

Light microscopy images, Symbiodiniaceae electron micrographs, and NCBI Sequence Read Archive (SRA) accession numbers associated with diseased and healthy *Pseudodiploria strigosa* corals collected from the Flower Garden Banks National Marine Sanctuary

Website: <https://www.bco-dmo.org/dataset/1010240>

Data Type: Other Field Results

Version: 1

Version Date: 2026-10-20

Project

» [Collaborative Research: RAPID: A multi-scale approach to predicting coral disease spread: leveraging an outbreak on coral-dense isolated reefs](#) (FGB Disease)

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Abstract

This dataset includes microscopy and omics data associated with 15 apparently healthy and diseased *Pseudodiploria strigosa* corals collected from the Flower Garden Banks National Marine Sanctuary (Northwest Gulf of Mexico) in September 2022, one month after a coral disease outbreak. Samples were collected from pairs of apparently healthy corals (HH tissue; n=5) and diseased corals (n=5). From diseased corals, two tissue samples were taken: apparently healthy tissue (HD) and disease-adjacent tissue (DD). Histopathology light microscopy images and electron micrographs of Symbiodiniaceae cells generated with transmission electron microscopy (TEM) are included as PDF files sorted by sample. These data also include NCBI Sequence Read Archive (SRA) accession numbers for raw fastq files of 16S rRNA gene sequencing, internal transcribed spacer-2 (ITS-2) sequencing, and RNA-Seq. This dataset supports an integrative approach for characterizing signatures of marine diseases at cellular, sub-cellular, and gene expression levels spanning multiple holobiont members: the coral host, Symbiodiniaceae microeukaryotes, bacteria/archaea communities, and viruses.

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Coverage

Location: Flower Garden Banks National Marine Sanctuary

Spatial Extent: N:27.9086 E:-93.597183 S:27.875317 W:-93.814817

Temporal Extent: 2022-09-20 - 2022-09-21

Methods & Sampling

Sample Collection:

Following the disease outbreak, fifteen samples of *Pseudodiploria strigosa* corals were collected in the Flower Garden Banks National Marine Sanctuary at the West Flower Garden Bank (Buoy 2: 27.875433, -93.813933 and Buoy 5: 27.875317, -93.814817) and East Flower Garden Bank (Buoy 2: 27.9086, -93.597183). Samples were collected on SCUBA using a hammer and chisel at a depth range of 61 to 70 feet. Corals (n = 10 colonies) were sampled *in situ* as sets of diseased and apparently healthy *P. strigosa*, where two samples were collected per diseased coral (DD: adjacent to the tissue loss lesion, n = 5; HD: apparently healthy tissue on the same coral, n = 5) and one sample was collected from a neighboring apparently healthy conspecific coral (HH; n = 5). Each sample was divided into three fragments that were preserved for histopathology (data not included herein), transmission electron microscopy (TEM), and DNA/RNA sequencing. Histopathology tissue samples were fixed in zinc-buffered formalin (Z-fix concentrate from Anatech Ltd. diluted with filtered seawater) for 24 hours, washed with seawater for 24 hours, then stored in 70% ethanol for transport to Louisiana State University, Baton Rouge, LA, USA. TEM samples were preserved in 750 microliters (μL) of 2% PFA in 3X PBS at 4 degrees Celsius (°C) for transport to Rice University, Houston, TX, USA. For DNA/RNA extraction, samples were collected, flash frozen in liquid nitrogen, and stored at -150°C for transport to the University of Texas at Arlington, Arlington, TX, USA.

