NCBI accessions and metadata associated with Caribbean sponge metagenomes collected from Curacao, Belize, Cayman Islands and St. Croix, 2009 and 2017-2018

Website: https://www.bco-dmo.org/dataset/775451
Data Type: Other Field Results
Version: 1
Version Date: 2019-08-15

Project
» Collaborative Research: Dimensions: Evolutionary Ecology of Sponges and Their Microbiome Drives Sponge Diversity on Coral Reefs (DimensionsSponge)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
Lesser, Michael P.	University of New Hampshire (UNH)	Principal Investigator
Slattery, Marc	University of Mississippi	Co-Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
NCBI accessions and metadata associated with Caribbean sponge metagenomes collected from Curacao, Belize, Cayman Islands and St. Croix, 2009 and 2017-2018.

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Coverage

Spatial Extent: **N**:19.4023 **E**:-64.673501 **S**:12.0828 **W**:-88.0878
Temporal Extent: 2009-01-01 - 2018-08-10

Dataset Description

This dataset includes NCBI Accessions for Raw sequence data for 16S rRNA amplicon microbiomes.

The NCBI BioProject number is PRJNA555077 which covers 1547 samples of 16S libraries where the metadata are also available but the sequences themselves are still embargoed. [2019-08-15]

Samples were collected at 15 m by SCUBA diving in the Caribbean near Curacao, Belize, Cayman Islands and St. Croix, in 2009 and 2017-2018. Samples were cleaned, frozen whole, or placed in a DNA/RNA preservation buffer and shipped back to the University of New Hampshire where DNA was extracted and metagenetic, shotgun or cDNA sequencing was conducted.

Data was quality controlled and analyzed in spreadsheets for descriptive statistics, and statistical software was used for bioinformatic analyses.

Data Processing Description

BCO-DMO Processing Notes:
- data were downloaded from NCBI BioProject PRJNA555077 on 2019-08-14 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA555077] and reformatted as a flat table.
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions

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Data Files

File
sponge_accessions.csv (Comma Separated Values (.csv), 203.35 KB) MD5:4d0a47e9493f47c52737085eb3f7c258
Primary data file for dataset ID 775451

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Parameters

Parameter	Description	Units
BioProject	NCBI BioProject accession number	unitless
BioSample	NCBI BioSample accession number	unitless
Sample_name	Lab sample name	unitless
sample_type	sample type and genomic analysis	unitless
host	host taxon	unitless
collection_date	date collected	unitless
geographic_location	geographic location of collection	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
source_material_identifiers	sample identifier	unitless
depth	collection depth guage measurement	feet seawater (fsw) or meters

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Instruments

Dataset-specific Instrument Name	
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	in situ light sensor
Generic Instrument Name	Light Meter
Generic Instrument Description	Light meters are instruments that measure light intensity. Common units of measure for light intensity are umol/m2/s or uE/m2/s (micromoles per meter squared per second or microEinsteins per meter squared per second). (example: LI-COR 250A)

Dataset-specific Instrument Name	in situ temperature sensor
Generic Instrument Name	Thermometer
Generic Instrument Description	A device designed to measure temperature.

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Project Information

Collaborative Research: Dimensions: Evolutionary Ecology of Sponges and Their Microbiome Drives Sponge Diversity on Coral Reefs (DimensionsSponge)

Coverage: Curacao, Belize, Florida, Cayman Islands

NSF Award Abstract:
Coral reefs, the tropical rain forests of the marine environment, are under significant threat from a variety of stressors such as pollution, overfishing, coastal development and climate change. There is increasing interest by the coral reef research community in the ecology and evolution of other groups of organisms besides corals on coral reefs with sponges being of particular interest. Sponges are a very old group of organisms essential to reef health because of their roles in nutrient cycling, providing food and homes for many other reef organisms, and their ability to synthesize diverse chemical compounds of ecological importance on the reef, and of interest to the biomedical community. Many of these important functions would not be possible without the symbiotic microbes (e.g., bacteria) that live within sponges. In this project, the investigators will examine relationships between the sponge host and its microbiome in the ecological roles described above. Like the human microbiome, understanding the sponge micobiome may be the key to understanding their ecology and biodiversity. The investigators will use a combination of classical ecological approaches combined with sophisticated biochemical and molecular analyses to unravel the role of the symbionts in the ecology and evolution of sponges. Both the University of New Hampshire and the University of Mississippi will provide training opportunities for undergraduate and graduate students as well as veterans and post-doctoral researchers, especially from underrepresented groups. Additionally, the investigators will develop unique outreach programs for public education on the importance of coral reef ecosystems.

The goal of this study is to examine the relationships between marine sponges and their microbiomes, and reveal the phylogenetic, genetic, and functional biodiversity of coral reef sponges across the Caribbean basin. This research will provide a better understanding of sponges as a major functional component of the biodiversity of coral reef communities. This transformative project will examine important paradigms relative to sponge communities worldwide that will provide unique insights into the integrative biodiversity of sponges on coral reefs and enhance our understanding of the ecology and evolution of this extensive, yet understudied, group of marine organisms. This is essential because sponges continue to emerge as the dominant taxon on many coral reefs, particularly following regional declines in coral cover over the last three decades, and their ecological importance to shallow coral reef communities is unequivocal. In addition, many marine sponges host a diverse assemblage of symbiotic microorganisms that play critical functional roles in nutrient cycling within sponges themselves and in the coral reef communities where they reside, and many sponges can potentially transfer photoautotrophically derived energy to higher trophic levels. As shallow coral reefs continue to decline, the phylogenetic, genetic, and functional diversity of coral reefs will increasingly be found in taxa other than scleractinian corals, such as soft corals and sponges. The investigators predict that co-evolution of the sponge host and microbiome leads to emergent functional properties that result in niche diversification and speciation of sponges. To assess this, they will quantify trophic modes (e.g., DOM and POC uptake, photo-autotrophy) of sponges in the Caribbean, as well as the production of chemical defenses. These character states will be analyzed in the context of the phylogenetic composition of the sponge hosts and their microbiomes, and the functional activities of the host and symbionts at the genetic level (i.e., transcriptomics and metatranscriptomics). These data will provide unique insights into the co-evolution of sponges and their microbiomes, and how these symbioses influence the functional attributes of sponges within coral reef communities.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1638296

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