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

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Data Type: Other Field Results
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Project
» Collaborative Research: Investigations into microbially mediated ecological diversification in sponges (Ecological Diversification in Sponges)

Contributors	Affiliation	Role
Baker, David M.	University of Hong Kong	Co-Principal Investigator
Easson, Cole G.	Middle Tennessee State University	Co-Principal Investigator
Freeman, Christopher J.	College of Charleston (CofC)	Co-Principal Investigator, Contact
Matterson, Kenan	University of Alabama at Birmingham (UA/Birmingham)	Co-Principal Investigator
Paul, Valerie J.	Smithsonian Marine Station (SMS)	Co-Principal Investigator
Thacker, Robert W.	Stony Brook University (SUNY Stony Brook)	Co-Principal Investigator
Soenen, Karen	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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 (δ13C and δ15N) 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 δ13C and δ15N values and microbiome community structure among individual samples within a site. There was also a strong phylogenetic signal in both δ15N values and microbial community diversity across host phylogeny, as well as a correlation between microbial community structure and variation in δ13C and δ15N 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 δ13C and δ15N 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 °C for analyses of microbial community structure.

Stable isotope and chlorophyll *a* analyses: Stable isotope values (δ13C and δ15N) of bulk sponge tissue serve as a time-integrated record of the sources of carbon and nitrogen assimilated by a holobiont (including activities of both sponge and microbial cells) and any fractionation associated with symbiont or host metabolism or nutrient recycling. Within an individual reef, δ13C and δ15N values of sponge tissue therefore act as a metabolic “fingerprint” that integrates the physiological, metabolic, and ecological differences present across individual sponges. Bulk sponge tissue samples were analyzed in the Stable Isotope Ratio Mass Spectrometry Laboratory at the University of Hong Kong as in. Mean (±SE) precision during analysis was 0.1 (0.001) ‰ and 0.2 (0.03) ‰ for δ13C and δ15N, respectively. Isotope values are expressed in delta (δ) notation in units per mille (‰). Values of the elemental composition (%C, %N, and C:N) of each sample of sponge tissue were also provided. Elemental values provide important information about how biomass-associated pools of carbon and nitrogen vary across sponge species and allowed us to test whether our trends in δ13C and δ15N values were strongly influenced by structural differences in sponge tissue. Photosymbiont abundance (as determined by chlorophyll *a* [chl *a*] concentration) was quantified in sponges from sites in Honduras, Panama, and the Florida Keys as in and expressed as µg chl *a* [g dry sponge tissue]−1. *Scopalina ruetzleri* samples were not analyzed for chl *a* because they were too small to provide tissue for both isotope and chl *a* analyses.

BCO-DMO Curation Notes

* converted date to ISO format
* Adjusted field names to comply with database requirements

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Data Files

File
954333_v1_isotope.csv (Comma Separated Values (.csv), 110.60 KB) MD5:491e95491461da65eb8da7e53a724e20 Primary data file for dataset ID 954333, version 1

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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
Species_name	Scientific name for sponge species	unitless
Region_Country	Broad region of collection (by country: Belize, Honduras, Panama, and Florida Keys)	unitless
Lat	Latitude of collection site	decimal
Lon	Longitude of collection site	decimal
Month_and_year_of_collection	Month-year	unitless
Ave_depth_ft	Average water depth at collection site	feet
Freeman_Mean_Chla_Dry_wt	Concentration of chlorophyll a in sponge tissue (as a proxy for photosymbiont abundance)	micrograms of chlorophyll a per gram of sponge tissue
HL_Chla	Discrete chlorophyll a concentration category (high: greater than 125; low: less than 125)	unitless
HMA_LMA	Overall microbial symbiont abundance (high: HMA or low: LMA)	unitless
Site_Name	Specific site name within broader region	unitless
Site_Number	Specific site or dive number within a site if multiple dives were made at one site	unitless
Site_ID	Site abbreviation	unitless
Species_Abbreviation	Abbreviation of species name	unitless

d15N	nitrogen isotope value	permille
d13C	carbon isotope value	permille
Percentage_N	percent nitrogen in tissue	percent
Percentage_C	percent carbon in tissue	percent
C_N	carbon to nitrogen ratio in tissue	unitless

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Instruments

Dataset-specific Instrument Name	Eurovector EA3028 coupled to a Perspective IRMS (Nu Instruments)
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	Sponge isotope samples were analyzed in the Stable Isotope Ratio Mass Spectrometry laboratory (SIRMS) at the University of Hong Kong via combustion in a Eurovector EA3028 coupled to a Perspective IRMS (Nu Instruments).
Generic Instrument Description	The Isotope-ratio Mass Spectrometer is a particular type of mass spectrometer used to measure the relative abundance of isotopes in a given sample (e.g. VG Prism II Isotope Ratio Mass-Spectrometer).

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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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1929293

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