Transmission Electron Microscopy (TEM) Imaging:

Coral fragments ~3 square millimeters (mm²) in size (fixed in 750 μL of 2% PFA in 3X PBS) were decalcified in 1000 μL of 1.5% ascorbic acid for 7-14 days, replacing the ascorbic acid solution daily until the entire skeleton was dissolved. The decalcified samples were fixed in Karnovsky's fixative for at least 24 hours before being post-fixed and processed according to (Howe-Kerr et al., 2023). Electron micrographs were imaged using a 120 kV JEOL JEM-1400Flash Transmission Electron Microscope equipped with a high-contrast pole piece and a 15 megapixel AMT NanoSprint15 sCMOS camera. Electron micrographs showed 438 total Symbiodiniaceae cells: 123 from HH tissue (20-30 cells per sample), 142 from HD tissue (23-38 cells per sample), and 173 from DD tissue (27-46 cells per sample). Electron micrographs were labelled by cell ID and grouped into separate pdf files per sample.

Nucleic Acid Extraction and Sequencing:

Subsets of the fifteen *P. strigosa* samples were first extracted for total RNA using a pea-sized amount of coral tissue harvested from the frozen samples using stainless steel sterilized bone cutters. For DD samples, the tissue was taken ~1 to 2 centimeters from the visible lesion line. Extractions were conducted using the Invitrogen RNAqueous Kit (AM1914). Potential DNA and chromatin contamination was removed from each sample using the Ambion DNase I (RNase-free) kit from Invitrogen (Life Technologies AM2222). Total RNA aliquots were sent to Novogene Co., LTD for library preparation and paired-end sequencing. All 15 *P. strigosa* samples had an RNA integrity number (RIN) ≥ 4 and were pre-processed with poly-A tail enrichment to capture all eukaryotic reads. Library prep was completed using the NEBNext Ultra II RNA Library Prep kit by Illumina and samples were processed for 150bp, paired-end sequencing on the Illumina Novaseq 6000 platform with raw read file sizes at a minimum of 5 million.

Upon confirmation of successful RNA extraction, DNA was extracted from the remainder of each coral. Coral

samples were airbrushed with a PBS solution to remove coral tissue from the skeleton. The resulting tissue slurry was spun in a centrifuge at maximum speed at 4°C for 40 minutes or until there was a well-formed pellet with near-transparent supernatant. DNA was extracted from ~0.040 grams (g) of the pelleted coral holobiont biomass with the Qiagen DNeasy PowerBioFilm Kit (Qiagen, Inc., Germantown, MD, 24000-50) according to the manufacturer's protocol and stored at -80°C until further processing. One 50 µL aliquot of extracted DNA was transferred to Rice University and another was transferred to Woods Hole Oceanographic Institution for sequencing of *Symbiodiniaceae* ITS-2 rDNA and 16S rRNA genes for bacteria/archaea, respectively.

To characterize *Symbiodiniaceae* composition, the ITS-2 region of *Symbiodiniaceae* rDNA was PCR amplified with the Sym_VAR primer set (Sym_VAR_5.8SII and Sym_VAR_REV; Hume et al., 2018). Each 16 µL PCR reaction contained: 1 µL DNA template, 9 µL EconoTaq PLUS GREEN 2X Master Mix (Biosearch Technologies), 0.42 µL each of forward and reverse primer at 100 µM, and 5.16 µL DNase/RNase-free water. PCR reactions were cycled as: initial denaturation at 94°C for 3 minutes; followed by 35 cycles of 94°C for 75 seconds, 58°C for 75 seconds, and 74°C for 90 seconds; and a final extension at 74°C for 7 minutes, before holding at 4°C. Library preparation and ITS-2 sequencing were performed at Oregon State University's Center for Quantitative Life Sciences (OSU CQLS, Corvallis, OR, USA) with 2x300 bp paired-end reads on an Illumina MiSeq platform. Blanks (nuclease-free PCR-grade water) were used as negative controls during sequencing.

