Prokaryote and eukaryote abundance in phytodetrital aggregates (PA), fecal aggregates (FA), and the ambient seawater from samples collected during R/V Atlantic Explorer cruises AE1718 and AE1809 in 2017 and 2018 at BATS in Bermuda

Website: https://www.bco-dmo.org/dataset/855296
Data Type: Cruise Results
Version: 1
Version Date: 2021-07-08

Project
» Aggregation of Marine Picoplankton (Marine Plankton Aggregation)

Contributors	Affiliation	Role
Neuer, Susanne	Arizona State University (ASU)	Principal Investigator
Cruz, Bianca N.	Arizona State University (ASU)	Contact
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Abundances of prokaryotic classes and eukaryotic orders and species found in phytodetrital aggregates (PA), fecal aggregates (FA), and the ambient seawater in the fall and spring seasons, as well as of species in DNA extraction negative controls. Abundance values are prior to (raw) and following rarefaction. These data were published in Neuer et al. (2021).

Table of Contents

Coverage

Spatial Extent: **N**:31.97 **E**:-64.42 **S**:31.57 **W**:-64.57
Temporal Extent: 2017-09-12 - 2018-03-15

Acquisition Description

Particles were collected on the monthly sampling cruises affiliated with the Bermuda Atlantic Time-series Study (BATS) in fall 2017 (AE1718) and spring 2018 (AE1809) using surface-tethered Particle Interceptor Traps deployed at 150 m, 200 m, and 300 m depths for 72 h (Table 1). To collect particles with minimal

alteration to their structure, traps containing a polycarbonate jar with 100 mL of 12% polyacrylamide gel were deployed at each depth. Seawater was collected from the surface, deep chlorophyll maximum (DCM) or 20 m above the mixed layer depth (MLD), and at every trap deployment depth using 12 L Niskin bottles mounted on a CTD rosette.

8 particles were categorized and manually picked based on their morphology using characteristics described in the literature (phytodetrital aggregates or fecal aggregates), washed three times using ultrapure nuclease-free distilled water (Invitrogen), and pooled in Eppendorf LoBind tubes stored at -80C. For DNA analysis of the microbial community in the ambient seawater, 2 L from each sampling depth was filtered onto GF/F and stored in Eppendorf LoBind tubes at -80C.

DNA from the pooled particles and GF/F were extracted using a DNeasy Blood and Tissue extraction kit, and bacterial and eukaryotic paired-end V4 amplicon sequences were acquired via an Illumina MiSeq platform.

Problem report:
As a result of low DNA yield, five samples of pooled aggregates failed PCR amplification attempts using eukaryotic (18S, V4) primers: fall 200m and 300m phytodetrital aggregates, fall 200m fecal aggregates, spring 300m phytodetrital aggregates, and spring 300m fecal aggregates.

Supplemental file "16S_Control-Blanks_Species_Raw.csv" contains the taxa excluded from downstream analyses.

Processing Description

Bioinformatic analyses were performed using QIIME2 v2019.1. PhiX reads and chimeric sequences were removed and remaining reads were assembled, demultiplexed, and trimmed to salvage reads with a median quality score above 25 using DADA2 within the QIIME2 pipeline.

BCO-DMO data manager processing notes:
* After correspondence with the submitter, the final format of this dataset was combined into one table with added columns for sample name, and transformed to have abundances for the samples in an additional "abundance" column instead of an abundance column per sample.
* Data originally submitted in excel sheets was combined into one data table. The originally named Sheet "16S_Control-Blanks_Species_Raw" with the description "Taxa excluded from downstream analyses" was not combined into the dataset and was instead served as an independent data table in the supplemental files section.

[table of contents | back to top]

Data Files

File	Version
Abundance of species in negative controls filename: 16S_Control-Blanks_Species_Raw.csv (Comma Separated Values (.csv), 1.05 KB) MD5:5b5225084eaa05ea852a843565ebc711 *Abundance of prokaryotic species found in blank negative control samples, samples include empty microcentrifuge tubes and blank GF/F filters. These taxa were excluded from downstream bioinformatic and statistical analyses.*	original

[table of contents | back to top]

Related Publications

Cruz, B. N., Brozak, S., & Neuer, S. (2021). Microscopy and DNA-based characterization of sinking particles

at the Bermuda Atlantic Time-series Study station point to zooplankton mediation of particle flux. Limnology and Oceanography. doi:10.1002/lno.11910
Results

[table of contents | back to top]

Related Datasets

IsRelatedTo

Arizona State University (2020). Prokaryotic and eukaryotic microbial communities within sinking particles from the Bermuda Atlantic Time-series Study (BATS) site. 7-Nov-2020. In: NCBI:BioProject: PRJNA675293. [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA675293.

Neuer, S. (2021) **Images corresponding to some of the samples that underwent 16S and 18S V4 amplicon sequencing of microbial communities in sinking particles collected during R/V Atlantic Explorer cruises AE1718 and AE1809 in 2017 and 2018 at BATS in Bermuda.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-07-08 http://lod.bco-dmo.org/id/dataset/855320 [view at BCO-DMO]
Relationship Description: Images of the same sinking particle samples.

Neuer, S., Cruz, B. N. (2020) **Sample information for 16S and 18S V4 amplicon sequencing of microbial communities in sinking particles and water column samples collected during R/V Atlantic Explorer cruises AE1718 and AE1809 in 2017 and 2018 at BATS in Bermuda.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-11-16 http://lod.bco-dmo.org/id/dataset/828922 [view at BCO-DMO]
Relationship Description: Data from the same sinking particle samples.

