Microbiome profiling of bacterioplankton communities on sponge excurrent water, coral exudate water, and surface reef water.

Website: https://www.bco-dmo.org/dataset/964182
Data Type: experimental
Version: 1
Version Date: 2025-06-17

Project
» Collaborative Research: The Influence of Sponge Holobiont Metabolism on Coral Reef Dissolved Organic Matter and Reef Microorganisms (Sponge Holobiont DOM)

Contributors	Affiliation	Role
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Abstract
Sponge exhalent water was collected from Looe Key reef, coral exudates water was collected from a coral incubation at Mote Marine lab, and ambient reef water was collected from Looe Key Reef surface water. All seawater was 0.2 um filtered to use as media in 2L bottles for an incubation experiment. Inoculum from reef surface water (1.6 um filtered) was used for the incubation. Bottles were incubated in the dark for 48 hours and samples were taken at the start (T0) and end (T48) for nutrient and microbiome analysis.

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Coverage

Location: Looe Key Reef, Florida Keys National Marine Sanctuary.
Spatial Extent: **Lat**:24.562002777778 **Lon**:-81.40871111
Temporal Extent: 2022-01-06 - 2022-01-08

Methods & Sampling

Seawater sampled from the incubation ‘soup’ or bottles was used for multiple nutrient analyses and DNA

extraction.

The rest of the seawater was filtered through an Omnipore 0.2 um filter using a peristaltic pump and acid and milliQ water rinsed Pharmed BP tubing and Teflon filter holders. The filter was stored at -80C until DNA extraction.

The NCBI dataset is the microbiome profiling data of the incubation experiment. These are the reads of 16S rRNA genes for each sample in the incubation experiment. Bottle incubations were set up as described in the methods for dataset 963872. The seawater from the bottles were filtered at T0 and at T48 and the filters were used for DNA extraction, amplification of the v4 region of the 16S rRNA gene, and Illumina sequencing. Additional details available through the NCBI accession link.

Data Processing Description

DNA from the Omnipore filters was extracted using a commercial kit and the 16S rRNA gene was amplified using the modified earth microbiome primer set for the V4 region (515F and 806R, Apprill et al. 2015). PCRs were sent to Middle Tennessee State University for library construction and sequencing on an Illumina MiSeq, producing FASTQ files as output.

BCO-DMO Processing Description

*Added sampling date to dataset

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Data Files

File
964182_v1_ncbi.csv (Comma Separated Values (.csv), 54.15 KB) MD5:2a3b2a60824d28a21e5b850328e7f272
Primary data file for dataset ID 964182, version 1

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Related Datasets

IsRelatedTo

Appalachian State University. Sponge Coral Picoplankton Incubation Experiment. 2025/02. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA1227475. NCBI:BioProject: PRJNA1227475. https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1227475

Apprill, A., Easson, C. G., Fiore, C. L., Reigel, A. M. (2025) **Effects of sponge excurrent seawater on coral reef picoplankton composition in the Florida Keys January 2022.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-06-17 doi:10.26008/1912/bco-dmo.963872.1 [view at BCO-DMO]
Relationship Description: Incubation experiment.

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Parameters

Parameter	Description	Units
Bioproject_Accession	NCBI Bioproject accession ID	unitless
Biosample_accession	NCBI Biosample accession ID	unitless
Sample_Name	Submitter sample name	unitless
SRA_run_ID	NCBI SRA run accession ID	unitless
SRA_run_link	Link to SRA data on NCBI	unitless
SPUID	SPUID (Submitter Provided Unique Identifier), a unique identifier assigned by the submitter to a sample in the NCBI BioSample database	unitless
Organism	Biological entity	unitless
Tax_ID	Unique numerical identifier assigned by unique numerical identifier assigned by the NCBI Taxonomy database to each organism or taxonase to each organism or taxon	unitless
library_ID	Unique identifier for the sequencing library (can be the sample name repeated).	unitless
SRA_study_ID	NCBI study accession ID	unitless
SRA_title	Title of SRA run	unitless
library_strategy	Sequencing library strategy	unitless
library_source	Source of sequencing library	unitless
library_selection	Selection used for sequencing library	unitless
library_layout	single or paired end sequencing reads	unitless
platform	Sequencing platform manufacturer	unitless
instrument_model	Sequencer model	unitless

design_description	Description explaining how this library was prepared and sequenced	unitless
filetype	File type	unitless
filename	Forward reads file name	unitless
filetype2	File type	unitless
filename2	Reverse reads file name	unitless
depth	Sampling depth	meters (m)
latitude	Sampling latitude, south is negative	decimal degrees
longitude	Sampling longitude, west is negative	decimal degrees
sample_date	Sample date	

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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.