To characterize bacteria and archaea, single barcoded PCR reactions were performed to amplify the V4 region of the small subunit rRNA gene using primers 515FY and 806RB (Apprill et al., 2015; Parada et al., 2015). As a sequencing control, we used genomic DNA from Microbial Mock Community B (even, low concentration), v5.1L, HM-782D, and nuclease-free PCR-grade water for the negative control. Each 50 µL PCR reaction contained: 2 µL DNA template, 0.5 µL GoTaq DNA Polymerase (Promega), 1 µL of each forward and reverse primer at 10 micromolar (µM), 1 µL of 10 millimolar (mM) deoxynucleoside triphosphate (dNTP) mix (Promega), 5 µL MgCl₂, 10 µL GoTaq 5X colourless flexi buffer (Promega), and 29.5 µL nuclease-free water. The PCR cycling conditions were as follows: initial denaturation at 95°C for 2 minutes; followed by 34 or 37 cycles of 95°C for 20 seconds, 55°C for 15 seconds, and 72°C for 5 minutes; and a final extension at 72°C for 10 minutes, before holding at 4°C. We used 34 or 37 cycles for samples to obtain comparable amounts of amplified DNA for subsequent purification and sequencing. Barcoded PCR products were purified using the MinElute PCR Purification Kit (Qiagen, Inc., Germantown, MD), and concentrations were measured using a Qubit 2.0 fluorometer. Purified samples were diluted to 1 nanogram per microliter (ng/µL) and pooled for sequencing. Sequencing was performed with 2x250 bp paired-end reads on an Illumina MiSeq platform at the University of Illinois at Urbana-Champaign (Kozich et al., 2013). During analysis of the resulting fastq files, two samples (HD and DD tissues from coral 007) were excluded from analysis due to a mislabeling error during laboratory processing.

Data Processing Description

Histology images and electron micrographs were sorted into separate pdf files per sample. Electron micrographs were labelled with a cell ID (starting with 1 per sample). Raw ITS-2, 16S, and RNA-seq sequences were uploaded to the NCBI Sequence Read Archive (SRA).

BCO-DMO Curation Notes

This section documents curation actions performed prior to publication review with the submitter, and additional information relevant to understanding and reusing this dataset. It distinguishes changes made to the submitted (meta)data from unresolved issues and/or enhancements that improve future reuse and interoperability.

CURATION ACTIONS PERFORMED ON DATA

- Imported original file "FGB22_BCO-DMO_metadata_SRA.xlsx" (sheet 1) into the BCO-DMO data processing system.
- Treated "NA" as a missing value (Note: missing values are empty/blank in the final CSV file).
- Converted collection_date from format %d-%b-%y to format %Y-%m-%d.
- Saved the final file as "1010240_v1_fgb22_pstr_coral_disease.csv".

CURATION ACTIONS PERFORMED ON METADATA

- BCO-DMO's standard metadata entry and text formatting steps were performed. See: <https://www.bco->

ISSUES POTENTIALLY IMPACTING REUSE

- N/A

Problem Description

Two samples (007_HD and 007_DD) do not have associated 16S data due to labeling errors during sample processing. One sample (004_HH) does not have an associated histology image due to data loss post-analysis.

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Data Files

File
1010240_v1_fgb22_pstr_coral_disease.csv (Comma Separated Values (.csv), 3.01 KB) MD5:e49ebab80a8b0bd0387e9110319b3cf2
Primary data file for dataset ID 1010240, version 1

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Supplemental Files

File
Microscopy images filename: FGB22_PSTR_microscopy.tar.gz (GZIP (.gz), 1.46 GB) MD5:98f65b0d0d3edc22fee605a2a4beeb10
Supplemental file for dataset ID 1010240, version 1. Compressed folder containing all histopathology (i.e., light microscopy) images and Symbiodiniaceae electron micrographs.

