

# Microbiome data from sponges collected in 2013 and 2014 from reefs in Honduras, Belize, Panama and the Florida Keys.

**Website:** <https://www.bco-dmo.org/dataset/954346>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2025-02-25

## Project

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

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## Abstract

Marine sponges host diverse communities of microbial symbionts that expand the metabolic capabilities of their host, but the abundance and structure of these communities is highly variable across sponge species. Specificity in these interactions may fuel host niche partitioning on crowded coral reefs by allowing individual sponge species to exploit unique sources of carbon and nitrogen, but this hypothesis is yet to be tested. Given the presence of high sponge biomass and the coexistence of diverse sponge species, the Caribbean Sea provides a unique system in which to investigate this hypothesis. To test for ecological divergence among sympatric Caribbean sponges and investigate whether these trends are mediated by microbial symbionts, we measured stable isotope ( $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$ ) ratios and characterized the microbial community structure of sponge species at sites within four regions spanning a 1700 km latitudinal gradient. Samples were collected in 2013 and 2014 from reefs in Honduras, Belize, Panama, and the Florida Keys. There was a low (median of 8.2 %) overlap in the isotopic niches of sympatric species; in addition, host identity accounted for over 75% of the dissimilarity in both  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values and microbiome community structure among individual samples within a site. There was also a strong phylogenetic signal in both  $\delta^{15}\text{N}$  values and microbial community diversity across host phylogeny, as well as a correlation between microbial community structure and variation in  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values across samples. Together, this evidence supports a hypothesis of strong evolutionary selection for ecological divergence across sponge lineages and suggests that this divergence is at least partially mediated by associations with microbial symbionts.

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## Coverage

**Location:** Caribbean Sea

**Spatial Extent:** N:24.578192 E:-81.442467 S:9.243206 W:-88.113819

**Temporal Extent:** 2013-05 - 2014-05

## Methods & Sampling

Sponge collection: Sponge species were collected from at least one site within four geographic regions spanning more than 15° of latitude (~1700 km) within the Caribbean Sea. Individual regions included the Bocas del Toro archipelago of Panama, the Miskito Cays of Honduras, the Mesoamerican barrier reef of Belize, and the Florida Keys. At each site, replicate small (3–5 ml) samples of dominant and conspicuous sponge species were collected by SCUBA using a dive knife and placed into individual bags containing seawater for transport back to the laboratory. Sponge samples always included a cross section with both inner and outer tissue regions to standardize collections and sample across the entire body of the sponge. Collections frequently included eight of the ten most dominant Caribbean species and species previously designated as both HMA and LMA sponges. Samples were preserved, processed, and prepared for  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  analysis. Sponges were identified to species and, if necessary, identities were verified via tissue histology and spicule preparations. Replicate subsamples of each sponge species were also preserved in 95% EtOH in 5 ml cryovials and frozen at  $-20\text{ }^{\circ}\text{C}$  for analyses of microbial community structure.

## Data Processing Description

Analyses of microbiomes: We surveyed the microbiomes within 294 individuals of the 14 most dominant sponge species from our isotope surveys within the Caribbean. Sponge sampling was most comprehensive within sites in the Bocas del Toro archipelago of Panama (10–13 species within each site) and on Wonderland Reef in the Florida Keys (12 species). Sponges from sites within three regions (Belize and North and South sites in Honduras) were pooled to provide a regional assessment of microbiome structure across species. In short, polymerase chain reaction was performed on extracted total genomic DNA following the 16S Illumina Amplicon protocol of the Earth Microbiome project (earthmicrobiome.org) and with barcoded 16S rRNA primers (515F and 806R); sequencing on an Illumina MiSeq resulted in paired-end 250 base pair amplicons.

Bioinformatics processing was conducted in R using the DADA2 pipeline and taxonomic assignments of amplicon sequence variants (ASVs) were carried out using the Silva database release 128. Prior to analysis, singleton reads were removed and ASV abundance was transformed to relative abundance.

## BCO-DMO Processing Description

- \* converted date to ISO format
- \* Adjusted field names to comply with database requirements
- \* Added bioproject number to dataset

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## Related Publications

Freeman, C. J., Easson, C. G., & Baker, D. M. (2014). Metabolic diversity and niche structure in sponges from the Miskito Cays, Honduras. *PeerJ*, 2, e695. <https://doi.org/10.7717/peerj.695>  
*Results*

Freeman, C. J., Easson, C. G., Matterson, K. O., Thacker, R. W., Baker, D. M., & Paul, V. J. (2020). Microbial symbionts and ecological divergence of Caribbean sponges: A new perspective on an ancient association. *The ISME Journal*, 14(6), 1571–1583. <https://doi.org/10.1038/s41396-020-0625-3>  
*Results*

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## Parameters

Parameter	Description	Units
Bioproject	Bioproject NCBI accession number	unitless
Accession	Biosample NCBI accession number	unitless
Region	Broad region of the Caribbean where samples were collected (by country: Panama, Belize, Honduras, or Florida Keys)	unitless
Dive_Site	Specific site within each region	unitless
Lat	GPS latitude, south is negative	decimal degrees
Lon	GPS longitude, west is negative	decimal degrees
Collection_date	Collection date	unitless
File_id	File name for barcoding data	unitless
Sample_name	Sample name for barcoding data	unitless
Seq_count_post_proc	Number of sequences	number
Sponge_Species	Scientific name for each sponge species; also includes seawater for water microbiome samples	unitless
Read_direction	Primer read direction (forward or reverse)	unitless

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## Instruments

<b>Dataset-specific Instrument Name</b>	Illumina MiSeq
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	Microbiome sequencing was carried out on an Illumina MiSeq.
<b>Generic Instrument Description</b>	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

## 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.

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1929293</a>

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