Bacterial and viral cell counts, and nutrients from 5 cruises on the R/V Hugh R. Sharp in Delaware and Chesapeake Bays, 2014-2016 (Coastal Bacterial Growth Rates project)

Website: https://www.bco-dmo.org/dataset/565451
Data Type: Cruise Results
Version: waiting for validation
Version Date: 2016-03-31

Project
» Growth Rates of Bacterial Taxa in Coastal Marine Ecosystems (Coastal Bacterial Growth Rates)

Contributors	Affiliation	Role
Campbell, Barbara	Clemson University (Clemson)	Principal Investigator
Allison, Dicky	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Dataset Description

Standard oceanographic measurements collected from CTD casts during 5 cruises in Delaware and Chesapeake Bays, representing coastal marine ecosystems. Measurements included nutrients, chlorophyll and light attenuation, bacterial and viral production.

This is a new version with both new data and updated older data. March 31, 2016

DMO notes:

changed ND to nd
,, to ,nd,
space between degree_decimal minutes to no space
change nutrient names to chemical symbols
added toplevel to put all three cruises in the same object
got rid of extra lines in ACTII
fixed bad lat/lon points in each cruise with PI input

Methods & Sampling

The water samples were collected with a Seabird 911+ CTD.

Nutrient concentrations were measured by standard wet chemical methods using a SEAL Analytical AA3 Continuous Segmented Flow Analyzer.

Samples for chlorophyll a concentrations were collected by filtering 100 ml of water through Whatman GF/F filters and stored at -20 ^{o}C until analysis. To estimate concentrations, the filters were placed into 90% acetone and 40% dimethyl sulfoxide *(DMSO)* and then the fluorescence in the extract was measured with a Turner

Designs 10-AU fluorometer.

The attenuation coefficient was estimated by measuring photosynthetically active radiance with a Biospherical PNF-210 radiometer over a depth profile. In nearly all cases, the downcast and upcast profiles of radiance were indistinguishable and all data were used. When differences between the down and upcasts were apparent, only the downcast data were used.

Data Processing Description

Nutrient concentrations were not processed except for converting raw spectrometric or fluorometric readings to concentrations.

Radiance values at very shallow or very deep depths were excluded from the analysis to calculate the attenuation coefficient when these values were clearly not along the ln (radiance) vs. depth line.

Bacterial Production: Assumes average C per cell = 15 fg and 0.125 nmol-C/pmol of leucine.

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Data Files

File
newACT_cruises_rs.csv (Comma Separated Values (.csv), 54.62 KB) MD5:b6c40914994ffdba93181c24f0fce795 Primary data file for dataset ID 565451

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Parameters

Parameter	Description	Units
cruise_informal	project name for the cruise	text
cruiseid	official name of the cruise	text
date_local	date of measurement	m/dd/yyyy
time_local	local time of day	HH:MM
lat	the latitude of the CTD or station	decimal degrees
lon	the longitude of the CTD or station; negative means West of Greenwich	decimal degrees
station	sequential cruise station number	number
CTD	sequential CTD cast number	number

temp	water temperature	degrees centrigrade
sal	water salinity	PSU
secchi_depth	depth at which the Secchi disk could no longer be distinguished	meters
PAR	Photosynthetically active radiation; designates the spectral range (wave band) of solar radiation from 400 to 700 nanometers that photosynthetic organisms are able to use in the process of photosynthesis	microEinsteins per square meter per second
atten	attenuation coefficient	per meter
atten_err	error for attenuation coefficient	calculated number
depth_sample	depth of the sample data	meters
cell_counts	cell counts	cells per milliliter
counts_sd	standard deviation of cell counts (i.e.difference from the mean/average)	cells per ml
counts_se	standard error of cell counts (taking into account the number of samples tested. Error is used to get a better representation of the deviation/error with larger numbers of samples; such as cell counts where we average 10 fields of view to get a number)	cells per milliliter
bact_prod	bacterial production of the whole sample	nanograms of Carbon per Liter per hour
bact_prod_sd	standard deviation of measurement of bacterial production	nanograms of Carbon per Liter per hour
bact_prod_lt_pt8	bacterial production of the part of the sample less than 0.8 microns	nanograms of Carbon per Liter per hour
bact_prod_lt_pt8_sd	standard deviation of bacterial production of the part of the sample less than 0.8 microns	nanograms of Carbon per Liter per hour
bact_size_frac	percentage of the whole sample that is less than 0.8 microns	percentage
chla	chlorophyll a concentration	micrograms per liter
chla_sd	standard deviation of chlorophyll measurements	micrograms per liter

NO3	Nitrate concentration	micromoles per liter
NO3_sd	standard deviation of Nitrate measurements	micromoles per liter
NH4	Ammonium concentration	micromoles per liter
NH4_sd	standard deviation of Ammonium measurements	micromoles per liter
PO4	Phosphate concentration	micromoles per liter
PO4_sd	standard deviation of Phosphate measurements	micromoles per liter
SiO4	Silicate concentration	micromoles per liter
SiO4_sd	standard deviation of Silicate measurements	micromoles per liter
viral_count	number of viruses in the sample	numbers per milliliter
viral_count_sd	standard deviation of the count of the number of viruses in the sample	numbers per milliliter

