# Bacteria cell counts and virus-like particle abundances from Espelandsvegen Fjord, Bergen Norway, May 2017

**Website**: https://www.bco-dmo.org/dataset/752722
**Data Type**: Other Field Results, experimental
**Version**: 1
**Version Date**: 2021-01-06

**Project**
» Light-dependent regulation of coccolithophore host-virus interactions: mechanistic insights and implications for structuring infection in the surface ocean (Light-dependent host virus interactions)


| Contributors | Affiliation | Role |
|---|---|---|
| Thamatrakoln, Kimberlee | Rutgers University | Principal Investigator |
| Bidle, Kay D. | Rutgers University | Co-Principal Investigator |
| Copley, Nancy | Woods Hole Oceanographic Institution (WHOI BCO-DMO) | BCO-DMO Data Manager |


**Abstract**
This dataset includes bacterial and virus abundances using flow cytometry from seawater collected in the Norwegian National Mesocosm Centre at the Espegrend (Espeland) Marine Biological Station near Bergen, Norway, in May 2017.

## Table of Contents



## Coverage

**Spatial Extent**: **Lat**:60.269602 **Lon**:5.218738
**Temporal Extent**: 2017-05-08 - 2017-05-30

## Dataset Description

This dataset includes bacterial and virus abundances using flow cytometry from seawater collected in the Norwegian National Mesocosm Centre at the Espegrend (Espeland) Marine Biological Station near Bergen, Norway, in May 2017.

### Methods & Sampling

#### Environmental Sample Collection

1. Transfer 1 ml of whole seawater to a 2 ml cryovial.
2. Add 20 µl of 25% glutaraldehyde for a final concentration of 0.5%.
3. Incubate at 4°C for 15 min.

4. Flash freeze in liquid N2 and store at -80°C.

**Fluorescent DNA staining (for bacterial and viral abundances)**

1. Thaw samples.
2. To 20 µl of sample, add 980 µl 1X TE buffer with SYBR Gold (see recipe below)
3. Heat to 80°C for 10 min in the dark
4. Cool at RT for 10 min in the dark
5. Analyze via flow cytometry

**Analysis (for bacterial and viral abundances)**

Samples are analyzed on Influx Model 209S Mariner flow cytometer using BD Sortware (BD Biosciences).

1. An initial Forward Scatter (FSC) vs Side Scatter (SSC) configuration is determined using Molecular Probes Flow Cytometry Sub-micron particles size reference kit (Cat#F13839) consisting of 0.02, 0.1, 0.5, 1.0 and 2.0 µm fluorescent beads.
2. A gating hierarchy is established using both beads and previously determined virus and bacteria populations as reference (Sybr Gold Fluorescence versus SSC cytogram).
3. Samples are analyzed using a 488 nm laser for excitation and a minimum trigger threshold is established using 542/15 nm (SYBR Gold) emission. Flow rates are determined using the volumetric method.
4. Collected data are analyzed using FlowJo v9.9.6. Virus Like Particles (VLPs) are differentiated from bacteria using the gating hierarchy established at time of collection.

**TE buffer with SYBR Gold recipe**
1X TE (for 100 mls)
1 ml of 1M Tris, pH 8.0
1 ml of 0.5 mM EDTA
98 mls MQ water
Store 4ºC

1X TE + SYBR Gold (for 10 mls)
1. Filter 10 mls 1 TE buffer, 0.22 µm filter
2. 1:20,000 dilution of SYBR Gold stock (Molecular Probes) (0.5 µl stock to 10 mls TE buffer)

**Data Processing Description**

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- re-formatted date from d-Mon-yy to yyyy-mm-dd
- replaced commas with semicolons
- reordered columns; sorted records by Treatment, Bag#, Depth
- changed column name Depth to Depth_description (shallow, deep) and added column Depth (1, 5)

[ table of contents | back to top ]

## Data Files

| File |
|---|
| **bact_virus_abund.csv** (Comma Separated Values (.csv), 19.87 KB) MD5:049dd458625af1689c89a2bbcec9e7fa<br>Primary data file for dataset ID 752722 |

[ table of contents | back to top ]

## Parameters

| Parameter | Description | Units |
|---|---|---|
| Treatment | nutrient amendment and/or manipulation: Fjord = water sampled directly from fjord adjacent to mesocosm bags Ambient = unamended P-limited=N:P (66:1; 4 µmol L-1 sodium nitrate:0.06 µmol L-1 sodium phosphate) added on 13-May, 14-May, 15-May-Redfield = N:P (16:1; 4 µmol L-1 sodium nitrate:0.25 µmol L-1 sodium phosphate ) added on 13-May, 14-May, 15-May Redfield/Shaded = N:P (16:1; 4 µmol L-1 sodium nitrate:0.25 µmol L-1 sodium phosphate) added on 13-May, 14-May, 15-May-; bags shaded to 20% surface irradiance on 24-May-2017) | unitless |
| Bag | Bag # | unitless |
| Date | Date formatted as yyyy-mm-dd | unitless |
| Bacteria_abund | Bacteria cell counts | cells/milliliter |
| Virus_like_particles_abund | virus-like particle counts | viruses/milliliter |
| Depth | sampling depth | meters |
| Depth_description | depth of sampling: surface = ~1 m; deep = ~5 m | unitless |

