Metabarcoding samples collected from surface and chlorophyll maximum depths from R/V Pt. Sur PS 18-09 Legs 01 and 03, Hurricane Harvey RAPID Response cruise (western Gulf of Mexico) September-October 2017.

Website: https://www.bco-dmo.org/dataset/824599
Data Type: Cruise Results
Version: 1
Version Date: 2020-09-11

Project
» RAPID: Hurricane Impact on Phytoplankton Community Dynamics and Metabolic Response (HRR)

Contributors	Affiliation	Role
Campbell, Lisa	Texas A&M University (TAMU)	Principal Investigator
Henrichs, Darren W.	Texas A&M University (TAMU)	Co-Principal Investigator
Gaonkar, Chetan	Texas A&M University (TAMU)	Contact
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Metabarcode samples collected from surface and chlorophyll maximum depths from R/V Pt. Sur PS 18-09 Legs 01 and 03, Hurricane Harvey RAPID Response cruise (western Gulf of Mexico) September-October 2017.

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Coverage

Spatial Extent: **N**:29.0649 **E**:-94.9 **S**:27.2286 **W**:-97.268
Temporal Extent: 2017-09-23 - 2017-10-01

Dataset Description

Metabarcode samples collected from surface and chlorophyll maximum depths from R/V Pt. Sur PS 18-09 Legs 01 and 03, Hurricane Harvey RAPID Response cruise (western Gulf of Mexico) September-October 2017.

Acquisition Description

On each of 2 cruise legs 01 and 03, samples were collected at 7 stations (S01, S06, S11, S16, S21, SS and GI) from 2 depths [surface and chlorophyll maximum depth when possible; see HRR-bottle data]) and triplicate 500-1000 ml samples were filtered and immediately fixed in RNALater. Triplicate samples from each station/depth were extracted with AllPrep DNA/RNA MiniKit (Qiagen, USA) following the manufacturer's instructions. DNA concentration and quality were evaluated using a Nanodrop spectrophotometer (Thermo Fisher Scientific Inc, USA). All the samples extracted for DNA were normalized to 5ng/µl concentration for the amplicon library construction.

The V4 regions of the 18S rRNA genes were amplified using customized V4 primers (Bradley et al. 2016; Kozich et al. 2013). Library construction and amplicon sequencing was performed at Texas A&M University Agrilife's Genomics and Bioinformatics Services (https://www.txgen.tamu.edu) using custom designed primers (Bradley et al. 2016; Kozich et al. 2013). Output of MiSeq results as fasta files were deposited in GenBank under the project number PRJNA592369.

Leg 01 Station 01 sample was not collected.

Sampling locations:

Sample ID	Station	Leg	Location Lat ^{o}N/Long ^{o}W
na		1	27.2286 -97.2686
L3_S01	S01	3	
L1_S06	S06	1	27.8358 -96.9874
L3_S06	S06	3	
L1_S11	S11	1	28.2614 -96.4129
L3_S11	S11	3	
L1_S16	S16	1	28.5366 -95.8656
L3_S16	S16	3	
L1_S21	S21	1	28.7644 -95.2978
L3_S21	S21	3	
L1_SS	SS	1	28.9600 -95.0946
L3_SS	SS	3	
L1_GI	GI	1	29.0649 -94.9000
L3_GI	GI	3	

Processing Description

Fastq files for all 13 station samples were quality checked using FastQC. Illumina paired end reads (2x300 bp) were processed in mothur v1.39.0 (Schloss et al. 2009). Contigs were assembled and pre-cleaned processed for homopolymers and ambiguities. These sequences were then screened for chimera using UCHIME in denovo mode (Edgar et al. 2011). Sequences were de-noised by pre-clustering at 1 bp per 100 bp and generate unique sequence for taxonomic annotation and characterization. Sequences less than three were eluted out in our study and rest OTUs were characterized using BLAST search using PR2 database v4.12.0. The BLAST analysis used a assignment approach with similarity was ≥ 90% and query coverage was ≥ 70% against the reference sequence. Any OTU that did not compile with this criterion was not used in this study. The following thresholds for identity with BLAST results were used for taxonomic assignment clustering: species (97%), genus (94%), family (93%), class (92%) and order (90%).

