A compilation from the scientific literature of burst size and latent period of lytic viruses infecting phytoplankton, as well as data on virus and host size and genome length, and host growth rate.

Website: https://www.bco-dmo.org/dataset/809379
Data Type: Other Field Results
Version: 1
Version Date: 2020-04-14

Project
» Eating themselves sick? Ecological interactions among a mixotrophic flagellate, its prokaryotic prey, and an ingestible giant virus. (Giant virus ecology)

Contributors	Affiliation	Role
Edwards, Kyle F.	University of Hawaiʻi at Mānoa (SOEST)	Principal Investigator, Contact
Steward, Grieg	University of Hawaiʻi at Mānoa (SOEST)	Co-Principal Investigator
Soenen, Karen	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
A compilation from the scientific literature of burst size and latent period of lytic viruses infecting phytoplankton, as well as data on virus and host size and genome length, and host growth rate.

Table of Contents

Dataset Description

These data were published in Edwards, K.F. and Steward, G.F., 2018 (Table S1). The data reside at Dryad with following DOI:10.5061/dryad.31sm2.

Methods & Sampling

The literature was searched for studies that measured burst size and latent period of viruses isolated on phytoplankton or other microalgal hosts. We only included experiments where the host was grown under nutrient-replete conditions. We recorded the name of the virus strain, virus genome type (dsDNA/dsRNA/ssDNA/ssRNA), virus source location, host species, host taxon (chlorophyte/cryptophyte/cyanobacterium/diatom/dinoflagellate/haptophyte /pelagophyte/raphidophyte), and environment (marine/freshwater). We also recorded whether burst size was estimated by counting infectious units or free virions. Virus capsid size (diameter) and genome size estimates were taken from the same study, or other studies on the same isolate. Host genome size and cell volume estimates were taken from the literature, and if an estimate for the host species was not available, an estimate from a congener was used if available. It is noteworthy that 10 of the 13 single-stranded viruses have been isolated from *Chaetoceros* species, and, in the absence of published information on genome sizes for most of the hosts, we assigned all of the host species the same genome size (measured for *C. muelleri*). For the double-stranded viruses, genome size estimates were available for nearly all host species. When possible, host exponential growth rate was extracted from growth curves measured on uninfected hosts, or hosts growing prior to infection. Temperature and irradiance under which the hosts were cultured during one-step growth experiments were also recorded.

Data Processing Description

BCO-DMO processing notes:

- BCO-DMO did not reprocess these data. The data reside at Dryad and already had a DOI:10.5061/dryad.31sm2.

[table of contents | back to top]

Supplemental Files

File
model_example filename: model.example.code.amnat.R (Octet Stream, 2.49 KB) MD5:42f1d1cb3118b9d567d7cb2e5f78ba69 model example: Host traits drive viral life histories across phytoplankton viruses
supplementary_figures filename: supplementary_figures.pdf (Portable Document Format (.pdf), 2.69 MB) MD5:e378b9a134a49505c7afc147b36c7060 Host traits drive viral life histories across phytoplankton viruses, supplementary virusses

[table of contents | back to top]

Related Publications

Edwards, K. F., & Steward, G. F. (2018). Host Traits Drive Viral Life Histories across Phytoplankton Viruses. The American Naturalist, 191(5), 566–581. doi:10.1086/696849
Results

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Project Information

Eating themselves sick? Ecological interactions among a mixotrophic flagellate, its prokaryotic prey, and an ingestible giant virus. (Giant virus ecology)

Coverage: North Pacific Subtropical Gyre - Station ALOHA; and North Pacific tropical embayment, Oahu, HI - Kaneohe Bay

NSF Award Abstract:
Phytoplankton support the biological bounty of our seas, so understanding what controls their growth and death is one of the central issues in oceanography. In much of the nutrient-depleted surface waters of the open ocean, the most successful phytoplankton are tiny photosynthetic bacteria known as Prochlorococcus.

These bacteria are highly successful competitors for the ocean's limited nutrients and commonly outcompete larger phytoplankton. Yet, many larger types of phytoplankton persist in the ocean. One reason why this coexistence may occur is that some of the weaker competitors called mixotrophs have evolved a clever alternative strategy best summed up as "If you can't beat them, eat them". In addition to directly competing for nutrients dissolved in the water, these larger phytoplankton can acquire nutrients by consuming and digesting their smaller rivals. The dual ability to photosynthesize and eat competitors has clear advantages, but there can be hidden costs of this intraguild predation strategy. While feeding on Procholorococcus, mixotrophs may also inadvertently ingest giant viruses that are so large they are mistaken for food. Infection is often fatal. Mixotrophy and viral infection are ubiquitous in the ocean; however these processes are often understudied and missing from traditional models of marine food webs that generally consider photosynthesis and predation independently. In this project, the interactions among a common mixotroph (Florenciella), its prey (Prochlorococcus), and a virus that infects the mixotroph (FloV1) will be studied in the lab and field. This research will also help guide the development of a cohesive mixotroph-virus-prey trophic model. Improving these trophic models to account for more complex processes could fundamentally change our understanding of marine trophic dynamics. The project will directly support the training of a post-doc, graduate and undergraduate student in inter-disciplinary science that includes field, lab, and modeling activities. The project will support a major component of the graduate student's dissertation and the progressive training of an undergraduate student, culminating in an independent project. The concepts of mixotrophy and viral ecology investigated here will be translated into a public display seen by hundreds of children and members of the public. The PIs will engage a K-12 teacher in the fieldwork at sea through a "Science Teachers Aboard Research Ships (STARS)" program and will recruit an undergraduate researcher through the CMORE Scholars program at the University of Hawaii.

The advantages and drawbacks of a mixotrophic strategy will depend on the availability of resources and competitors and the likelihood of viral infection. The timing of grazing will be tested to determine whether Florenciella grazes continuously or separates it grazing and photosynthetic activities by only feeding at night. Prey preferences of Florenciella will be tested in competitive grazing experiments offering Prochlorococcus as prey in the presence of varying amounts of other bacteria and cyanobacteria. Electron microscopy will be used to determine whether prey and virus enter Florenciella by the same pathway and whether the presence of prey competitively interferes with viral infection. The kinetics of grazing by Florenciella and infection of Florenciella by FloV1 will be quantified. The results from these lab experiments will be used to parameterize a numerical model. The model will be used to answer questions and make predictions about the dynamics of the mixotroph-virus-prey system and those predictions will be compared to field data. Collectivity, these observational, experimental and quantitative analyses will provide a detailed exploration of the ecological complexity hidden at the base of the marine food web.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1559356

[table of contents | back to top]