[table of contents | back to top]

Parameters

Parameter	Description	Units
prokaryotic_or_eukaryotic	Prokaryotic or eukaryotic	unitless
Taxonomy	Taxonomy	unitless
abundance	Abundances of prokaryotic classes and eukaryotic orders and species. Abundance values are prior to (raw) and following rarefaction.	unitless
sample_name	Sample name	unitless
sample_type	Sample type ("Seawater";"PA_Particles" = phytodetrital aggregate (PA) particles;"FA_Particles"= fecal aggregate (FA) particles)	unitless
depth	Nominal depth of sample	meters (m)
season	Season of the sample	unitless
sample_group	Sample group (e.g. 16s classes raw)	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Niskin bottle
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird SBE 911plus
Dataset-specific Description	CTD Rosette with 12L Niskin bottles used to collect seawater samples: 12L Niskin bottles affixed to a SBE9/11+ CTD Rosette, Sea-Bird Electronics, Inc.
Generic Instrument Description	The Sea-Bird SBE 911plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911plus includes the SBE 9plus Underwater Unit and the SBE 11plus Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9plus and SBE 11plus is called a SBE 911plus. The SBE 9plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3plus and SBE 4). The SBE 9plus CTD can be configured with up to eight 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	Illumina MiSeq
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	Stemi 2000-C, Carl Zeiss
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Stemi 2000-C, Carl Zeiss 3.2MP Digital USB Microscope Camera, OMAX Microscope
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

[table of contents | back to top]

Deployments

AE1718

Website	https://www.bco-dmo.org/deployment/775032
Platform	R/V Atlantic Explorer
Start Date	2017-09-11
End Date	2017-09-16

AE1809

Website	https://www.bco-dmo.org/deployment/828987
Platform	R/V Atlantic Explorer
Start Date	2018-03-12
End Date	2018-03-15

[table of contents | back to top]

Project Information

Aggregation of Marine Picoplankton (Marine Plankton Aggregation)

Coverage: Bermuda Atlantic Time-Series station

NSF abstract:

Marine phytoplankton are microscopic algae that live in the sunlit zone of the ocean. They play an important role in the uptake of carbon dioxide from the atmosphere through photosynthesis, similar to what plants do on land, and are the basis of the marine food web. However, instead of storing this organic carbon in leaf tissue and roots, marine phytoplankton are grazed by planktonic animals, or die and subsequently sink out of the sunlit zone in the form of aggregates, also called "Marine Snow". These

particles not only export the organic carbon contained in their cells to the deep ocean, but also serve as food for animals and bacteria that live in the deep. A considerable portion of these phytoplankton are extremely small, among the tiniest of all organisms known. These extremely small cells have not been thought to play an important role in the formation and sinking of marine snow; however, recent findings challenge this view. This project will investigate how the smallest of these phytoplankton contribute to the rain of sinking particles from the sunlit surface to the deep ocean. This research is important because, in some of the largest expanses of the open oceans, these minute cells dominate the phytoplankton community, and larger plankton organisms are very sparse. The project, through a combination of work in the laboratory and at a field station, will shed light on how these tiny phytoplankton cells make aggregates, which ultimately enable them to sink as "Marine Snow". The project also provides unique opportunities for undergraduate students at Arizona State University, a land-locked public university, to gain experience in working with marine research. The project will serve to educate one PhD student, one MS student in an accelerated BS-MS program, and 8-10 undergraduate students/semester in a unique, inquiry based learning effort termed Microbial EducatioN Training and OutReach (MENTOR). The undergraduate students will also participate in Arizona State University (ASU)'s School of Life Sciences, Undergraduate Research Program (SOLUR), which seeks to increase the participation of minorities in science. They will also contribute towards developing web and classroom materials, based on this project, which will then be distributed through a partnership with the award-winning ASU-sponsored Ask A Biologist K-12 web site.

The oceanic "biological carbon pump", the photosynthetically mediated transformation of dissolved inorganic carbon into particulate and dissolved organic carbon and its subsequent export to deep water, functions as a significant driver of atmospheric carbon uptake by the oceans. The traditional view of the biological carbon pump in the ocean is that of sinking of large aggregates (marine snow) or fecal pellets, which are made up of large, mineral ballasted cells of phytoplankton. However, recent evidence, stemming from in situ investigations of particulate matter, trap studies and modelling studies, have shown that micron-sized phytoplankton such as picocyanobacteria as well as picoeukaryotes can contribute significantly to the sinking of particulate matter. The specific mechanisms behind the sinking of these micrometer sized cells remain elusive as the cells are too small to sink on their own, and mesozooplankton is likely unable to ingest single cells. Intriguingly, recent research by the investigators has shown that the ubiquitous picocyanobacteria Synechococcus are able to form aggregates and sink at velocities comparable to those of marine snow. They found that the matrix of the Synechococcus aggregates was made of Transparent Exopolymeric Particles (TEP), and that TEP production was enhanced under nutrient limited culture conditions. Interaction with clays and presence of heterotrophic bacteria also enhanced aggregation and sinking velocity. This study aims to further investigate aggregation of other common picoplankton in the laboratory and aggregation occurring in natural settings at an oligotrophic open ocean site, the Bermuda Atlantic Time-series Site (BATS). Ultimately, this project will increase and refine our understanding of the role of the smallest phytoplankton in aggregation and sinking - information vital to understanding carbon cycling processes in the oceans.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658527

[table of contents | back to top]