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Related Publications

Apprill, A., McNally, S., Parsons, R., & Weber, L. (2015). Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquatic Microbial Ecology*, 75(2), 129–137. doi:[10.3354/ame01753](https://doi.org/10.3354/ame01753)

Methods

Howe-Kerr, L. I., Knochel, A. M., Meyer, M. D., Sims, J. A., Karrick, C. E., Grupstra, C. G. B., Veglia, A. J., Thurber, A. R., Vega Thurber, R. L., & Correa, A. M. S. (2023). Filamentous virus-like particles are present in coral dinoflagellates across genera and ocean basins. *The ISME Journal*, 17(12), 2389–2402. <https://doi.org/10.1038/s41396-023-01526-6>

Methods

Hume, B. C. C., Ziegler, M., Poulain, J., Pochon, X., Romac, S., Boissin, E., de Vargas, C., Planes, S., Wincker, P., & Voolstra, C. R. (2018). An improved primer set and amplification protocol with increased specificity and sensitivity targeting the Symbiodinium ITS2 region. *PeerJ*, 6, e4816. Portico. <https://doi.org/10.7717/peerj.4816>

Methods

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. doi:[10.1128/aem.01043-13](https://doi.org/10.1128/aem.01043-13)

Methods

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2015). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. *Environmental*

Microbiology, 18(5), 1403–1414. doi:[10.1111/1462-2920.13023](https://doi.org/10.1111/1462-2920.13023)
Methods

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Related Datasets

IsRelatedTo

Woods Hole Oceanographic Institution. Flower Garden Banks Reefs Pseudodiploria Strigosa disease. 2025/07. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA1292163>. NCBI:BioProject: PRJNA1292163. <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1292163/>

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Parameters

Parameter	Description	Units
sample_id	Sequencing library ID	unitless
coral_id	ID of coral colony assigned at time of sampling	unitless
col_health	Health of coral colony	unitless
coral_species	Genus and species of the sampled coral	unitless
coral_aphiaID	Aphia ID of the host (coral) species	unitless
collection_date	Date collected	unitless
site	The sampling site	unitless
buoy	The sampling buoy	unitless
depth_ft	The sampling depth	feet
latitude	The sampling latitude	decimal degrees
longitude	The sampling longitude	decimal degrees
ncbi_bioproject	The associated NCBI BioProject	unitless
ncbi_biosample	The associated NCBI BioSample	unitless
ncbi_16S_sra	The associated NCBI SRA accession number for 16S data	unitless
ncbi_ITS2_sra	The associated NCBI SRA accession number for ITS-2 data	unitless
ncbi_RNAseq_sra	The associated NCBI SRA accession number for RNA-seq data	unitless
TEM_file	The pdf file name of TEM images	unitless
histo_file	The pdf file name of histology images	unitless

Instruments

Dataset-specific Instrument Name	Airbrush
Generic Instrument Name	Airbrush
Dataset-specific Description	Airbrush: An airbrush was used to create coral tissue slurry for DNA extraction.
Generic Instrument Description	Device for spraying liquid by means of compressed air.

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina MiSeq: 16S and ITS-2 sequencing was performed on an Illumina MiSeq platform (PE250 and PE300, respectively).
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Illumina Novaseq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina Novaseq 6000: RNA-seq was performed on an Illumina Novaseq 6000 platform.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Bone cutters
Generic Instrument Name	bone cutter
Dataset-specific Description	Bone cutters: Sterile bone cutters were used to scrape coral tissue for RNA extraction.
Generic Instrument Description	A bone cutter is a surgical instrument used to cut bones or coral fragments.

Dataset-specific Instrument Name	Centrifuge
Generic Instrument Name	Centrifuge
Dataset-specific Description	Centrifuge: A 4°C centrifuge was used to create a pellet of coral tissue slurry.
Generic Instrument Description	A machine with a rapidly rotating container that applies centrifugal force to its contents, typically to separate fluids of different densities (e.g., cream from milk) or liquids from solids.

