

New insights into global ocean microbe-virus interactions, drivers of Earth's ecosystems

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Seawater samples are being prepared for extraction of marine viruses aboard the Tara Oceans vessel. Credit: Anna Deniaud/Tara Oceans

Hidden among Earth's vast oceans are some of the tiniest and most vital organisms to the health of delicate ecosystems. Ocean microbes produce

half of the oxygen we breathe, and are important drivers in chemical reactions and energy transfers that fuel critical ecological processes.

Much like other organisms, marine microbes are susceptible to [viral infections](#) that can alter their metabolic output, or even kill them. For example, certain ocean viruses invade algae and take control over the photosynthetic process, which replenishes the oxygen we breathe. Others simply kill off vast amounts of organisms, putting a cap on the biomass that can support food webs in the world's oceans.

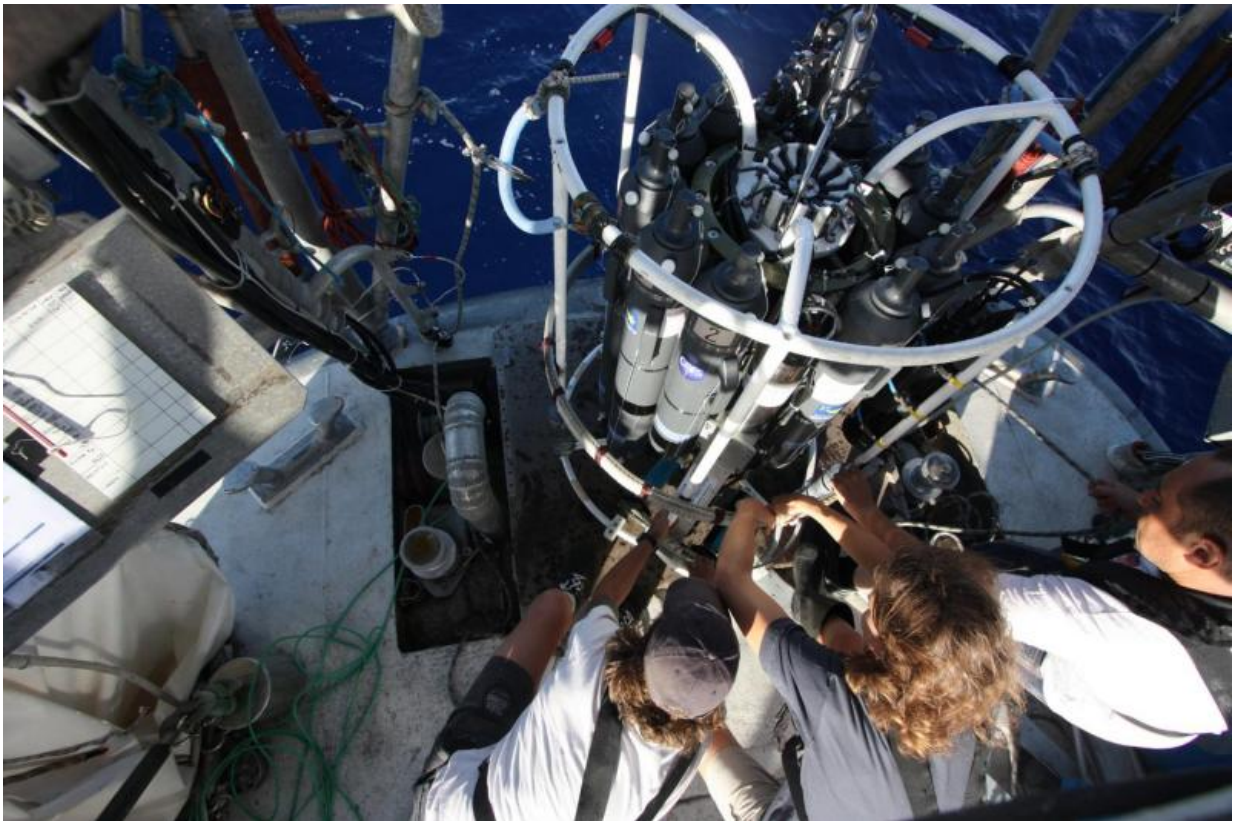
A new study from an international team led by UA scientists Matthew Sullivan, Jennifer Brum, Simon Roux and Julio Cesar Ignacio Espinoza draws on viral genome data to explain how oceanic viral communities maintain high regional diversity on par with global diversity. The findings may help researchers to predictively model the virus-microbe interactions driving Earth's ecosystems. The paper is one of five landmark studies borne from the Tara Oceans Expedition featured this week in a special issue of the journal *Science*.