HTS-metabarcoding procedures were followed as mentioned in Gaonkar et al., (2020). Only HTS

metabarcodes haplotypes (OTUs) with reads more than 3 allocated to Chaetocerotaceae (Chaetoceros and Bacteriastrum) were used with a selection criterion of ≥ 90% similarity and ≥ 70% similarity after BLAST analysis using the protistan PR2 dataset. A total of 206 (n=82881) OTUs annotated as Chaetocerotacean haplotypes were obtained from the HRR dataset. See figures 1 and 2 in the Supplemental Files section.

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions

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Related Publications

Bradley, I. M., Pinto, A. J., & Guest, J. S. (2016). Design and Evaluation of Illumina MiSeq-Compatible, 18S rRNA Gene-Specific Primers for Improved Characterization of Mixed Phototrophic Communities. Applied and Environmental Microbiology, 82(19), 5878–5891. doi:10.1128/aem.01630-16 https://doi.org/10.1128/AEM.01630-16
Methods

Edgar, R. C., Haas, B. J., Clemente, J. C., Quince, C., & Knight, R. (2011). UCHIME improves sensitivity and speed of chimera detection. Bioinformatics, 27(16), 2194–2200. doi:10.1093/bioinformatics/btr381
Methods

Edler, D., Klein, J., Antonelli, A., & Silvestro, D. (2019). raxmlGUI 2.0: a graphical interface and toolkit for phylogenetic analyses using RAxML. doi:10.1101/800912
Software

Gaonkar, C. C., Piredda, R., Sarno, D., Zingone, A., Montresor, M., & Kooistra, W. H. C. F. (2020). Species detection and delineation in the marine planktonic diatoms Chaetoceros and Bacteriastrum through metabarcoding: making biological sense of haplotype diversity. Environmental Microbiology, 22(5), 1917–1929. doi:10.1111/1462-2920.14984
Results

Guillou, L., Bachar, D., Audic, S., Bass, D., Berney, C., Bittner, L., ... & Christen, R. (2012). The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote small sub-unit rRNA sequences with curated taxonomy. Nucleic acids research, 41(D1), D597-D604. https://doi.org/10.1093/nar/gks1160
General

Kozich, J. J., Westcott, S. L., Baxter, N. T., Highlander, S. K., & Schloss, P. D. (2013). Development of a Dual-Index Sequencing Strategy and Curation Pipeline for Analyzing Amplicon Sequence Data on the MiSeq Illumina Sequencing Platform. Applied and Environmental Microbiology, 79(17), 5112–5120. https://doi.org/10.1128/AEM.01043-13
Methods

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Parameters

Parameter	Description	Units
Sequence_ID	OTU sequence generated from the HRR data	Unitless
Taxonomy	Taxonomic annotation of the OTU	Unitless
Similarity	percentage of identical matches	Unitless
Length	alignment length (sequence overlap)	Unitless
Mismatches	number of mismatches	Unitless
Gaps	number of gap openings	Unitless
Q_start	start of alignment in query	Unitless
Q_end	end of alignment in query	Unitless
R_start	start of alignment in reference sequence	Unitless
R_end	end of alignment in reference sequence	Unitless
e_value	number of expected hits of similar quality	Unitless
Score	Bit-score	Unitless
OTU	representative OTUs	Unitless
L1_S06	number of copies of the OTU at Leg 1 Station 06	Unitless
L1_S11	number of copies of the OTU at Leg 1 Station 11	Unitless
L1_S16	number of copies of the OTU at Leg 1 Station 16	Unitless
L1_S21	number of copies of the OTU at Leg 1 Station 21	Unitless
L1_SS	number of copies of the OTU at Leg 1 Surfside station SS	Unitless
L1_GI	number of copies of the OTU at Leg 1 Galveston Island station GI	Unitless
L3_S01	number of copies of the OTU at Leg 3 Station 01	Unitless
L3_S06	number of copies of the OTU at Leg 3 Station 06	Unitless
L3_S11	number of copies of the OTU at Leg 3 Station 11	Unitless
L3_S16	number of copies of the OTU at Leg 3 Station 16	Unitless
L3_S21	number of copies of the OTU at Leg 3 Station 21	Unitless
L3_SS	number of copies of the OTU at Leg 3 Surfside station SS	Unitless
L3_GI	number of copies of the OTU at Leg 3 Galveston Island station GI	Unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Used to collect samples
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used to obtain DNA sequences. See https://www.illumina.com/systems/sequencing-platforms/miseq.html
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.

Dataset-specific Instrument Name	Nanodrop spectrophotometer (Thermo Fisher Scientific Inc, USA)
Generic Instrument Name	Spectrophotometer
Dataset-specific Description	Used for DNA concentration and quality evaluation.
Generic Instrument Description	An instrument used to measure the relative absorption of electromagnetic radiation of different wavelengths in the near infra-red, visible and ultraviolet wavebands by samples.

