

Coral gene expression Sequence Read Archive (SRA) accession numbers and information for samples collected at the Flower Garden Banks National Marine Sanctuary in the Gulf of Mexico in September and October of 2017 to capture effects of Hurricane Harvey

Website: <https://www.bco-dmo.org/dataset/817298>

Data Type: Other Field Results

Version: 1

Version Date: 2020-06-30

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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Abstract

To capture the immediate effects of storm-driven freshwater runoff on coral and symbiont physiology, we leveraged the heavy rainfall associated with Hurricane Harvey in late August 2017 by sampling FGB coral gene expression at two time points: September 2017, when surface water salinity was reduced (~34 ppt); and 1 month later when salinity had returned to typical levels (~36 ppt in October 2017). This dataset includes Sequence Read Archive (SRA) and BioSample accessions under BioProject PRJNA552981 at The National Center for Biotechnology Information. It also contains sample information and species names for samples collected the east and west banks of the Flower Garden Banks National Marine Sanctuary (FGBNMS) at 80ft. These data were published in Wright et al. (2019).

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Coverage

Spatial Extent: N:27.908 E:-93.60019 S:27.8819 W:-93.62828

Temporal Extent: 2017-09 - 2017-10

Dataset Description

To capture the immediate effects of storm-driven freshwater runoff on coral and symbiont physiology, we leveraged the heavy rainfall associated with Hurricane Harvey in late August 2017 by sampling FGB coral gene expression at two time points: September 2017, when surface water salinity was reduced (~34 ppt); and 1 month later when salinity had returned to typical levels (~36 ppt in October 2017).

This dataset includes Sequence Read Archive (SRA) and BioSample accessions under BioProject PRJNA552981 at The National Center for Biotechnology Information. It also contains sample information and species names for samples collected the east and west banks of the Flower Garden Banks National Marine Sanctuary (FGBNMS) at 80ft.

These data were published in Wright et al. (2019).

Methods & Sampling

Location:

East and west banks of the Flower Garden Banks National Marine Sanctuary (FGBNMS) 80ft

Sampling Events:

Hurricane Harvey FGB October 2017, Hurricane Harvey FGB October 2018.

Methodology:

Tagseq libraries were prepared and SE 50bp reads were generated using Illumina Hiseq 2500 platform.

Coral tissue samples were preserved midday underwater. RNA was isolated and samples were processed for tagseq profiling.

Data Processing Description

Coral tissue samples were preserved midday underwater. RNA was isolated and samples were processed for tagseq profiling.

BCO-DMO Data Manager Processing Notes:

- * Originally submitted Excel file Wright_et_al_metadada.xlsx extracted to csv file.
- * added a conventional header with dataset name, PI name, version date
- * modified parameter names to conform with BCO-DMO naming conventions (spaces, +, and - changed to underscores). Units in parentheses removed and added to Parameter Description metadata section.
- * blank values (originally submitted as NR) in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system.
- * Combined "Lat Lon" column (e.g. "27°52'54.84", 93°37'41.84") separated into separate lat and lon columns in decimal degree format.

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Data Files

File
hurr_harvey_sra_samples.csv (Comma Separated Values (.csv), 4.50 KB) MD5:2d62c2041a8d22c37330d36dc8c7c68a
Primary data file for dataset ID 817298

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Related Publications

Boston University (2019). Coral holobiont gene expression Hurricane Harvey. 2019/07. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA552981>. NCBI:BioProject: PRJNA552981.

References

Jari Oksanen, F. Guillaume Blanchet, Michael Friendly, Roeland Kindt, Pierre Legendre, Dan McGlinn, Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos, M. Henry H. Stevens, Eduard Szoecs, Helene Wagner (2019) vegan: Community Ecology Package (R package version 2.5-6) <https://cran.r-project.org/web/packages/vegan/index.html>

Software

Michael Love, S. A. (2017). *DESeq2*. Bioconductor. <https://doi.org/10.18129/B9.BIOC.DESEQ2>
<https://doi.org/10.18129/B9.bioc.DESeq2>

Software

R Core Team (2016) R: A language and environment for statistical computing. R Foundation for Statistical Computing. Vienna, Austria. <https://www.r-project.org>

Software

Wright, R. M., Correa, A. M. S., Quigley, L. A., Santiago-Vázquez, L. Z., Shamberger, K. E. F., & Davies, S. W. (2019). Gene Expression of Endangered Coral (*Orbicella* spp.) in Flower Garden Banks National Marine Sanctuary After Hurricane Harvey. *Frontiers in Marine Science*, 6. doi:[10.3389/fmars.2019.00672](https://doi.org/10.3389/fmars.2019.00672)

Methods

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Parameters

Parameter	Description	Units
Sample_Name	Sample name	unitless
Time	Sample time in format (Full month name and four digit year)	unitless
Bank	east or west bank of the Flower Garden Banks	unitless
Buoy	Buoy number samples were collected from	unitless
Lat	Sample latitude	decimal degrees
Lon	Sample longitude	decimal degrees
Species	Scientific name (Genus species)	unitless
Depth	Sample depth	meters (m)
SRA	Sequence Read Archive (SRA) accession number at NCBI	unitless
Accession	BioSample accession number at NCBI	unitless

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Instruments

Dataset-specific Instrument Name	Illumina Hiseq 2500 platform
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

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.

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1800904

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