SRA accessions and collection information for 16S-V4 rRNA amplicon data from invertebrates sampled at Flower Garden Banks National Marine Sanctuary, Gulf of Mexico following Tax Day Flooding (2016), Hurricane Harvey (2017), and a no flooding year (2018)

Website: https://www.bco-dmo.org/dataset/817436
Data Type: Other Field Results
Version: 1
Version Date: 2020-07-23

Project
» RAPID: Collaborative Research: Impact of freshwater runoff from Hurricane Harvey on coral reef benthic organisms and associated microbial communities (Rapid Reefs Harvey)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:27.9078 **E**:-93.6002 **S**:27.8819 **W**:-93.62829
Temporal Extent: 2016-07-27 - 2018-10-28

Dataset Description

To document the effects of storm-driven freshwater runoff on sponge-associated microbiomes, we leveraged the heavy rainfall associated with Tax Day Flooding (July 2016) and Hurricane Harvey (August 2017) to characterize sponge-associated bacterial communities at five time points: in July 2016 (at detection of the mortality event), one month after the mortality event (August 2016), immediately after Hurricane Harvey (September 2017), one month after Hurricane Harvey (October 2017), and approximately one year following Hurricane Harvey (October 2018).

These data contain Sequence Read Archive (SRA) and BioSample accession numbers associated with BioProject PRJNA605902 (see https://www.ncbi.nlm.nih.gov/bioproject/605902) at The National Center for Biotechnology Information.

Methods & Sampling

Location:

East and West Banks of the Flower Garden Banks National Marine Sanctuary (FGBNMS)

Sampling Events:

NOAA FGBNMS Cruise July 2016, NOAA FGBNMS Cruise August 2016
Hurricane Harvey FGB October 2017, Hurricane Harvey FGB October 2018

Methodology:

V4-16S bacterial communities libraries were prepared and PE 250bp reads were generated using Illumina MiSeq platform.

Sampling and analytical procedures:

Samples were flash frozen in liquid nitrogen and stored at -20°C until further processing. DNA was extracted from 250 mg of sponge sample using the Nucleospin Soil DNA extraction kit (Takara Bio) or the DNeasy PowerSoil DNA extraction kit (QIAGEN).

Data Processing Description

Processing description for data in the Sequence Read Archive:
Sequencing processing and statistical analysis were conducted through the QIIME2 2019.10 software package.

BCO-DMO Data Manager Processing notes:
* Made the following changes to the originally submitted file "sponges_ANSedits_7.23.2020.csv"
* converted variable date formatting to ISO8601 format yyyy-mm-dd
* converted lat/lon in degrees decimal minutes with format 27° 52'54.84”,"93° 37'41.84""" to degrees decimal minutes. Made Long negative so it correctly corresponds to the sample location.
* Checked taxonomic names for validity using WoRMS

Identification, lowest taxon match in WoRMS, LSID
Agaricia sp., Agaricia, urn: lsid: marinespecies.org: taxname: 204464
Agelas clathrodes, Agelas clathrodes, urn:lsid:marinespecies.org:taxname:164823, accepted
Xestospongia mute, Xestospongia mute, urn:lsid:marinespecies.org:taxname:166894, accepted

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Data Files

File
sponges.csv (Comma Separated Values (.csv), 13.02 KB) MD5:f96a637bbd09cd20e015f7df90eb20bf Primary data file for dataset ID 817436

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Related Publications

Caporaso, J. G., Kuczynski, J., Stombaugh, J., Bittinger, K., Bushman, F. D., Costello, E. K., … Knight, R. (2010). QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 7(5), 335–336. doi:10.1038/nmeth.f.303
Methods

Rice University (2020). Hurricane Harvey Rapid Response FGBNMS. Submitted 2020/02. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA605902. NCBI:BioProject: PRJNA605902.