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Deployments

PS1809

Website	https://www.bco-dmo.org/deployment/784313
Platform	R/V Point Sur
Start Date	2017-09-23
End Date	2017-10-01
Description	HRR study with three legs. Chief Scientists: Steve DiMarco (Leg 1); Kristen Thyng (Leg 2); Lisa Campbell (Leg 3)

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Project Information

RAPID: Hurricane Impact on Phytoplankton Community Dynamics and Metabolic Response (HRR)

Coverage: Texas coast

This project was recently funded by NSF award OCE-1760620. More information will be added as it becomes available.

Project summary from NSF RAPID proposal:
Overview: Tropical cyclones (hurricanes and tropical storms) can produce substantial impacts in marine ecosystems, including alteration of tidal regimes, upwelling, vertical mixing, sediment resuspension, and terrestrial runoff that affect estuaries, coastal areas and the open ocean. The drastic perturbations following tropical cyclones have also been shown to produce immediate shifts in phytoplankton community composition. High temporal resolution observations from the Imaging FlowCytobot (IFCB) revealed that hurricanes in the Gulf of Mexico (GOM) initially caused blooms of diatoms, which subsequently were replaced by blooms of dinoflagellates. This change in the community structure was hypothesized to be related to the ability of dinoflagellates compared to diatoms to assimilate organic nitrogen compounds supplied by the high river discharge that resulted from the rainfall. This RAPID project will address two hypotheses:
1. Community structure will be a flagellate-dominated system as long as the high river discharge continues. Community structure will shift to a diatom-dominated system when environmental conditions return to normal. Continuous, high temporal resolution data from the IFCB time series will provide estimates of abundance and biovolume to assess the temporal variability of phytoplankton from the aftermath of the hurricane until the return to normal conditions.
2. Nitrogen will be the main driver of shifts in community metabolic responses.
Analysis of gene expression profiles, environmental conditions, and water quality parameters will provide a time series of metabolic functional responses. Metatranscriptomic analysis may also provide insight into taxa-specific metabolic responses related to nutrient and other environmental stresses as a consequence of Hurricane Harvey.

We propose two rapid response cruises to sample at 5 sites along a transect from Galveston to Port Aransas. At each station, CTD profiles and water samples from surface and the chlorophyll maximum for nutrient and carbonate chemistry analysis and RNA sequencing will be collected. Concurrently, the IFCB will operate continuously onboard for comparison with the ongoing time series at Surfside Beach. If the water column is strongly stratified, samples will be collected at the low salinity surface layer and the high salinity deeper layer. Time series analyses of the response of the phytoplankton community will include high frequency data of physical and hydrological variables, water quality measurements, and metatranscriptome analyses. Results will provide novel insights on the impact that extreme hurricanes exert on the phytoplankton community and ultimately in ecosystem functioning and resilience.

Intellectual Merit: Hurricane Harvey is the strongest hurricane to hit the GOM in decades; therefore, the impact of this hurricane on the phytoplankton community may be unprecedented in terms of response and duration. It is unknown how the phytoplankton community will respond and the time to return to "normal" condition. Immediate high temporal resolution sampling is the only way to fully capture the effects of tropical cyclones on coastal phytoplankton communities. And, in combination with metatranscriptomic analysis, the time series of metabolic responses can be elucidated.

Broader Impacts: If extreme storms are predicted to increase with future climate change, the taxa-specific responses provided by the IFCB time series are tremendously valuable for detecting changes, which have implications for ecosystem functioning. Over the past decade, the high temporal resolution phytoplankton time series at TOAST has proven to be invaluable in providing early warning for 8 harmful algal blooms. Given the unknown impact of Hurricane Harvey on the Texas coast (or the duration of the impact), the IFCB time series are invaluable to resource managers. Time series data have been successfully implemented into undergraduate Oceanography laboratory courses at TAMU to teach the value of ocean observing and assessment to the students' lives. Data from this Hurricane Harvey rapid response will also be included in future problem sets for students. As a strategy for targeting general audiences, outcomes of this project will also be produced for "On the Ocean", a weekly radio program on KAMU, the public radio station on TAMU campus; podcasts are also archived linked to the Oceanography department's website.

Related data from the The Texas Observatory for Algal Succession Time-Series (TOAST) can be found at the following:
http://toast.tamu.edu/HRR_cruise

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1760620

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