Quantitative analysis of viral infection networks using previously published phytoplankton-virus networks newly compiled for results publication Edwards and Hayward (2024)

Website: https://www.bco-dmo.org/dataset/923515
Data Type: Synthesis
Version: 1
Version Date: 2024-03-26

Project
» Giant viruses in the open ocean: Is large size adaptive where cells are scarce? (GVs NPSG)

Contributors	Affiliation	Role
Edwards, Kyle F.	University of Hawaii at Manoa	Principal Investigator
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset contains results of a quantitative analysis performed using previously published phytoplankton-virus networks newly compiled for results publication Edwards and Hayward (2024). Network dimensionality (in terms of the minimum embedding dimensionality) was analyzed using R code with input files containing 11 phytoplankton-virus cross-infection matrices collected from published sources.

Table of Contents

Coverage

Temporal Extent: 1994 - 2023

Methods & Sampling

Cross-infection matrices for viruses infecting eukaryotic phytoplankton were collected from published sources.

The table provided in the "Data Files" section for this dataset corresponds to Table S1 of Edwards and Hayward (2024) and includes the results of a quantitative analysis of each viral infection network. Citations for the eukaryote-virus networks are listed in the column "Reference" with full citations listed in the "Related Datasets" section. The bacteria-virus networks were taken from a previous compilation: Flores et al. (2011).

Data Processing Description

The supplemental .zip packages containing R-code that performed the analysis and input files containing the compiled sources are available from the publication (Edwards, K. (2024), https://doi.org/10.6084/m9.figshare.24991041).

"R Code for analyzing network dimensionality" supplementary_file_S1.zip contains three scripts that analyze the

dimensionality of infection networks.

(1) The script ‘for_publication_nullmodel.R’ takes an infection matrix and uses a null model to test whether the infection matrix can be sorted in one dimension better than expected by chance. As noted in the script, the script assumes that the matrix is a csv file formatted such that rows correspond to viruses, columns correspond to hosts, the first column contains virus strain labels, and the first row contains host strain labels. 1 = infection, 0 = no infection. The script was written in R 4.3.2 and also uses a package called future.apply for parallelization.

(2) The script ‘for_publication_find_minimum_dimensionality.R’ takes and infection matrix and finds the smallest number of dimensions in which an infection matrix can be sorted with zero errors. The data input is the same as the null model script.

(3) The script ‘for_publication_dimensionality_plot_functions.R’ contains plotting functions that are referenced by the second script.

Other details of how the code works are included as annotations within the scripts themselves.

"Phytoplankton-virus infection networks" supplementary_file_S2.zip contains 11 phytoplankton-virus networks stored as .csv files, where the rows are virus strains and the columns are host strains. Within the matrix a value of 1 indicates that the virus strain can infect the phytoplankton strain, while 0 indicates that it cannot. The csv files are named with the last name of the first author of the publication, followed by the date of publication.

BCO-DMO Processing Description

* Sheet 1 of submitted file "Supplementary_Table_S1.xlsx" was imported into the BCO-DMO data system for this dataset. Parameter descriptions below the data table were removed from the data file and added in the "Parameters" section.
* previously published and DOI'ed supplemental files were not republished as part of this datasets and instead were linked as related publications and described in the metadata.
* Taxonomic names used in the data table were matched with identifiers using the World register of marine species (WoRMS) with gaps filled in by searching for non-marine taxa at ITIS.gov.

[table of contents | back to top]

Related Publications

Baudoux, A. -C., Lebredonchel, H., Dehmer, H., Latimier, M., Edern, R., Rigaut-Jalabert, F., Ge, P., Guillou, L., Foulon, E., Bozec, Y., Cariou, T., Desdevises, Y., Derelle, E., Grimsley, N., Moreau, H., & Simon, N. (2015). Interplay between the genetic clades of Micromonas and their viruses in the Western English Channel. Environmental Microbiology Reports, 7(5), 765–773. Portico. https://doi.org/10.1111/1758-2229.12309
IsDerivedFrom

Baudoux, A.-C., & Brussaard, C. P. D. (2005). Characterization of different viruses infecting the marine harmful algal bloom species Phaeocystis globosa. Virology, 341(1), 80–90. https://doi.org/10.1016/j.virol.2005.07.002
IsDerivedFrom

Bellec, L., Clerissi, C., Edern, R., Foulon, E., Simon, N., Grimsley, N., & Desdevises, Y. (2014). Cophylogenetic interactions between marine viruses and eukaryotic picophytoplankton. BMC Evolutionary Biology, 14(1). https://doi.org/10.1186/1471-2148-14-59
IsDerivedFrom

Clerissi, C., Desdevises, Y., & Grimsley, N. (2012). Prasinoviruses of the Marine Green Alga Ostreococcus tauri Are Mainly Species Specific. Journal of Virology, 86(8), 4611–4619. https://doi.org/10.1128/jvi.07221-11
https://doi.org/10.1128/JVI.07221-11
IsDerivedFrom

Edwards, K. (2024). Data from: The dimensionality of infection networks among viruses infecting microbial eukaryotes and bacteria [Data set]. figshare. https://doi.org/10.6084/M9.FIGSHARE.24991041
https://doi.org/10.6084/m9.figshare.24991041
Software

Edwards, K. F., & Hayward, C. (2024). The dimensionality of infection networks among viruses infecting microbial eukaryotes and bacteria. Ecology Letters, 27(2). Portico. https://doi.org/10.1111/ele.14383
Results