References

Shore, A. N., Sims, J. A., Grimes, M., Howe-Kerr, L. I., Stadler, L., Sylvan, J. B., … Correa, A. M. S. (2020). On a reef far, far away: Offshore transport of floodwaters following extreme storms impacts sponge health and associated microbial communities. doi:10.1101/2020.04.27.064568

Results

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Parameters

Parameter	Description	Units
Sample_Name	Sample name	unitless
Collection_Date_Start	Sample collection date (start of date range) in ISO 8601 format yyyy-mm-dd	unitless
Collection_Date_End	Sample collection date (end of date range) in ISO 8601 format yyyy-mm-dd	unitless
Depth_min	Sample collection depth (minimum of depth range)	meters (m)
Depth_max	Sample collection depth (maxiumum of depth range)	meters (m)
Bank	East or west bank of the Flower Garden Banks	unitless
Species	Identification (taxonomic name or organism description)	unitless
SRA	Sequence Read Archive (SRA) accession number at NCBI	unitless
Accession	BioSample accession number at NCBI	unitless
Lat	Sample latitude	decimal degrees
Long	Sample longitude	decimal degrees

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq Platform
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.

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Project Information

RAPID: Collaborative Research: Impact of freshwater runoff from Hurricane Harvey on coral reef benthic organisms and associated microbial communities (Rapid Reefs Harvey)

Coverage: Flower Garden Banks National Marine Sanctuary, Northwest Gulf of Mexico

NSF Award Abstract:
Coral reefs are ecologically and economically important ecosystems, and are threatened by a variety of global (climate change) and local (overfishing, pollution) stressors. Anthropogenic climate change is increasing the frequency and severity of storms, which can physically damage reef structures and reduce reef health through changes in seawater quality. In August of 2017, Hurricane Harvey caused widespread flooding in southeast Texas when it released more than 50 trillion liters of rain, which then accumulated along the Texas Shelf. This runoff is expected to impact nearby coral reefs in the Flower Garden Banks National Marine Sanctuary (FGBNMS, northwest Gulf of Mexico) via eddies and jets that transport coastal waters offshore. Findings from this project will allow managers to quickly predict whether extreme storm events are likely to induce reef mortality and ecosystem decline due to freshwater accumulation, by tracking of low salinity water masses coupled with microbial community characterization and metrics of coral health. These data are critical to managing coastal ecosystems, including the high coral cover reefs in the FGBNMS, and will help stakeholders (e.g., diving and fishing communities) plan for and minimize disruption to their livelihoods following these storms. Results will be communicated broadly across scientific arenas, in graduate and undergraduate education and training programs, and to the general public through outreach. The investigators have seven 7 square meter 2-D Reef Replicas from 2014 depicting representative FGBNMS reef bottoms, and will construct additional 2-D Reef Replicas from both banks following the arrival of Harvey runoff, allowing the public to directly experience and quantify the effects of Hurricane Harvey on local reefs using quadrats and identification guides. This project will also synergize with NSF REU programs at Boston University and Texas A&M University, providing transformative research experiences for undergraduates. One post-doctoral scholar, four graduate students, a technician and more than 5 undergraduates will be involved in all aspects of the research. All datasets will be made freely available to the public, and will serve as an important set of baselines for future lines of inquiry into the processes by which hurricanes and other extreme storms impact reef health.

Hurricanes and other extreme storm events can decimate coral reefs through wave-driven physical damage. Freshwater runoff from extreme storms is also potentially detrimental to reefs but has received comparatively less attention. This research will provide unprecedented resolution on how hurricanes and other extreme storm events may trigger cascading interactions among water chemistry, declines in metazoan health and shifts in their associated microbial communities, ultimately resulting in coral reef decline. The freshwater runoff initiated by Hurricane Harvey is likely to impact reefs within the FGBNMS, one of the few remaining coral-dominated reefs in the greater Caribbean. The effects of Harvey runoff will be compared to a previously documented storm-driven runoff event that was associated with invertebrate mortality on the same reef system. Sampling seawater chemistry, microbial communities (water column and benthic), and host gene expression and proteomics before, immediately after, and six months after Harvey runoff enters the FGBNMS will allow us to identify commonalities among large-scale freshwater runoff events and track the response of benthic invertebrate health, microbial community diversity, and the trajectory of reef community recovery or decline. The investigators will determine if changes in water chemistry induce pelagic microbial shifts, if microbial communities typically associated with corals and sponges are altered, and whether feedbacks occur between these potential drivers of benthic invertebrate mortality.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1800914

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