Bacteria Counts CTD Bottle Measurements from CTD samples collected during R/V Hugh R. Sharp cruise HRS2204 from Apr to May 2022

Website: https://www.bco-dmo.org/dataset/945987
Data Type: Cruise Results, Other Field Results
Version: 1
Version Date: 2025-02-28

Project
» Collaborative Research: The importance of particle disaggregation on biogeochemical flux predictions (Disaggregation)

Contributors	Affiliation	Role
Rau, Matthew	Pennsylvania State University (PSU)	Principal Investigator
Thamatrakoln, Kimberlee	Rutgers University	Scientist
Grubb, Austin	Rutgers University	Student
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
These data include measurements of free bacteria in whole seawater and particle-associated bacteria for particles larger than 1.2 microns from CTD bottle water samples collected during a cruise on the Northeast Continental Shelf to study particle disaggregation. One cruise was completed aboard the R/V Hugh R. Sharp from 2022-04-21 through 2022-05-02 (HRS 22-04), which visited a variety of stations and hydrodynamic environments associated with the Northeast Continental Shelf of the United States. Stations ranged from Georges Bank and the Great South Channel near the Gulf of Maine, Martha's Vineyard, the mouth of the Sakonnet River near Newport, Rhode Island, and Hudson Canyon near New York. These data were collected as part of a study to clarify the importance of hydrodynamic forces on the cohesion, aggregation, and breakup of marine particles. These data were collected by Dr. Austin Grubb of the Rutgers University on the cruise led by Dr. Matthew Rau (chief scientist) of the George Washington University.

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Coverage

Location: Northeastern U.S. Continental Shelf
Spatial Extent: **N**:41.7745 **E**:-67.4007 **S**:39.4554 **W**:-72.2765
Temporal Extent: 2022-04-23 - 2022-04-28

Methods & Sampling

This cruise visited eight stations on the Northeastern U.S. Continental Shelf. Latitudes and longitudes provided per sample in the data, but general station descriptions are below.

- Station 1 - Station 3: Georges Bank near the Gulf of Maine. Approximate location was 41.7 N, 68 W. Samples acquired from 0 m to 25 m depths.
- Station 4: The Great South Channel near the Gulf of Maine. Approximate location was 41.6 N, 69 W. Samples acquired from 0 m to 150 m depths.
- Station 5: Only one CTD profile was taken before this station was aborted due to weather. No data acquired. Station location was 40.8 N, 70.5 W.
- Station 6: Off the coast of Martha's Vineyard. Approximate location was 41.3 N, 70.5 W. Samples acquired from 0 m to 10 m depths.
- Station 7: At the mouth of the Sakonnet River near Newport, Rhode Island. Approximate location was 41.5 N, 71.2 W. Samples acquired from 0 m to 10 m depths.
- Station 8: Hudson Canyon near New York. Approximate location was 39.5 N, 72.3 W. Samples acquired from 0 m to 200 m depths.

Whole seawater and 1.2 um filtrates were fixed in final concentration of 0.5% glutaraldehyde for 15 min at 4 degrees, then flash frozen in liquid N2 and stored at -20 degree until analysis. Samples were thawed at room temperature and 10 ug/ml Tween-80 (final concentration) was added to each. Samples were sonicated for 1 min in a water bath (50W). A 20,000-fold dilution of Sybr Green I Nucleic Acid stain (Thermo-Fisher) was made in 0.2 um filtered 1XTE. 5ul of sample was mixed with 245 ul of 1X TE/Sybr Green I in a 96 well microtiter plate. Samples were counted on an Accrui C6 Plus flow cytometer on a fast flow rate, triggered off FL1-H<1000 for 30 sec.

Data Processing Description

Particle associated bacteria were calculated by subtracting concentrations of the 1.2 micron filtrate from the concentrations obtained for whole seawater. Free and particle-associated bacteria concentrations were calculated from raw counts accounting for dilutions. Other data processing was not applicable.

BCO-DMO Processing Description

- Imported "HRS22-04_BacteriaCounts.xlsx" with excel formatting into the BCO-DMO system
- Combined date and times to create datetime field
- Removed original date and time fields
- Renamed fields to comply with BCO-DMO naming conventions
- Exported final file as "945987_v1_bacteria_counts_ctd.csv"

Problem Description

The particle-associated bacteria counts at some stations/depths were quite low, resulting in negative values after subtracting as described in the data processing above.