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Project Information

Collaborative Research: The Influence of Sponge Holobiont Metabolism on Coral Reef Dissolved Organic Matter and Reef Microorganisms (Sponge Holobiont DOM)

Coverage: Caribbean Sea

NSF Award Abstract:
The seawater around coral reefs is typically low in nutrients, yet coral reefs are teeming with life and are often compared to oases in a desert. Life exists in these 'marine deserts' in large part, due to symbiotic associations between single-celled microbes and invertebrates such as corals and sponges. The concentration and type of dissolved organic matter (DOM), a complex pool of organic nutrients such as amino acids, vitamins, and other diverse compounds, also affects the health of coral reefs. The composition of DOM on coral reefs is linked to

both the composition of free-living microbes in the seawater and to the nutrition of filter-feeding organisms, such as corals and sponges. However, the factors that influence the composition of DOM on coral reefs and the consequences of how it changes are not well understood. Recent work suggests that sponges could have a significant impact on the composition of reef dissolved organic nutrients, depending on sponge species due to differences in filtration capacity and in their symbiotic microbial communities. This project characterizes how diverse sponge species process DOM on coral reefs and determines the impacts of this processing on the free-living microbial community. Seawater is collected from sponges (pre- and post- sponge filtration) on coral reefs in the relatively pristine region of Curacao, and incubation experiments measure the impact of sponge filtration on the growth of the free-living microbial community. The organic nutrients of seawater samples are analyzed using cutting-edge techniques to distinguish the types of nutrients that are processed by sponges. The incubation experiments, using free-living microbes collected from the coral reef, quantify the impact of sponge filtration on the growth and composition of this community. This project provides fundamental understanding of how sponges contribute to the base of the coral reef food web. As the human-driven impacts continue to alter the composition of organisms on reefs, this understanding is necessary to predict changes to reef microbial food webs and is thus essential for scientists, reef managers, and policy decision makers. This project trains undergraduate students and a postdoctoral scholar and contributes to undergraduate and K-12 education through development of sponge-centric lessons that focus on local U.S. east coast aquatic environments as well as coral reef ecosystems.

Sponges vary in their capacity to filter seawater and in their associated microbial communities, leading to diverse metabolic strategies that often coexist in one habitat. While it is well-established that sponges are important in processing dissolved organic matter (DOM), an important reservoir of reduced carbon compounds, and transferring this energy to benthic food webs, there has been limited work to understand the consequences of sponge processing on the composition of coral reef DOM and on pelagic food webs. Specifically, while studies have shown that exudates of corals and algae select for specific groups of picoplankton (autotrophic and heterotrophic, respectively), similar data for sponges are required to understand the multiple factors that shape the composition of DOM and of the picoplankton community on coral reefs. Thus, this project is aimed at addressing a major knowledge gap of the role of sponge-derived DOM (sponge exometabolome) in coral reef biogeochemistry. An in situ sampling design targeting prominent Caribbean sponges and picoplankton incubation experiments is coupled to address both the composition of sponge exometabolomes and delineate shifts in the picoplankton community derived from sponge exometabolomes. Molecular-level changes to seawater DOM by sponge processing and the impact of these changes on the overall coral reef DOM profile is assessed with two DOM analysis techniques: a commonly used fluorometry technique (fDOM analysis) and with high-resolution mass spectrometry (LC-MS/MS). Additionally, microbiome and functional gene profiling, growth metrics, and nutrient analyses are employed to assess changes in the picoplankton community in response to sponge exometabolomes. Advanced data analysis techniques then synthesize data generated by each approach to provide novel insight on a poorly uncharacterized biogeochemical pathway on coral reefs. The work outlined here represents entirely novel information on the impact of sponge metabolism on the composition of DOM, sheds light on biologically important molecules involved in benthic-pelagic coupling, and importantly, generates data using standardized methods, thus facilitating comparison to previous and future DOM datasets.

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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1924540
NSF Division of Ocean Sciences (NSF OCE)	OCE-1923962

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