[ table of contents | back to top ]

## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Influx Model 209S Mariner Flow Cytometer |
| **Generic Instrument Name** | Flow Cytometer |
| **Dataset-specific Description** | Use to make cell counts of bacteria and virus particles. |
| **Generic Instrument Description** | Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm) |

[ table of contents | back to top ]

## Deployments

**MesoHux_2017**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/752756 |
| **Platform** | National Mesocosm Centre |
| **Start Date** | 2017-05-01 |
| **End Date** | 2017-05-31 |
| **Description** | Mesocosm experiments on bacteria and viruses. |

[ table of contents | back to top ]

## Project Information

**Light-dependent regulation of coccolithophore host-virus interactions: mechanistic insights and implications for structuring infection in the surface ocean (Light-dependent host virus interactions)**

**Coverage**: Norwegian National Mesocosm Centre at the Espegrend Marine Biological Station (60 16'25N, 5 14'10E)

*Description from the NSF award abstract:*
Phytoplankton, microscopic photosynthetic algae, form the basis of marine foodwebs and are responsible for producing nearly half the oxygen on the planet, yet represent <1% of Earth's biomass. Steady-state maintenance of a high production to biomass ratio implies that, on average, these organisms grow, die and are replaced once every week. Predatory infection by viruses has emerged as the primary mechanism responsible for the high mortality rates of phytoplankton populations. Despite the importance of viral mortality in structuring marine microbial ecosystems, little is known about the fundamental mechanisms that regulate host-virus interactions. Phytoplankton are inherently dependent on light and photosynthesis. Given the need for host resources, the viruses that infect these organisms must, therefore, also fundamentally depend on light and photosynthesis. This project will explore the relationship between light and viral infection to develop a framework for how light influences viral infection and phytoplankton mortality in the surface ocean. The widespread phytoplankton species Emiliania huxleyi, and its associated virus, Coccolithovirus, has emerged as the prominent model system for investigating algal-viral interactions due to its ecological relevance and collective mechanistic insight from numerous physiological, molecular, biochemical, genomic, and field studies. Laboratory-based culture studies will be used to elucidate the role light plays in mediating infection in E. huxleyi, specifically addressing whether light is required for viral infection as well as identifying the light-regulated host metabolic processes that viruses may co-opt for successful infection and production. These observations will then be extended to natural populations using manipulative, field-based experiments to elucidate the role light plays in structuring infection in the surface ocean. This project provides hands-on training for a Rutgers University undergraduate student, as well as a postdoctoral researcher. To facilitate ocean literacy, researchers will work with the Education and Public Outreach staff and Tilapia Film, LLC to develop an educational video based on research findings and the Next Generation Science Standards. This video, aimed at middle, high school, and undergraduate students, expands on an already successful video series that highlights scientific practices through real research investigations. It will be open access and disseminated through existing connections to the New Jersey Science Teacher Association, the National Science Teachers Association, the National Marine Educators Association, and the National Biology Teachers Association.

Predatory infection by viruses is the primary mechanism responsible for the high lysis rates observed in phytoplankton populations. As the most abundant biological entities in aquatic environments, viruses turn over more than a quarter of the photosynthetically-fixed carbon, thereby fueling microbial foodwebs and short-circuiting carbon export to higher trophic levels and the deep sea. Despite its importance, estimates of viral-induced mortality are rarely included in global models of net primary productivity and deep carbon export, in part because we lack a mechanistic understanding of the fundamental factors that regulate host-virus interactions. For viruses infecting obligate photoautotrophs, there is an inherent and fundamental interaction between light and the infection process, as well as a dependence on light-regulated host metabolic processes that may be required for viral replication. Using the model algal host, Emiliania huxleyi and its associated Coccolithovirus, this project addresses the hypotheses that: 1) infection dynamics in E. huxleyi are driven through light-dependent processes, specifically that light mediates viral entry and replication, and that viruses redirect host energy to maximize viral replication, and 2) light increases viral decay relieving hosts of viral pressure. This mechanistic, cellular framework will then be used to elucidate the role light plays in structuring infection in natural coccolithophore populations using manipulative field-based experiments. Given that light is one of the most fundamental, readily, and easily measured features of the ocean, this work will ultimately provide a context for modeling the biogeochemical impact of viral infection in the global ocean.

[ table of contents | back to top ]

## Funding

| Funding Source | Award |
| --- | --- |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1559179 |


[ table of contents | back to top ]