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Instruments

Dataset-specific Instrument Name	CTD Seabird 911+
Generic Instrument Name	CTD Sea-Bird 911
Dataset-specific Description	Standard Seabird CTD911+
Generic Instrument Description	The Sea-Bird SBE 911 is a type of CTD instrument package. The SBE 911 includes the SBE 9 Underwater Unit and the SBE 11 Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9 and SBE 11 is called a SBE 911. The SBE 9 uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 and SBE 4). The SBE 9 CTD can be configured with auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorescence, light (PAR), light transmission, etc.). More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	Flow Cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Viruses were counted using a flow cytometer at Xiamen University, following their published method: Horizontal and Vertical Distribution of Marine Virioplankton: A Basin Scale Investigation Based on a Global Cruise. Y. Liang, et al. PLOS ONE www.plosone.org November 2014 9:11; e111634
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)

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Deployments

HRS1402

Website	https://www.bco-dmo.org/deployment/565457
Platform	R/V Hugh R. Sharp
Start Date	2014-03-18
End Date	2014-03-22
Description	One of several ACT cruises to study Bacterial Growth Rates.

HRS1416

Website	https://www.bco-dmo.org/deployment/565535
Platform	R/V Hugh R. Sharp
Start Date	2014-08-27
End Date	2014-09-01
Description	One of several cruises to Delaware Bay to study bacterial growth activity.

HRS1422

Website	https://www.bco-dmo.org/deployment/565616
Platform	R/V Hugh R. Sharp
Start Date	2014-10-31
End Date	2014-11-02
Description	One of several cruises in Delaware Bay to study bacterial growth rate ACTivity.

HRS1501

Website	https://www.bco-dmo.org/deployment/641729
Platform	R/V Hugh R. Sharp
Start Date	2015-04-11
End Date	2015-04-17
Description	This is a continuation of the series of cruises to study Bacterial Growth Rates **Processing Description** Originally in BCO-DMO as HSR1502. Changed after consult with CLC plus R2R to HRS1501.

HRS1511

Website	https://www.bco-dmo.org/deployment/641730
Platform	R/V Hugh R. Sharp
Start Date	2015-08-17
End Date	2015-08-22
Description	Another cruise in the series of Cruises to study Bacteria Growht Rates in Delaware and Chesapeake Bays

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Project Information

Growth Rates of Bacterial Taxa in Coastal Marine Ecosystems (Coastal Bacterial Growth Rates)

Coverage: Delaware and Chesapeake Bays, coastal Atlantic Ocean

Description from NSF award abstract:
Prokaryotic organisms in marine systems are highly diverse and carry out many types of metabolic processes important in biogeochemical cycles. However, the contribution of individual bacterial taxa to biochemical processes is not well understood. Similarly, previous studies have had limited success in understanding the regulation of bacterial communities by looking at correlations between abundance of individual taxa and environmental factors. Estimates of growth rates will help understand both problems. The contribution of specific bacterial taxa to biogeochemical cycles is likely to scale with growth rate as well as abundance, and these rates are also likely to be more sensitive to environment fluctuations than abundance.

This project will examine the following questions and hypotheses about a fundamental property of organisms, growth rates: 1) what is the relationship between growth rate and abundance of specific bacterial taxa in controlled experiments? Do 16S rRNA:rDNA ratios or other growth-regulated transcript:gene ratios reflect real differences in growth rates? The PIs hypothesize that growth responsive transcript:gene ratios will correlate with growth rates independent of metabolic strategy and phylogeny, even though ratios and absolute rates will vary among bacterial species or within a taxa growing under different conditions. This hypothesis will be explored in environmentally relevant isolated bacteria whose genomes have been sequenced as well as in individual taxa in natural communities, whose genomes will be sequenced via a single cell approach. 2) What is the relationship between growth rate and abundance in situ? How are variations in the environment reflected in bacterial growth rates? The PIs hypothesize that growth rates, estimated by either 16S rRNA:rDNA ratios or by other growth responsive transcript:gene ratios, will be better correlated to environmental factors than abundance alone. Variation in growth rates within and between taxa will correlate with changes in the environment, especially with light and nutrients. The project will test this hypothesis by analyzing three well--studied diverse marine ecosystems: a coastal Microbial Observatory site which has been sampled since 2006, and the Delaware and Chesapeake Bays.

To investigate the questions and hypotheses outlined above, the PIs will use a combination of single cell genomics, high throughput sequencing, and QPCR approaches to examine levels of 16S rRNA and other

growth-regulated transcripts as well as their corresponding genes under various nutrient conditions and different in situ temporal and spatial scales. High throughput sequencing avoids amplification and cloning artifacts and is cost effective. Growth-responsive transcript:gene ratios, microbial abundance, and biogeochemical properties will be examined over hourly, daily, weekly and monthly time scales to investigate the influence of environmental factors on growth rates of individual bacterial taxa and to explore bottom-up control of microbial communities.

The results from this project will do much to alter our perception of microbial processes in the oceans and estuaries by providing answers to long-standing questions about relationships between activity and standing stocks of bacterial populations. It will begin to link quantitative rate measurements of specific bacterial taxa to the extensive genomic data now becoming available.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1261359

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