Tara Oceans on marine plankton has enabled the discovery of a major group of DNA viruses found abundantly from

the equator to the poles: mirusviruses. These viruses play a role in regulating plankton by infecting a considerable number of single-cell organisms at any given time.

They are highly complex with a surprising genomic composition: the genes key to forming their viral particle, a characteristic of these DNA viruses, have a direct evolutionary link with herpes viruses. The latter are common in animals (half of the world's [human population](#) is infected with the [herpes virus](#)) but non-existent in other life forms, leaving the question of their evolutionary origin unanswered.

The discovery of mirusviruses suggests that the ancestors of herpes viruses once infected marine single-cell organisms. The evolutionary history of mirusviruses held other surprises. Despite the obvious link to herpes viruses, the majority of mirusvirus genes, including those involved in viral genome replication, are similar to those of giant viruses, a completely distinct virus group that intrigues scientists for their amazing properties. This evolutionary "chimerism" in mirusviruses is unique and could provide information about the evolution of DNA viruses.

"In 2019, our research team observed an unusual evolutionary signal in the massive amounts of sequencing data provided by the Tara Oceans project. By tracking this signal, we discovered and then characterized a major DNA virus group: mirusviruses. The publication of this discovery in *Nature* marks the start of a new adventure and a gateway for the scientific community to detect and study mirusviruses in any number of ecosystems," explains Tom Delmont, an expert in [microbial ecology](#) at CNRS and last author of the study.

"Tara Oceans has transformed our understanding of plankton ecology. Our study proves that this incredible expedition also provides answers to fundamental evolutionary questions. Much remains to be discovered and

understood about mirusviruses. They have yet to be cultivated, no images of their [viral particle](#) exist, and we have yet to study them in places other than the oceans," said Morgan Gaïa, a [virus](#) evolution expert at the CEA and first author.

## More about the Tara Oceans Expedition (2009–2013)

For nearly four years, the schooner Tara sailed every oceanic basin on a unique mission: to obtain a global picture of [marine plankton](#) ecosystems around the world. This overlooked and invisible biodiversity is a crucial marker of the health of our planet and its climate system. Nearly 35,000 samples of viruses, bacteria, algae and plankton have been collected and analyzed and are still being analyzed.

The largest genetic sequencing effort ever carried out on a marine ecosystem, the expedition has highlighted a majority of previously unknown microbial genes. Led in collaboration with the Tara Ocean Foundation, this expedition mainly involved teams from CNRS, CEA and EMBL, which are members of the Tara Oceans consortium and the GO-SEE (Global Oceans Systems Ecology & Evolution) research network.

**More information:** Morgan Gaïa et al, Mirusviruses link herpesviruses to giant viruses, *Nature* (2023). [DOI: 10.1038/s41586-023-05962-4](https://doi.org/10.1038/s41586-023-05962-4)

Provided by CNRS

Citation: New viruses related to both giant viruses and herpesviruses (2023, April 29) retrieved 25 April 2024 from <https://phys.org/news/2023-04-viruses-giant-herpesviruses.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private

study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.