16S microbiome metadata collected from shallow artificial reef sponges and seawater in the Florida Keys, USA from Apr 2021 to Aug 2021

Website: https://www.bco-dmo.org/dataset/953999
Data Type: Other Field Results
Version: 1
Version Date: 2025-02-21

Project
» Collaborative Research: Investigations into microbially mediated ecological diversification in sponges (Ecological Diversification in Sponges)

Contributors	Affiliation	Role
Easson, Cole G.	Middle Tennessee State University	Principal Investigator
Fiore, Cara L.	Appalachian State University	Co-Principal Investigator
Freeman, Christopher J.	College of Charleston (CofC)	Co-Principal Investigator
Thacker, Robert W.	Stony Brook University (SUNY Stony Brook)	Co-Principal Investigator
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Sponges are a dominant component of coral reefs worldwide and in the Caribbean, where their biomass exceeds that of reef-building corals. For almost a quarter century, the success of sponges in the Caribbean has been linked to their filter-feeding ability. However, recent work demonstrated that coexisting sponges on Caribbean reefs host unique communities of bacteria that might allow sponges to access multiple pools of nutrients that are not available to other organisms. In this project, the investigators will test the hypothesis that ecologically dominant sponge species in the Caribbean have unique metabolic strategies that are mediated by their associations with microbes that live within the sponge body. In this dataset, we present the 16S rRNA microbiome NCBI accession and sample collection metadata for an artificial reef experiment where sponges of 10 species were placed on this temporary reef from April to August of 2021 and sampled using VacuSIP. VacuSIP methods capture incurrent (In) and excurrent (Ex) water from each sponge specimen. Incurrent represents the bacteria that are available for the sponge to consume via filter feeding and excurrent represents the bacteria that remain once sponges have consumed their preferred taxa. Additionally, we have provided microbiome metadata for the host sponges for several of these paired In/Ex samples. See the related dataset, NCBI Bioproject PRJNA1179970, for all sequence data. Microbiome data was generated using protocols from the Earth Microbiome project and sequencing was conducted on an Illumina MiSeq at Middle Tennessee State University. The data available at NCBI represents raw sequencing data, and no quality checks or sequencing filtering has been done on the uploaded sequences.

Table of Contents

Coverage

Location: These data were generated on shallow reefs (<10m) in the Florida Keys, USA.
Spatial Extent: **N**:24.576 **E**:-81.369 **S**:24.538 **W**:-81.423
Temporal Extent: 2021-04 - 2021-08

Methods & Sampling

Location
Samples were collected on shallow reefs (<10m) in the Florida Keys, USA. The temporary artificial reef was constructed adjacent to patch reefs within the Looe Key special preservation area. At the conclusion of the experiment, the reef was completely dismantled. The environment was well mixed by wave action within minimal tidal influence.

Collection and Analysis

Seawater samples were collected via VacuSIP and filtered through 0.2 µm membranes with a peristaltic pump to collect samples of ambient microbes. Total genomic DNA was extracted from cross sections of sponge tissue (~0.25 grams) and ½ of seawater filter membranes using Qiagen PowerSoil Powerlyzer extraction kit and following the manufacturers protocol. After DNA extraction, polymerase chain reaction (PCR) was performed following the 16S Illumina Amplicon protocol of the Earth Microbiome project (Caporaso, 2018) with barcoded 16S rRNA primers (515F and 806R; (Apprill et al. 2015, Parada et al. 2016) and PCR products were cleaned using AMPure beads (Beckman Coulter). DNA concentration in cleaned products was measured using a Qubit fluorometer (Qubit). The concentration of each sample was diluted to 4 nM and then all samples were pooled in equal volumes. Pooled samples were then sequenced on an Illumina MiSeq platform following standard Illumina protocols for sample preparation and loading except that custom sequencing primers from the EMP protocol were used. A 500 cycle V2 chemistry MiSeq kit was used during sequencing, which yielded paired-end 250 base pair (bp) amplicons.

Data Processing Description

Sample barcodes were input into the MiSeq to demultiplex samples. No additional data processing was done to these samples.

BCO-DMO Processing Description

- Imported "PRJNA1179970_attributes_11_22.tsv" into the BCO-DMO System
- Removed columns without values
- Imported WoRMS report on all species included in the dataset as "easson_organisms_matched.txt" into the BCO-DMO System
- Join "easson_organisms_matched.txt" to "PRJNA1179970_attributes_11_22.tsv" on the species name, including the AphiaID and the LSID in the dataset
- Split the lat_lon field into Latitude and Longitude and removed the string components
- Convert West Long values to negative
- Exported file as "953999_v1_16s_reef_microbiome.csv"

Problem Description

No known issues with these data.

[table of contents | back to top]

Related Publications

Apprill, A., McNally, S., Parsons, R., & Weber, L. (2015). Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. Aquatic Microbial Ecology, 75(2), 129–137. doi:10.3354/ame01753

Methods

Greg Caporaso, J., Ackermann, G., Apprill, A., Bauer, M., Berg-Lyons, D., Betley, J., Fierer, N., Fraser, L., A. Fuhrman, J., A. Gilbert, J., Gormley, N., Humphrey, G., Huntley, J., K. Jansson, J., Knight, R., L. Lauber, C., A. Lozupone, C., McNally, S., M. Needham, D., … Weber, L. (2018). EMP 16S Illumina Amplicon Protocol v1. https://doi.org/10.17504/protocols.io.nuudeww
Methods

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2015). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. Environmental Microbiology, 18(5), 1403–1414. doi:10.1111/1462-2920.13023
Methods

[table of contents | back to top]

Related Datasets

Related Research

Middle Tennessee State University (2024). InEx and Sponge microbiome samples. 2024/10. NCBI:BioProject: PRJNA1179970. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1179970.