Flores, C. O., Meyer, J. R., Valverde, S., Farr, L., & Weitz, J. S. (2011). Statistical structure of host–phage interactions. Proceedings of the National Academy of Sciences, 108(28). https://doi.org/10.1073/pnas.1101595108
IsDerivedFrom

Nagasaki, K. (1999). Cluster analysis on algicidal activity of HaV clones and virus sensitivity of Heterosigma akashiwo (Raphidophyceae). Journal of Plankton Research, 21(11), 2219–2226. https://doi.org/10.1093/plankt/21.11.2219
IsDerivedFrom

Nagasaki, K., Shirai, Y., Tomaru, Y., Nishida, K., & Pietrokovski, S. (2005). Algal Viruses with Distinct Intraspecies Host Specificities Include Identical Intein Elements. Applied and Environmental Microbiology, 71(7), 3599–3607. https://doi.org/10.1128/aem.71.7.3599-3607.2005 https://doi.org/10.1128/AEM.71.7.3599-3607.2005
IsDerivedFrom

Nagasaki, K., Tomaru, Y., Katanozaka, N., Shirai, Y., Nishida, K., Itakura, S., & Yamaguchi, M. (2004). Isolation and Characterization of a Novel Single-Stranded RNA Virus Infecting the Bloom-Forming Diatom Rhizosolenia setigera. Applied and Environmental Microbiology, 70(2), 704–711. https://doi.org/10.1128/aem.70.2.704-711.2004 https://doi.org/10.1128/AEM.70.2.704-711.2004
IsDerivedFrom

R Core Team (2023). R: A language and environment for statistical computing. R v4.3.2. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Ruiz, E., Oosterhof, M., Sandaa, R.-A., Larsen, A., & Pagarete, A. (2017). Emerging Interaction Patterns in the Emiliania huxleyi-EhV System. Viruses, 9(3), 61. https://doi.org/10.3390/v9030061
IsDerivedFrom

Tarutani, K., Nagasaki, K., & Yamaguchi, M. (2000). Viral Impacts on Total Abundance and Clonal Composition of the Harmful Bloom-Forming Phytoplankton Heterosigma akashiwo. Applied and Environmental Microbiology, 66(11), 4916–4920. https://doi.org/10.1128/aem.66.11.4916-4920.2000 https://doi.org/10.1128/AEM.66.11.4916-4920.2000
IsDerivedFrom

Tomaru, Y., Shirai, Y., Suzuki, H., Nagasaki, T., & Nagumo, T. (2008). Isolation and characterization of a new single-stranded DNA virus infecting the cosmopolitan marine diatom Chaetoceros debilis. Aquatic Microbial Ecology, 50, 103–112. https://doi.org/10.3354/ame01170
IsDerivedFrom

Tomaru, Y., Shirai, Y., Toyoda, K., & Nagasaki, K. (2011). Isolation and characterisation of a single-stranded DNA virus infecting the marine planktonic diatom Chaetoceros tenuissimus. Aquatic Microbial Ecology, 64(2), 175–184. https://doi.org/10.3354/ame01517
IsDerivedFrom

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Project Information

Giant viruses in the open ocean: Is large size adaptive where cells are scarce? (GVs NPSG)

Coverage: North Pacific

NSF Award Abstract:
Viruses can infect all forms of life. Viruses are highly diverse, and one aspect of diversity is size: genomes of viruses vary more than a thousandfold in length, and the size of viral particles varies nearly a millionfold. The discovery of “giant” viruses was astounding because they can be physically larger and code for more genes than many free-living microorganisms. There is growing evidence that giant viruses are widespread and diverse in the ocean, but much about their ecology remains unknown. What critical ecological tradeoffs vary with virus size, allowing small and large viruses to coexist? Do these tradeoffs cause the distribution of virus sizes to vary across habitats? This project aims to answer these questions for viruses that infect phytoplankton, the microscopic plants that are the foundation of ocean productivity. This research can also influence a diverse array of scientific fields because virus size varies greatly in other ecosystems and host-associated microbiomes. The fundamental constraints on size may be broadly similar across systems, but the processes driving virus size have not been thoroughly investigated in any of them. This project supports the training of a postdoctoral researcher, two graduate students, and undergraduate students in integrative science that includes field, laboratory, and modeling components. National Science Foundation-supported Research Experience for Undergraduates and Tribal Colleges and Universities programs at UH Manoa that serve Pacific Islanders and other underrepresented groups are used for recruiting students. In addition, science outreach at public events in Hawai’i includes an interactive game to communicate ideas about giant viruses and their role in the ocean.

Large viruses may have four advantages over smaller viruses: i) ability to infect a greater diversity of host genotypes, ii) better control of host metabolism, iii) large enough size to enter host cells by ingestion, and iv) greater persistence in the extracellular environment. These advantages may compensate for the advantages held by smaller viruses: higher contact rates with their hosts and greater offspring number per infection. The advantages of large size may be more consequential in oligotrophic habitats, where the microbial eukaryote community is primarily small phagotrophic flagellates (mixotrophs and heterotrophs), at low population densities, with resource-limited growth. The project goals are: (1) To test whether giant viruses indeed dominate in the oligotrophic ocean compared to a productive coastal location, as suggested by initial observations of this research team; (2) To test the above four hypotheses about the advantages of large size by conducting laboratory experiments with diverse viral isolates, and (3) To use an eco-evolutionary model of eukaryotic microbes and their viruses to explain observed size patterns.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2129697
Simons Foundation (Simons)	566853
NSF Office of Integrative Activities (NSF OIA)	OIA-1736030

[table of contents | back to top]