Bacteria and virus abundance data collected from the R/V Melville MV1405 along the California coastline during 2014

Website: https://www.bco-dmo.org/dataset/652259
Data Type: Cruise Results
Version: 1
Version Date: 2016-07-21

Project
» Linking physiological and molecular aspects of diatom silicification in field populations (Diatom Silicification)

Contributors	Affiliation	Role
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Abstract
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Coverage

Spatial Extent: **N**:42.6495 **E**:-120.02587 **S**:34.23125 **W**:-126.6157
Temporal Extent: 2014-07-04 - 2014-07-24

Dataset Description

Bacteria and virus abundance data from the MV1405 cruise. Samples were collected by CTD.

Methods & Sampling

Environmental Sample Collection

1. Transfer 1 ml of whole seawater to a 2 ml cryovial.
2. Add 20 ul of 25% glutaraldehyde for a final concentration of 0.5%.
3. Incubate at 4 degrees celsius for 30 min.
4. Flash freeze in liquid N_2 and store at -80 degrees celsius.

Fluorescent DNA staining (for bacterial and viral abundances)

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

Analysis (for bacterial and viral abundances)

Samples are analyzed on Influx Model 209S Mariner flow cytometer using BD Software (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 um 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.

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 4 degrees celsius

1X TE + SYBR Gold (for 10 mls)

1. Filter 10 mls 1 TE buffer, 0.22 um filter
2. 1:20,0000 dilution of SYBR Gold stock (Molecular Probes) (0.5 ul stock to 10 mls TE buffer)

Data Processing Description

DMO notes:

- added cruise_id column
- changed column names to meet BCO-DMO standards
- added ISO_DateTime_UTC column
- reformatted lat/lon to appear in decimal degrees
- removed prefix "stn" and "sta" from numbers in station column

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Data Files

File	
bact_virus_counts.csv	(Comma Separated Values (.csv), 2.55 KB) MD5:7774822eedb47e1802b8406e8fb52b08
Primary data file for dataset ID 652259	

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Parameters

Parameter	Description	Units
cruise_id	cruise where samples were collected	unitless
station	station where samples were collected	unitless
CTD	CTD cast	unitless
depth	depth of sample collection	meters
date_GMT	GMT date of cast; mm/dd/yy	unitless
yearday_GMT	GMT day of year.	unitless
time_GMT	GMT time of cast; HH:MM	unitless
lat	latitude	decimal degrees
lon	longitude	decimal degrees
bacteria	bacteria-like particle abundance	bacteria per milliliter
virus	virus-like particle abundance (VLP)	VLP per milliliter
ISO_DateTime_UTC	DateTime (UTC) ISO formatted	unitless

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Instruments

Dataset-specific Instrument Name	Influx Model 209S Mariner Flow Cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Samples analyzed on flow cytometer using BD Software (BD Biosciences).
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. Description from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm

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Deployments

MV1405

Website	https://www.bco-dmo.org/deployment/559966
Platform	R/V Melville
Start Date	2014-07-03
End Date	2014-07-26
Description	Deployment MV1405 on R/V Melville. Cruise took place during July 2014.

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Project Information

Linking physiological and molecular aspects of diatom silicification in field populations (Diatom Silicification)

Coverage: Oregon/California Coastal Upwelling Zone, between 34-44N and 120-124W

Description from NSF award abstract:
Diatoms, unicellular, eukaryotic photoautotrophs, are among the most ecologically successful and functionally diverse organisms in the ocean. In addition to contributing one-fifth of total global primary productivity, diatoms are also the largest group of silicifying organisms in the ocean. Thus, diatoms form a critical link between the carbon and silicon (Si) cycles. The goal of this project is to understand the molecular regulation of silicification processes in natural diatom populations to better understand the processes controlling diatom productivity in the sea. Through culture studies and two research cruises, this research will couple classical measurements of silicon uptake and silica production with molecular and biochemical analyses of Silicification-Related Gene (SiRG) and protein expression. The proposed cruise track off the West Coast of the US will target gradients in Si and iron (Fe) concentrations with the following goals: 1) Characterize the expression pattern of SiRGs, 2) Correlate SiRG expression patterns to Si concentrations, silicon uptake kinetics, and silica production rates, 3) Develop a method to normalize uptake kinetics and silica production to SiRG expression levels as a more accurate measure of diatom activity and growth, 4) Characterize the diel periodicity of silica production and SiRG expression.

It is estimated that diatoms process 240 Teramoles of biogenic silica each year and that each molecule of silicon is cycled through a diatom 39 times before being exported to the deep ocean. Decades of oceanographic and field research have provided detailed insight into the dynamics of silicon uptake and silica production in natural populations, but a molecular understanding of the factors that influence silicification processes is required for further understanding the regulation of silicon and carbon fluxes in the ocean. Characterizing the genetic potential for silicification will provide new information on the factors that regulate the distribution of diatoms and influence in situ rates of silicon uptake and silica production. This research is expected to provide significant information about the molecular regulation of silicification in natural populations and the physiological basis of Si limitation in the sea.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1333929
NSF Division of Ocean Sciences (NSF OCE)	OCE-1334387

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