[table of contents | back to top]

Parameters

Parameter	Description	Units
collection_date	Date of sample collection	unitless
latitude	Latitude of sample collection; north is positive	Decimal Degrees
longitude	Longitude of sample collection; west is negative	Decimal Degrees
accession	NCBI BioSample accession number	unitless
sample_name	Sample identifier	unitless
species_ab	Species abbreviation of sponge ajacent to the sampler	unitless
sample_type	Description of sample type: tissue, incurrent (In), or excurrent (Ex) water	unitless
organism	Organism that corresponds to tissue samples	unitless
AphiaID	AphiaID of organism that corresponds to tissue samples	unitless
LSID	LSID of organism that corresponds to tissue samples	unitless
isolation_source	Type of source: environmental	unitless
geo_loc_name	Geographic location of sample source	unitless
data_day	data_day	days
seq_attempt	seq_attempt	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina MiSeq - sequencer used to generate sequence libraries from prepared samples
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Qubit
Generic Instrument Name	Qubit fluorometer
Dataset-specific Description	Qubit - fluorometer used for quantitation of double-stranded DNA
Generic Instrument Description	Benchtop fluorometer. The Invitrogen Qubit Fluorometer accurately and quickly measures the concentration of DNA, RNA, or protein in a single sample. It can also be used to assess RNA integrity and quality. Manufactured by Invitrogen, Carlsbad, CA, USA (Invitrogen is one of several brands under the Thermo Fisher Scientific corporation.)

Dataset-specific Instrument Name	Vortex
Generic Instrument Name	Shaker
Dataset-specific Description	Vortex - standard laboratory vortex for mixing samples and extracting DNA
Generic Instrument Description	A Shaker is a piece of lab equipment used to mix, blend, or to agitate substances in tube(s) or flask(s) by shaking them, which is mainly used in the fields of chemistry and biology. A shaker contains an oscillating board which is used to place the flasks, beakers, test tubes, etc.

Dataset-specific Instrument Name	Thermal cycler
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Thermal cycler - Used for polymerase chain reaction
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

[table of contents | back to top]

Project Information

Collaborative Research: Investigations into microbially mediated ecological diversification in sponges (Ecological Diversification in Sponges)

Coverage: Caribbean coast of Panama

NSF Award Abstract:
Coral reefs represent a paradox because, despite their immense productivity and biodiversity, they are found in nutrient-poor habitats that are equivalent to "marine deserts." High biodiversity is often associated with a division of resources that allows many types of organisms to coexist with minimal competition. Indeed, unlike many other organisms on coral reefs, sponges are adapted to efficiently remove bacteria, phytoplankton, and dissolved organic matter from seawater by filter-feeding. Sponges are a dominant component of coral reefs worldwide and in the Caribbean, where their biomass exceeds that of reef-building corals. For almost a quarter century, the success of sponges in the Caribbean has been linked to their filter-feeding ability. However, recent work demonstrated that coexisting sponges on Caribbean reefs host unique communities of bacteria that might allow sponges to access multiple pools of nutrients that are not available to other organisms. In this project, the investigators will test the hypothesis that ecologically dominant sponge species in the Caribbean have unique metabolic strategies that are mediated by their associations with microbes that live within the sponge body. This research will combine manipulative field experiments with a novel combination of modern analytical tools to investigate both filter-feeding by sponge hosts and the metabolic pathways of their microbes. This work will advance our understanding of the ecological and evolutionary forces that have helped shape the species present on Caribbean coral reefs. Additionally, this project will support three early-career investigators and provide training opportunities for graduate and undergraduate students at Nova Southeastern University, Appalachian State University, Stony Brook University, and Smithsonian Marine Station. The investigators will also develop innovative outreach programs that expand existing platforms at their institutions to increase public engagement and scientific literacy.

Marine sponges have been widely successful in their expansion across ecological niches in the Caribbean, with biomass often exceeding that of reef-building corals and high species diversity. However, whether this success is linked to efficient heterotrophic filter-feeding on organic carbon in the water column or to their evolutionary investment in microbial symbionts is yet to be fully elucidated. Microbial symbionts expand the metabolic capabilities of host sponges, supplementing heterotrophic feeding with inorganic carbon and nitrogen, mediating the assimilation of dissolved organic matter, and facilitating recycling of host-derived nitrogen. Despite these benefits, microbial symbiont communities are widely divergent across coexisting sponge species and there is substantial variation in host reliance on symbiont-derived carbon and nitrogen among host sponges; therefore, these associations likely mediate the ecological diversification of coexisting sponge species. The goal of this project is to test this transformative hypothesis by adopting an integrative approach to assess the individual components of holobiont metabolism (i.e., microbial symbionts and sponge host) in ten of the most common sponge species in the Caribbean. The investigators will isolate autotrophic and heterotrophic metabolic pathways and explore potential links between microbial symbiont community composition and the assimilation of particulate and dissolved organic matter (POM and DOM) from seawater. This project will elucidate whether Caribbean sponge species are on similar or divergent evolutionary trajectories, and will provide information that is critical for our understanding of how conditions in the Caribbean basin have shaped the evolution of benthic organisms.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1915949
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756799
NSF Division of Ocean Sciences (NSF OCE)	OCE-1929293
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756114
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756249
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756171

[table of contents | back to top]