Dataset-specific Instrument Name	Invitrogen RNAqueous Kit (AM1914)
Generic Instrument Name	DNA Analysis Kit
Dataset-specific Description	Invitrogen RNAqueous Kit (AM1914): RNA was extracted with the Invitrogen RNAqueous Kit (AM1914).
Generic Instrument Description	A laboratory kit containing reagents and materials used to extract, purify, detect, measure, or otherwise evaluate genetic material from a sample.

Dataset-specific Instrument Name	Ambion DNase I (RNase-free) kit from Invitrogen (Life Technologies AM2222)
Generic Instrument Name	DNA Analysis Kit
Dataset-specific Description	Potential DNA and chromatin contamination was removed from each sample using the Ambion DNase I (RNase-free) kit from Invitrogen (Life Technologies AM2222).
Generic Instrument Description	A laboratory kit containing reagents and materials used to extract, purify, detect, measure, or otherwise evaluate genetic material from a sample.

Dataset-specific Instrument Name	NEBNext Ultra II RNA Library Prep kit by Illumina
Generic Instrument Name	DNA Analysis Kit
Dataset-specific Description	NEBNext Ultra II RNA Library Prep kit by Illumina: Library preparation for RNA sequencing was completed with the NEBNext Ultra II RNA Library Prep kit by Illumina.
Generic Instrument Description	A laboratory kit containing reagents and materials used to extract, purify, detect, measure, or otherwise evaluate genetic material from a sample.

Dataset-specific Instrument Name	Qiagen DNeasy PowerBioFilm Kit
Generic Instrument Name	DNA Analysis Kit
Dataset-specific Description	Qiagen DNeasy PowerBioFilm Kit (Qiagen, Inc., Germantown, MD, 24000-50): DNA was extracted with the Qiagen DNeasy PowerBioFilm Kit (Qiagen, Inc., Germantown, MD, 24000-50).
Generic Instrument Description	A laboratory kit containing reagents and materials used to extract, purify, detect, measure, or otherwise evaluate genetic material from a sample.

Dataset-specific Instrument Name	MinElute PCR Purification Kit
Generic Instrument Name	DNA Analysis Kit
Dataset-specific Description	MinElute PCR Purification Kit (Qiagen, Inc., Germantown, MD): Barcoded 16S PCR products were purified with the MinElute PCR Purification Kit (Qiagen, Inc., Germantown, MD).
Generic Instrument Description	A laboratory kit containing reagents and materials used to extract, purify, detect, measure, or otherwise evaluate genetic material from a sample.

Dataset-specific Instrument Name	Hammer and chisel
Generic Instrument Name	Manual Biota Sampler
Dataset-specific Description	Hammer and chisel: A hammer and chisel were used to collect coral samples.
Generic Instrument Description	"Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool.

Dataset-specific Instrument Name	Qubit 2.0 fluorometer
Generic Instrument Name	Qubit fluorometer
Dataset-specific Description	Qubit 2.0 fluorometer: DNA concentrations were measured with a Qubit 2.0 fluorometer.
Generic Instrument Description	Benchtop fluorometer. The Invitrogen Qubit Fluorometer accurately and quickly measures the concentration of DNA, RNA, or protein in a single sample. It can also be used to assess RNA integrity and quality. Manufactured by Invitrogen, Carlsbad, CA, USA (Invitrogen is one of several brands under the Thermo Fisher Scientific corporation.)

Dataset-specific Instrument Name	SCUBA
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	SCUBA: Coral samples were collected on SCUBA (self-contained underwater breathing apparatus).
Generic Instrument Description	The self-contained underwater breathing apparatus or scuba diving system is the result of technological developments and innovations that began almost 300 years ago. Scuba diving is the most extensively used system for breathing underwater by recreational divers throughout the world and in various forms is also widely used to perform underwater work for military, scientific, and commercial purposes. Reference: https://oceanexplorer.noaa.gov/technology/technical/technical.html

Dataset-specific Instrument Name	Polymerase chain reaction (PCR)
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	PCR: Polymerase chain reaction (PCR) reactions were used to amplify 16S rRNA genes and ITS-2 rDNA.
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