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Data Files

File	
945987_v1_bacteria_counts_ctd.csv	(Comma Separated Values (.csv), 3.28 KB) MD5:88d03f32f3e26a67b384c674860888a5
Primary data file for dataset ID 945987, version 1	

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Parameters

Parameter	Description	Units
ID	ID of the CTD cast sample, formatted as (station#_CTDcast#_depth)	unitless
Station	Station number	unitless
CTD	CTD cast number	unitless
Depth	Depth in meters that the CTD bottle was triggered for sampling	meters (m)
ISO_DateTime_UTC	ISO datetime the sample was acquired in UTC	unitless
Latitude	Ship's latitude when the sample was taken	decimal degrees
Longitude	Ship's longitude when the sample was taken	decimal degrees
Free_bacteria	Bacteria concentration in 1.2 micron filtered fraction	cells/ml
Particle_associated_bacteria_concentration	Bacteria concentration of whole seawater minus that in 1.2 micron filtered fraction	cells/ml

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Instruments

Dataset-specific Instrument Name	CTD
Generic Instrument Name	CTD Sea-Bird 911
Dataset-specific Description	These data include measurements of free bacteria in whole seawater and particle-associated bacteria for particles larger than 1.2 microns from CTD bottle water samples collected during a cruise on the Northeast Continental Shelf to study particle disaggregation.
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	Accuri C6 Plus flow cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Samples were counted on an Accuri C6 Plus flow cytometer.
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

HRS2204

Website	https://www.bco-dmo.org/deployment/946038
Platform	R/V Hugh R. Sharp
Start Date	2022-04-21
End Date	2022-05-02
Description	See additional cruise information in R2R: https://www.rvdata.us/search/cruise/HRS2204

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Project Information

Collaborative Research: The importance of particle disaggregation on biogeochemical flux predictions (Disaggregation)

Coverage: Northeast United States Continental Shelf

NSF abstract:

Particle settling is one of the major ways that material in surface waters reaches the deep ocean. Particulate matter in the open ocean consists primarily of organic material from plankton and other biological detritus, which can readily aggregate to form large flocs. A combination of physical, chemical, and biological processes transforms these flocs as they settle, redistributing material throughout the water column and potentially sequestering elements such as carbon in the deep ocean. The impact of these transformations is affected by the sinking speed of these flocs, with larger and denser particles settling faster than smaller, less-dense ones. One of the key questions facing oceanographers today is what controls particle settling speed (for example, particle size, shape, and density). There is considerable evidence that particles readily break apart as they settle, decreasing their average size and settling speed, but it is not yet understood what conditions cause these disaggregation events. This work will measure the breakup characteristics of organic settling particles both in the laboratory and at sea to quantify the importance of these breakup processes relative to particle transport. The work will be done at the Pennsylvania State University in collaboration with the University of Georgia to target the development of future marine particle disaggregation models for use by the

oceanographic community.

This research will play an important role in determining the importance of disaggregation on the vertical transport of particulate matter in the ocean. The project will quantify the breakup of organic marine aggregates due to fluid forces caused by turbulence or swimming organisms. Phytoplankton will be cultured and formed into aggregates in the lab prior to disaggregation using calibrated turbulence. The size, shape, and structure of these aggregates before and after breakup will be quantified using high-speed visualization and holographic imaging. In addition to the laboratory measurements, a deployable instrument that can disrupt particles in-situ and measure their size and shape will be built and deployed in the North Atlantic during the spring bloom of phytoplankton. Detailed measurements of particle concentrations, breakup characteristics, organic content, and ambient turbulence as a function of depth in the water column will be collected. This work will represent the first study of marine aggregate breakup in-situ. Specifically, the project will clarify: (1) under what conditions disaggregation is important, (2) how strong different types of natural marine aggregates are and how their strength varies with size, composition, and morphology, and (3) how aggregate size, composition, and structure influences the distribution of its breakup mass. This project will advance the career of a doctoral student and engage numerous undergraduate researchers with the field of ocean science.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

Additional Project Output (supplement to Data Collections section below):

Model Code Description:

Adrian Burd's Research Lab. (2023). BurdLab/Dissaggregation: Disaggregation (Disaggregation). Zenodo. https://doi.org/10.5281/zenodo.8226166

Associated Github Repository: https://github.com/BurdLab/Dissaggregation/tree/Disaggregation

This is the initial release of model code for particle aggregation and disaggregation in the ocean. The referenced Github Repository contains Matlab code to calculate the evolution of the particle size distribution in a single layer of the water column. The code numerically solves the aggregation-disaggregation mass balance equations using a so-called sectional approach developed by Gelbard and Seinfeld (J. Colloid and Interface Sci., 68:363-382, 1979). The model allows for particle aggregation, disaggregation, and sinking, and also changes in aggregate size from cell growth (see SetUpCoag.m), and will form the basis of a suite of particle aggrgation/disaggregation models. All documentation is provided within the code itself. Please see Associated Github Repository link above for detailed description and files.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1948283
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