# Pseudo-nitzschia species diversity, viral titers and environmental data collected semi-monthly in 2013-2014 in Puget Sound and the Washington coast

**Website**: https://www.bco-dmo.org/dataset/762928
**Data Type**: Other Field Results
**Version**: 1
**Version Date**: 2019-03-25

**Project**
» Ecology of diatom viruses: connecting physiology and field dynamics through host transcriptional responses (Diatom Viruses)

| Contributors | Affiliation | Role |
|---|---|---|
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## Coverage

**Spatial Extent**: **N**:48.2397 **E**:-122.6795 **S**:46.7625 **W**:-124.0898
**Temporal Extent**: 2013-04-13 - 2014-04-11

## Dataset Description

Pseudo-nitzschia species diversity, viral titers and environmental data collected semi-monthly in 2013-2014 in Puget Sound and the Washington coast.

These data were published in Carlson et al. (2016).

### Methods & Sampling

Samples were collected on foot from shore. Temperature and salinity were measured with a handheld YSI device. Nutrients were measured at the UW Marine Chemistry Lab following the protocols of the WOCE Hydrographic Program using a Seal Analytical AA3.

Approximately 15 L of surface water was filtered through triplicate 3.0 and 0.2 µm 147 mm polyethersulfone filters (Millepore) with a peristaltic pump within 2 h of sampling. The filters were frozen at −80◦C for molecular analysis. The viruses in the filtrate were precipitated by adding iron chloride (1 g L− 1 ) and incubating for 12 h at 13◦ C in the dark.

Pseudo-nitzschia species diversity was assessed by extracting DNA from the 3.0 µm filters and performing

ARISA with Pseudo-nitzschia-specific primers. Abundances are expressed as a percent of the total Pseudo-nitzschia community detected.

Viral titer was assessed by incubating viral communities concentrated from each sample in a series of 10-fold dilutions of with 8 independent Pseudo-nitzschia isolates. Cultures were monitored for death via chlorophyll-a fluorescence. The infectious units were determined
based on MPN tables.

Full details of these methods are in Carlson et al. (2016).

Location:
Puget Sound: Penn Cove, Washington (48.2397, −122.6795) and
Washington coast: Grays Harbor, Washington (46.7625, −124.0898)

**Data Processing Description**

BCO-DMO Data Manager Processing Notes:
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* Converted date to ISO 8601 format
* parsed column with lat and lon into separate latitude and longitue columns in decimal degrees. "48.58 N 125.50 W" -> lat:"48.58" lon:"-125.50"

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## Related Publications

Carlson, M. C. G., McCary, N. D., Leach, T. S., & Rocap, G. (2016). Pseudo-nitzschia Challenged with Co-occurring Viral Communities Display Diverse Infection Phenotypes. Frontiers in Microbiology, 7. doi:10.3389/fmicb.2016.00527
*Results*

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## Parameters

*Parameters for this dataset have not yet been identified*

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Illumina HiSeq 2500 |
| **Generic Instrument Name** | Automated DNA Sequencer |
| **Generic Instrument Description** | General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | CTD - profiler |
| **Generic Instrument Description** | The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934. |

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## Project Information

**Ecology of diatom viruses: connecting physiology and field dynamics through host transcriptional responses (Diatom Viruses)**

**Coverage**: Puget Sound, North Pacific

*Extracted from the NSF award abstract:*

Overview: Viruses play critical roles in aquatic ecosystems. Phages infecting marine bacteria are abundant members of the plankton that contribute to cell mortality, structure population diversity and drive genome evolution though horizontal gene transfer. Viruses infecting eukaryotic phytoplankton have been demonstrated to induce both life cycle switching and programmed cell death in coccolithophorids and be significant agents of mortality in blooms of pelagophytes, haptophytes and raphidophytes. However, much less is known about viruses infecting one of the largest, most diverse and most productive groups of algae, the diatoms. Only thirteen diatom infecting viruses have been reported, and little is known about their mechanisms of infection, effects on host metabolism or diversity and dynamics in the field. This is a remarkable knowledge gap considering the ecological importance of the diatoms. Infection with a clonal virus on Pseudo-nitzschia multiseries can result in complete host lysis within 12-16 hours. The P. multiseries virus (PmDNAV) is a single stranded DNA virus with an icosahedral capsid of 50 nm. The PmDNAV infects the widest host range of any marine eukaryote-infecting virus, lysing other strains of P. multiseries, other species of Pseudo-nitzschia, and other genera of diatoms including many centric diatoms. With the recent completion of the genome of the host, P. multiseries, we now have a model system to investigate the response of the host to viral infection and the potential impacts of viruses on diatom mortality in the field. The objectives of this project are to:
1. isolate and characterize additional diatom viruses utilizing established methods, using a variety of host strains and field viral concentrate combinations
2. use RNA-Seq to determine the transcriptional profiles of three diatoms (P. multiseries, P. pungens and T. pseudonana) during the course of viral infection
3. determine a surface water metavirome at four stations on a coastal to open ocean transect in diatom dominated waters in the Pacific Northwest (line P), with an emphasis on diversity and biogeography of ssDNA and ssRNA viruses.
Viral and host genes whose expression is diagnostic of viral infection, will be identified by observing genomic responses to infection in culture. These genes, along with viruses assembled in the metaviromes, will be combined with eukaryotic metatranscriptomes already available from the same waters to assess virus activity in the field.

Intellectual Merit: This project seeks to strengthen the model system initiated by the discovery of the Pseudo-nitzschia multiseries DNA virus. The host-virus transcriptomics will lay the groundwork for assessing the

impact of viruses on diatom communities in the environment. In turn, the paired metaviromes and metatranscriptomes will reveal new questions about both diatom virus diversity and function that can then be further explored by controlled, culture-based experiments. This research will be the first extensive exploration of diatom virus ecology and function and will ultimately help further connect viruses and diatoms to global biogeochemical cycles, unravel complex organismal interactions, and inform ocean-related public health.

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## Funding


| Funding Source | Award |
| --- | --- |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1356779 |


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