Literature review of sponge-microbe interactions on sixteen characteristics of 82 sponges.

Website: https://www.bco-dmo.org/dataset/955245
Data Type: Synthesis
Version: 1
Version Date: 2025-04-23

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

Contributors	Affiliation	Role
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Thacker, Robert W.	Stony Brook University (SUNY Stony Brook)	Co-Principal Investigator
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Abstract

This dataset compiles information from a literature review (Freeman et al., 2021) of seminal and recent papers focusing on sponge ecology and sponge-microbe interactions. Data (when available in the literature) on sixteen characteristics of 82 sponge species from diverse subclasses are included. These data include enumeration of overall microbial abundance (High and Low Microbial Abundance: HMA and LMA), chemical defense allocation patterns and overall palatability in feeding assays, nutritional quality (carbohydrate, protein, lipid, and energy content), physical characteristics (tensile strength, ash content, tissue density), photosymbiont abundance (chlorophyll a concentration) physiology and metabolism (pumping rate, NOx production), nutrition (% of carbon derived from dissolved organic matter, detritus, and living particulate organic matter), and microbial symbiont diversity (expressed as the inverse Simpson's index).

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Dataset Description

Scientific names in the data were checked using World Register of Marine Species (WoRMS) Taxon Match. Scientific names were corrected after working with the data contributor. All scientific names in the data are valid and accepted names as of 2025-03-04.

Methods & Sampling

Data compiled from the source papers for this dataset were generated using the following methods.

Microbial abundance (HMA vs LMA status) is enumerated using a combination of scanning and transmission electron microscopy (Weisz et al., 2007, 2008; Gloeckner et al., 2014); chemical defense allocation patterns and palatability are determined by incorporating chemical extracts from sponges into artificial food cubes that are then fed to generalist fish or fish assemblages on coral reefs (Loh and Pawlik, 2014); nutritional quality and physical characteristics of sponge tissue are determined by combustion of dried and weighed tissue in a muffle furnace at 450 C for 12 hours (ash); measuring the force required to tear tissue (tensile strength); NaOH-solube protein analysis using bovine serum albumen as a standard (protein); TCA-soluble carbohydrate content using glycogen as a standard (carbohydrate); a gravimetric lipid assay; and combustion in a bomb calorimeter for caloric energy content (Chanas and Pawlik, 1995). Photosymbiont abundance (chlorophyll a concentration) is determined by extracting sponge tissue in acetone and using a spectrophotometer to estimate the concentration of this pigment (Erwin and Thacker, 2007; Freeman et al., 2020); microbial community diversity (via the Inverse Simpson's index) is determined via 16S metabarcoding of the microbial symbiont community (Easson and Thacker, 2014; Thomas et al., 2016; Gantt et al., 2019; Freeman et al., 2020); NO_x production was assessed using *ex situ* experimental incubations or collections of water before and after passing through the sponge (Southwell et al., 2008); pumping rate is assessed based on the advancement of a dye front in the excurrent water plume or an acoustic Doppler velocimeter (Weisz et al., 2007; 2008; Pawlik et al., 2018); the proportion of carbon obtained from dissolved organic matter, detritus, and living particulate organic matter (DOC, DET, LPOC) is assessed by collection of incurrent (before entering the sponge) and excurrent (after entering the sponge) water, followed by analysis of water samples using a combination of flow cytometry to enumerate cells and high temperature catalytic oxidation to measure DOC (McMurray et al., 2018; Pawlik et al., 2018); and tissue density is measured as dry mass of tissue divided by volume (measured as water displacement) (Weisz et al., 2007; 2008). Lastly, phylogenetic signal analysis was carried out as in Freeman et al., 2020 using Pagel's K statistic (Pagel, 1999; Münkemüller et al., 2012). This statistic measures phylogenetic dependence of trait data, with K values close to zero indicating phylogenetic independence and a value of one suggesting that traits are distributed as would be expected under Brownian Motion.

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Data Files

File
955245_v1_review.csv (Comma Separated Values (.csv), 9.22 KB) MD5:0a0bb33292d9debc269ed6e7159a566c Primary data file for dataset ID 955245, version 1

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Supplemental Files

File
Sponge microbe review paper citations and topics filename: sponge_paper_refs_supp.xlsx (Microsoft Excel, 9.93 KB) MD5:0d4f0868010d44392ff3ca2dc56a0cc6 File capturing the references information from the original file

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Related Publications

Chanas, B., & Pawlik, J. (1995). Defenses of Caribbean sponges against predatory reef fish. II. Spicules, tissue toughness, and nutritional quality. Marine Ecology Progress Series, 127, 195–211. https://doi.org/10.3354/meps127195
Related Research

Easson, C. G., & Thacker, R. W. (2014). Phylogenetic signal in the community structure of host-specific microbiomes of tropical marine sponges. Frontiers in Microbiology, 5. https://doi.org/10.3389/fmicb.2014.00532
Related Research

Erwin, P. M., & Thacker, R. W. (2007). Incidence and identity of photosynthetic symbionts in Caribbean coral reef sponge assemblages. Journal of the Marine Biological Association of the United Kingdom, 87(6), 1683–1692. https://doi.org/10.1017/s0025315407058213 https://doi.org/10.1017/S0025315407058213
Related Research

Freeman, C. J., Easson, C. G., Fiore, C. L., & Thacker, R. W. (2021). Sponge–Microbe Interactions on Coral Reefs: Multiple Evolutionary Solutions to a Complex Environment. Frontiers in Marine Science, 8. https://doi.org/10.3389/fmars.2021.705053
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
Related Research

