Metagenome profiles of common emergent Caribbean sponges collected from temporary artificial reef in the Florida Keys, USA in Jan 2022

Website: https://www.bco-dmo.org/dataset/969228
Data Type: Other Field Results
Version: 1
Version Date: 2025-07-18

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

Contributors	Affiliation	Role
Apprill, Amy	Woods Hole Oceanographic Institution (WHOI)	Co-Principal Investigator
Easson, Cole G.	Middle Tennessee State University	Co-Principal Investigator
Fiore, Cara L.	Appalachian State University	Co-Principal Investigator
Zuniga, Luis	Middle Tennessee State University	Student
Moore, Danielle	Appalachian State University	Technician
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Sponges are prevalent on Caribbean coral reefs and are important filter-feeders that can influence seawater nutrient composition. This study examined the metagenome profiles of sponge species that were also used for examination of nutrient processing. The metagenome profiles (BioProject PRJNA1256488) showed convergence in several nitrogen pathways (e.g., dissimilatory, assimilatory nitrate reduction, denitrification) but differences in the taxonomic composition of those pathways. Additional analysis of the metagenome profiles is ongoing. Included in this dataset are accession information, collection metadata, and sample preparation data for common emergent Caribbean sponges collected from temporary artificial reef in the Florida Keys in January 2022.

Table of Contents

Coverage

Location: Shallow reefs (<10m) in the Florida Keys, USA. Acon (Agelas tubulata) samples were collected from Looe Key Reef at 6m depth in January 2022 (24.56200278, -81.40871111).
Spatial Extent: **N**:24.569055 **E**:-81.369452 **S**:24.56200278 **W**:-81.40871111
Temporal Extent: 2022-01-07 - 2022-01-13

Methods & Sampling

Using day boats from a local boat rental company, sponge tissue (about 3-4 cm3) was collected from the sponge in situ (3 - 6 m depth, FL Keys, USA) and put in a sterile Whirl-Pak bag with seawater. Bagged samples were stored on ice in the boat until return to the laboratory where they were removed from the water and stored in a cryovial (no buffer) at -80 degrees C. Total DNA was extracted from the sponge tissue and either host depleted ('hd' in sample name) using a QIAmp DNA microbiome kit or not host depleted (DNA extracted with the Qiagen powersoil powerlyser kit) before use in metagenome sequencing. Metagenome library preparation was completed with TruSeq DNA PCR-Free LP Illumina prep kit and sent to Azenta Life Sciences for sequencing. DNA sequencing was performed on an Ilumina HiSeq 4000 using 150 nucleotide length reads with paired end sequencing.

Data Processing Description

Low quality reads and adapter sequences were removed from the raw demultiplexed data using fastp version 0.23.2 (Chen et al 2018). Filtered short reads were assembled into longer nucleotide contiguous sequences (contigs) using SPAdes version 3.15.0 (Bankevich et al 2012). Gene prediction using the contigs was completed with Prodigal version 2.6.3 (Hyatt et al 2010). Functional annotation was completed with the KEGG GhostKoala server (Kanehisa et al 2016). An in-house script “koala_sort.py” (Zuniga Acuna, n.d.) was used to filter out genes of interest for pathway specific analysis. Visualization of gene abundance was performed with the output of GhostKoala and sorted with the Koala_sort.py and visualized using R statistical software version 4.3.2 (R Core Team 2023).

BCO-DMO Processing Description

- Imported "Caribbean Sponge Metagenome Accession Table.xlsx" into BCO-DMO system
- Split "Coordinates" parameter into Latitude and Longitude
- Formatted the collection date in ISO 8601 format YYYY-MM
- Renamed fields to remove spaces and replace with underscores
- Exported file as "969228_v1_metagenome_emergent_sponges.csv"

[table of contents | back to top]

Data Files

File	
969228_v1_metagenome_emergent_sponges.csv	(Comma Separated Values (.csv), 2.16 KB) MD5:25ac05ef926354a93fb472cf7b117e50
Primary data file for dataset ID 969228, version 1	

[table of contents | back to top]

Related Publications

Bankevich, A., Nurk, S., Antipov, D., Gurevich, A. A., Dvorkin, M., Kulikov, A. S., … Pevzner, P. A. (2012). SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. Journal of Computational Biology, 19(5), 455–477. doi:10.1089/cmb.2012.0021
Methods

Chen, S., Zhou, Y., Chen, Y., & Gu, J. (2018). fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics, 34(17), i884–i890. https://doi.org/10.1093/bioinformatics/bty560
Software

Hyatt, D., Chen, G.-L., LoCascio, P. F., Land, M. L., Larimer, F. W., & Hauser, L. J. (2010). Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics, 11(1). doi:10.1186/1471-2105-11-119
Methods

Kanehisa, M., Sato, Y., & Morishima, K. (2016). BlastKOALA and GhostKOALA: KEGG Tools for Functional Characterization of Genome and Metagenome Sequences. Journal of Molecular Biology, 428(4), 726–731. https://doi.org/10.1016/j.jmb.2015.11.006
Software

R Core Team (2023). R: A language and environment for statistical computing. R v4.3.2. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Zuniga Acuna, Luis. (n.d.) LuisZ_MS_supplemental. GitHub. https://github.com/la-zuniga/LuisZ_MS_supplemental
Software

[table of contents | back to top]

Related Datasets

References

Appalachian State University. Caribbean Sponge Metagenomes. 2025/04. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1256488. NCBI:BioProject: PRJNA1256488.

[table of contents | back to top]

Parameters

Parameter	Description	Units
Accession_Number	NCBI Biosample accession number	unitless
Sample_Name	Name of sample, unique identifier	unitless
Organism	Type of organism utilized for experimentation	unitless
Sample_Preparation	DNA extracted with selection for prokaryotic DNA (QIAmp DNA microbiome kit) or total DNA (Qiagen powersoil powerlyser kit)	unitless
Collection_Date	Date of sample collection	unitless
Latitude	Latitude of sample collection, positive is North	decimal degrees
Longitude	Longitude of sample collection, negative is South	decimal degrees

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina HiSeq 4000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Metagenome library preparation was completed with TruSeq DNA PCR-Free LP Illumina prep kit and sent to Azenta Life Sciences for sequencing. DNA sequencing was performed on an Ilumina HiSeq 4000 using 150 nucleotide length reads with paired end sequencing.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]