"We established a means to study viral populations within more complex communities and found that surface ocean viruses were passively transported on currents and that population abundances were structured by local environmental conditions," said Sullivan, associate professor in the Department of Ecology and Evolutionary Biology and member of the BIO5 Institute. The work was completed with the assistance of a Gordon and Betty Moore Foundation Investigator grant, a highly prestigious award given to researchers focused on environmental science and conservation.

Sullivan's work is part of the Tara Oceans Expeditions, a global effort to understand complex interactions between ocean ecosystems, climate and biodiversity. For the past ten years, the Tara Oceans research vessel has traversed over 180,000 miles across all the world's oceans collecting

biological samples and information about the oceans' physical parameters like depth, temperature and salinity.

"The Tara Oceans expedition provided a platform for systematically sampling ocean biota from viruses to fish larvae, and in a comprehensive environmental context," said Sullivan. "Until now, a global picture of ocean viral community patterns and ecological drivers was something we could only dream of achieving."



The Rosette. Credit: Anna Deniaud/Tara Oceans

To assess geographical diversity in marine viral communities, Sullivan

and his team looked at double-stranded DNA viral genomic sequence data, or viromes, and whole viral community morphological data across 43 Tara Oceans expedition samples. The samples were globally distributed throughout the surface oceans (only one deep sea sample) and represented diverse environmental conditions.

Specifically, Sullivan and his team were interested in the previous observation that the diversity of ocean viruses at any given site was as high as that observed globally. Such high local and low global diversity had been observed a decade ago and scientists proposed a seed-bank hypothesis to explain it. This hypothesis suggests that high local genetic diversity can exist by drawing variation from a common and relatively limited global gene pool. Local-dominant communities consist of viruses that are influenced by environmental conditions, which affect their microbial hosts and indirectly alter the structure of the viral community. These communities serve as the low-abundance "bank" for neighboring locations, as they are passively transported by way of [ocean currents](#).

Since viruses lack universal genes that could be used to identify global community patterns, Sullivan had to employ different techniques to study viral communities. The first approach involved looking at viral particles themselves, and comparing morphological characteristics like capsid size and tail length.

"This is the low resolution way to do things - viruses that appear identical may have completely different genomes," explained Sullivan. "The fact that all viruses don't share a single common gene calls for some clever approaches to investigating viral diversity."

Next, the researchers cataloged viral populations in terms of the proteins they shared in common, in a process called protein clustering. This allowed them to establish core genes that were shared across the viral communities studied. Finally, Sullivan and his team looked at the

distribution of viral populations, the majority of which had not been previously characterized, across all of the Tara Oceans sample sites.

When they investigated the distribution patterns, they found that the directionality of viral population flow closely corresponded to that of ocean currents, affirming the seed-bank hypothesis.

"Ocean virus-microbe interactions have a huge impact on global biogeochemistry," said Sullivan. "As they destroy microbial cells, they change the forms of nutrients available to other, larger organisms in ocean ecosystems. This recycling of nutrients through viral lysis is an important pathway that regulates how the oceanic ecosystem functions. Viral infections simultaneously reduce the amount of nutrients and materials available to larger organisms by killing microbial cells, but also stimulate microbial activity through the release of organic matter and nutrients, which provides increased biomass available for larger organisms including fish."

Sullivan's findings stem from key advances in methodology, including the ability to systematically collect biological samples on a global scale and pushing the analysis of marine viral characteristics into the realm of the quantitative.

"Up until recently, the methods used to study virus-microbe interactions were often qualitative," said Sullivan. "With this study, we have made great quantitative advances. The goal now is to determine how our quantitative estimates can be used to build predictive models."

Sullivan emphasized the uniqueness and importance of working with the Tara Oceans team: "This is an incredible new way of doing science. At Tara Oceans, we are united by a common goal rather than a common funding source. These first papers show the world that we're capable of doing science at this scale, and yet they represent just the tip of the

iceberg of what is hidden in these vast data sets. We've got years of work ahead of us."

Sullivan and his lab also contributed to three other papers in this special issue. Those three papers explore the global ocean microbiome and plankton interaction networks, as well as how plankton communities change across a key ocean circulation choke point off South Africa.

More information: Patterns and ecological drivers of ocean viral communities, www.sciencemag.org/lookup/doi/10.1126/science.1261498

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