Gantt, S. E., McMurray, S. E., Stubler, A. D., Finelli, C. M., Pawlik, J. R., & Erwin, P. M. (2019). Testing the relationship between microbiome composition and flux of carbon and nutrients in Caribbean coral reef sponges. Microbiome, 7(1). https://doi.org/10.1186/s40168-019-0739-x
Related Research

Gloeckner, V., Wehrl, M., Moitinho-Silva, L., Gernert, C., Schupp, P., Pawlik, J. R., Lindquist, N. L., Erpenbeck, D., Wörheide, G., & Hentschel, U. (2014). The HMA-LMA Dichotomy Revisited: an Electron Microscopical Survey of 56 Sponge Species. The Biological Bulletin, 227(1), 78–88. https://doi.org/10.1086/bblv227n1p78
Related Research

Loh, T.-L., & Pawlik, J. R. (2014). Chemical defenses and resource trade-offs structure sponge communities on Caribbean coral reefs. Proceedings of the National Academy of Sciences, 111(11), 4151–4156. doi:10.1073/pnas.1321626111
Related Research

McMurray, S., Stubler, A., Erwin, P., Finelli, C., & Pawlik, J. (2018). A test of the sponge-loop hypothesis for emergent Caribbean reef sponges. Marine Ecology Progress Series, 588, 1–14. https://doi.org/10.3354/meps12466
Related Research

Münkemüller, T., Lavergne, S., Bzeznik, B., Dray, S., Jombart, T., Schiffers, K., & Thuiller, W. (2012). How to measure and test phylogenetic signal. Methods in Ecology and Evolution, 3(4), 743–756. Portico. https://doi.org/10.1111/j.2041-210x.2012.00196.x https://doi.org/10.1111/j.2041-210X.2012.00196.x
Related Research

Pagel, M. (1999). Inferring the historical patterns of biological evolution. Nature, 401(6756), 877–884. https://doi.org/10.1038/44766
Related Research

Pawlik, J. R., Loh, T.-L., & McMurray, S. E. (2018). A review of bottom-up vs. top-down control of sponges on Caribbean fore-reefs: what's old, what's new, and future directions. PeerJ, 6, e4343. Portico. https://doi.org/10.7717/peerj.4343
Related Research

Southwell, M. W., Popp, B. N., & Martens, C. S. (2008). Nitrification controls on fluxes and isotopic composition of nitrate from Florida Keys sponges. Marine Chemistry, 108(1–2), 96–108. https://doi.org/10.1016/j.marchem.2007.10.005
Related Research

Thomas, T., Moitinho-Silva, L., Lurgi, M., Björk, J. R., Easson, C., Astudillo-García, C., Olson, J. B., Erwin, P. M., López-Legentil, S., Luter, H., Chaves-Fonnegra, A., Costa, R., Schupp, P. J., Steindler, L., Erpenbeck, D., Gilbert, J., Knight, R., Ackermann, G., Victor Lopez, J., … Webster, N. S. (2016). Diversity, structure and convergent evolution of the global sponge microbiome. Nature Communications, 7(1). https://doi.org/10.1038/ncomms11870
Related Research

Weisz, J. B., Hentschel, U., Lindquist, N., & Martens, C. S. (2007). Linking abundance and diversity of sponge-associated microbial communities to metabolic differences in host sponges. Marine Biology, 152(2), 475–483. https://doi.org/10.1007/s00227-007-0708-y
Related Research

Weisz, J. B., Lindquist, N., & Martens, C. S. (2007). Do associated microbial abundances impact marine demosponge pumping rates and tissue densities? Oecologia, 155(2), 367–376. https://doi.org/10.1007/s00442-007-0910-0

Related Research

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Parameters

Parameter	Description	Units
Sponge_Species	Sponge scientific name	unitless
Class	Sponge species class	unitless
Subclass	Sponge species subclass	unitless
Order	Sponge species order	unitless
Family	Sponge species family	unitless
HMA_LMA	Sponge species microbial abundance (High microbial abundance [HMA] or Low microbial abundance [LMA])	unitless
palatability	Palatability due to chemical defense production (mean number of pellets containing sponge chemical extracts that were consumed in trials with the bluehead wrasse)	unitless
ash	Ash content in sponge tissue	milligrams per ml of sponge tissue (mg/ml)
tensile	Tensile strength of sponge tissue	Newtons per m x 10^5 (N/m x 10^5)
carbohydrate	Carbohydrate content in sponge tissue	milligrams per ml of sponge tissue (mg/ml)
protein	Protein content in sponge tissue	milligrams per ml of sponge tissue (mg/ml)
lipid	Lipid content in sponge tissue	milligrams per ml of sponge tissue (mg/ml)
energy	Energy content in sponge tissue	Kilojoules per ml (kJ/ml)
mean_ChlA	Mean chlorophyll a content (from photosynthetic symbionts) in sponge tissue	Micrograms of chlorophyll a per gram of sponge tissue (ug chl a/gram of sponge tissue)
inverse_Simpson	Inverse Simpson’s diversity index for microbiome diversity	unitless

NOx	Production and release of NOx by sponge species (production or no production)	unitless
pump_Rate	Pumping rate of water through a sponge	liters per second per liter of sponge tissue
DOC	Percent dissolved organic carbon in sponge diet	percentage (%)
DET	Percent detritus in sponge diet	percentage (%)
LPOC	Percent living particulate organic carbon in diet	percentage (%)
Density	Sponge tissue density	grams per ml (g/ml)

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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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