Dataset-specific Instrument Name	120 kV JEOL JEM-1400Flash Transmission Electron Microscope
Generic Instrument Name	Transmission Electron Microscope
Dataset-specific Description	120 kV JEOL JEM-1400Flash Transmission Electron Microscope equipped with a high-contrast pole piece and a 15 megapixel AMT NanoSprint15 sCMOS camera: Electron micrographs were captured with this technology.
Generic Instrument Description	An electron microscope that transmits a beam of electrons through a finely sliced section of a specimen and creates an image of the sample based on its effect on the phase of the electrons that pass through.

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Deployments

FGB22

Website	https://www.bco-dmo.org/deployment/1010380
Platform	R/V Manta
Start Date	2022-09-20
End Date	2022-09-21
Description	R/V Manta "Coral Disease response cruise 2" East and West Flower Garden Banks EFGB Mooring #2 and WFGB Mooring #5 Cruise 2: Sept 20-21, 2022 Chief Scientist - Dr. Michelle Johnston (Flower Garden Banks NMS, 4700 Ave. U, Bld. 216, Galveston, TX 77551)

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Project Information

Collaborative Research: RAPID: A multi-scale approach to predicting coral disease spread: leveraging an outbreak on coral-dense isolated reefs (FGB Disease)

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

NSF Award Abstract:

Marine diseases have devastating impacts on ocean ecosystems and this work directly informs understanding of disease transmission in the ocean. To understand the cause and patterns of spread of a disease outbreak that began in late summer of 2022 at the Flower Garden Banks National Marine Sanctuary (northwest Gulf of Mexico, GoM), a team of ecologists, ocean connectivity and disease modelers, microbiologists, and coral immunologists (from Rice University, the University of Virgin Islands (UVI), Louisiana State University (LSU), and Woods Hole Oceanographic Institution) is monitoring the health of corals, and biopsy their tissues. This data aid in developing a model that predicts coral disease transmission and its impacts on economically valuable coral reefs in the GoM. This project supports multidisciplinary field and laboratory research experiences of graduate students at multiple minority-serving institutions, and provides undergraduate students with hands-on training in modeling, ecological and molecular analysis techniques. UVI and LSU are in EPSCoR jurisdictions and have diverse student bodies, including numerous under-represented minority (URM) students. The research team collaboratively provides URM students with research experiences in STEM fields. Project findings are being broadly communicated through virtual public programming, to the Disease Advisory Council, and via direct updates to managers of the Flower Garden Bank National Marine Sanctuary.

Over the last four decades, diseases decimated ecosystem engineers in marine coastal environments, including coral reefs. Recent results from studies of white plague and stony coral tissue loss disease (SCTLD) show coral species immune traits can influence disease resistance and therefore predict of coral community structure post-outbreak in the Caribbean. In late August of 2022, an unidentified multi-species acute tissue loss disease with signs and species susceptibility characteristics reminiscent of white plague or SCTLD was documented at the Flower Garden Banks (northwest Gulf of Mexico, GoM). This disease is having significant impacts on FGB and could become widespread across the GoM, offering an opportunity to test hypotheses about the influence of coral community composition and pathogen dispersal on disease spread during the early stages of an outbreak; few studies examine this on relatively isolated, deep, coral-dense reefs. The interdisciplinary research team employs photomosaics and colony fate-tracking, layered molecular datasets and microscopy approaches, as well as modeling of disease reservoirs and dispersal to assess the etiology of the disease and contribute to the development of a generalizable framework for disease spread on reefs. By parsing the impacts of reef-scale community composition versus seascape-scale dispersal in disease transmission and persistence, this work helps reveal the potential resistance and resilience of isolated, coral-dense reefs to diseases that decimate these ecosystems across the wider Caribbean.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2109622
NSF Division of Ocean Sciences (NSF OCE)	OCE-2530272

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