

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

Website: <https://www.bco-dmo.org/dataset/828922>

Data Type: Cruise Results

Version: 1

Version Date: 2020-11-16

Project

» [Aggregation of Marine Picoplankton](#) (Marine Plankton Aggregation)

Contributors	Affiliation	Role
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Abstract

Sample information for 16S and 18S V4 amplicon sequencing of phytodetrital aggregates, fecal aggregates, and water column at the Bermuda Atlantic Time-series Study (BATS) site. Particles were collected on the monthly sampling cruises affiliated with the BATS in fall 2017 (AE1718) and spring 2018 (AE1809) on the R/V Atlantic Explorer. These data were published in Neuer et al. (2021). Genetic sequences are available at the National Center for Biotechnology Information (NCBI) under BioProject PRJNA675293.

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Coverage

Spatial Extent: N:31.97 E:-64.42 S:31.57 W:-64.57

Temporal Extent: 2017-09-12 - 2018-03-15

Methods & Sampling

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, Neuer et al., 2021). 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 -80°C. 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 -80°C.

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.

Issues:

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

Data 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:

* converted lat and lon from degrees north and east to decimal degrees.

* replaced line returns separating image names within values for "associated_media" column to semicolons. Replacement made to support interoperable file formats.

* removed direct HTML links to accession pages at NCBI, these are accessible with the accession numbers in the dataset.

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Data Files

File
sample_metadata.csv (Comma Separated Values (.csv), 23.04 KB) MD5:1612f2769f57969ba76a21a1e11ca04f Primary data file for dataset ID 828922

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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](https://doi.org/10.1002/lno.11910)
Results

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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
doi:10.26008/1912/bco-dmo.855320.1 [[view at BCO-DMO](#)]
Relationship Description: Images of the same sinking particle samples.

Neuer, S. (2021) **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.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-07-08
doi:10.26008/1912/bco-dmo.855296.1 [[view at BCO-DMO](#)]
Relationship Description: Sample information and genetic accession info for the same sinking particle samples.

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Parameters

Parameter	Description	Units
sample_description	Sample description	unitless
depth	Nominal depth of sample collection	meters (m)
particle_trap_deployment_date	Particle trap deployment date (ISO 8601 format YYYY-MM-DD)	unitless
particle_trap_recovery_date	Particle trap recovery date (ISO 8601 format YYYY-MM-DD)	unitless
seawater_collection_date	Seawater collection date (ISO 8601 format YYYY-MM-DD)	unitless
latitude	latitude	decimal degrees
longitude	longitude	decimal degrees
associated_media	Filenames of images of the particles pertaining to this sample (list of image names delimited with semicolons)	unitless
sample_name	sample name	unitless
bioproject_accession	BioProject accession identifier at the National Center for Biotechnology Information (NCBI)	unitless
biosample_accession	BioSample accession identifier at the National Center for Biotechnology Information (NCBI)	unitless
SRA_run_ID	Sequence Read Archive (SRA) Run identifier at the National Center for Biotechnology Information (NCBI)	unitless

library_ID	library identifier	unitless
SRA_study_ID	Study identifier in the Sequence Read Archive (SRA) at the National Center for Biotechnology Information (NCBI)	unitless
SRA_title	Descriptive title of Sequence Read Archive (SRA) accession at the National Center for Biotechnology Information (NCBI)	unitless
library_strategy	Library strategy ("AMPLICON")	unitless
library_source	Library source ("GENOMIC")	unitless
library_selection	Library selection ("PCR")	unitless
library_layout	Library layout ("paired")	unitless
platform	Sequencing platform ("Illumina")	unitless
instrument_model	Sequencing instrument model ("Illumina MiSeq")	unitless
design_description	Sequencing design description	unitless
filetype	Type of file 1 at NCBI	unitless
filename	Name of file 1 at NCBI	unitless
filetype2	Type of file 2 at NCBI	unitless
filename2	Name of file 2 at NCBI	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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 911 plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911 plus 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 9 plus and SBE 11 plus is called a SBE 911 plus. The SBE 9 plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 plus and SBE 4). The SBE 9 plus 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	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".

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.

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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

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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.

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Funding

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

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