Bacterial communities and relative abundances of the pathogen Vibrio coralliilyticus in feces of coral reef fish collected on the north shore of Mo'orea, French Polynesia, Oct 2020

Website: https://www.bco-dmo.org/dataset/935908
Data Type: Other Field Results
Version: 1
Version Date: 2024-09-25

Project
» CAREER: Testing the effects of predator-derived feces on host symbiont acquisition and health (Fish transmit microbes)

Contributors	Affiliation	Role
Correa, Adrienne M.S.	Rice University	Principal Investigator
Grupstra, Carsten	Rice University	Co-Principal Investigator
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Understanding how microbial communities in consumer feces may impact ecosystem health may improve conservation and restoration efforts. To test how microbial communities in fish feces may affect coral reef health, we collected fecal samples from ten fish species, ranging from obligate corallivore to grazer/detritivore. Additionally, samples of corals, algae, sediments, and seawater were collected to test whether bacterial taxa in these samples were also represented in fish feces (N = 5-14 per fish, coral, or algae species/genus). All collections were conducted in October 2020 from the back reef (1-2 m depth) and fore reef (5-10 m depth) in Moorea, between LTER sites 1 and 2 of the Moorea Coral Reef (MCR) Long Term Ecological Research (LTER) site. We conducted bacterial 16S rRNA gene metabarcoding on all samples and found that fecal communities of bacteria differed among fish guilds (obligate corallivores, facultative corallivores, grazer/detritivores). We also used real-time PCR to quantify abundances of Vibrio coralliilyticus, a known coral pathogen, in all fecal samples. Samples were collected and processed, and data were analyzed, by the authors of Grupstra et al., 2023.

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Coverage

Location: The North shore of Mo'orea, French Polynesia.
Spatial Extent: **N**:-17.474444 **E**:-149.827222 **S**:-17.483056 **W**:-149.849444
Temporal Extent: 2020-10-01 - 2020-10-31

Methods & Sampling

All collections were conducted in October 2020 from the back reef (1-2 m depth) and fore reef (5-10 m depth)

in Moorea, between LTER sites 1 and 2 of the Moorea Coral Reef (MCR) Long Term Ecological Research (LTER) site. Obligate corallivores were defined as fish that eat corals nearly exclusively (>90% of stomach content or number of bites; Harmelin-Vivien and Bouchon-Navaro, 1983; Rotjan and Lewis, 2008), and facultative corallivores were defined as fish that were observed to feed on coral for a minor to major part of their diet, while also feeding on algae or other invertebrates (~5-80% of bites from corals; Harmelin-Vivien and Bouchon-Navaro, 1983; Rotjan and Lewis, 2008; Viviani et al., 2019; Ezzat et al., 2020). The selected species included four obligate corallivore species (butterflyfishes *Chaetodon ornatissimus*, "CHOR"; *Chaetodon lunulatus*, “CHLU”; *Chaetodon reticulatus*, “CHRE”; and the filefish *Amanses scopas*, “AMSC”), three facultative corallivore species (butterflyfishes *Chaetodon citrinellus*, “CHCI”; and *Chaetodon pelewensis*, “CHPE”; and the parrotfish *Chlorurus spilurus*, “CHSP”), and three grazer/detritivore species (surgeonfishes *Ctenochaetus flavicauda*, “CTFL”; *Ctenochaetus striatus*, "CTST"; and *Zebrasoma scopas*, “ZESC”). Coral and algal samples were collected from locally abundant coral and algae genera (Pratchett, 2014; Burkepile et al., 2020), including the corals *Acropora hyacinthus* (“ACR”), *Pocillopora* species complex (“POC”, Gélin et al., 2017; Johnston et al., 2018), and *Porites lobata* species complex (“POR”, Forsman et al., 2009; Forsman et al., 2015); and mixed communities of turf algae (“Turf”) as well as macroalgae in the general *Asparagopsis* (“Asp”), *Dictyota* (“Dict”), *Lobophora* (“Lob”), *Sargassum*(“Sarg”), and *Turbinaria* sp. (“Turb”). Sediment (“SED”; 250 ml) and water (“WAT”; 1.9 L) were collected concomitantly with fish and environmental samples using sterilized containers. Following collection, all samples (fish, coral, algae, sediments and water) were immediately transported on ice to the lab, where they were processed using sterile methods as described in Grupstra et al. (2021) and preserved in DNA/RNA Shield (Zymo Research, CA).

Sequencing and analysis of 16S rRNA gene amplicons from *in situ* samples

DNA was extracted from all samples using the ZymoBIOMICS DNA/RNA Miniprep kit (Zymo Research, CA) according to the manufacturer’s instructions, but with a 1hr proteinase K incubation (35°C) before the lysis buffer step. Library preparation and sequencing was conducted at the Genomics Core Lab at the Institute of Arctic Biology of the University of Alaska Fairbanks. All samples were sequenced using the 16S rRNA gene V4 primers 515f (GTGYCAGCMGCCGCGGTAA) and 806rB (GGACTACNVGGGTWTCTAAT) on Illumina MiSeq using v3 2x300bp chemistry (Apprill et al., 2015; Parada et al., 2016; Walters et al., 2016). Mock communities (HM-782D, BEI Resources, VA), extraction negatives, and plate negatives were included to facilitate the identification and removal of potential contaminants *in silico* (Davis et al., 2018).

Quantitative PCR of *Vibrio coralliilyticus* genes in fish feces

Quantitative PCR (qPCR) was conducted using vcpARTF and vcpARTR qPCR primers developed for the bacterial coral pathogen *Vibrio coralliilyticus* (Wilson et al., 2013) and results were standardized using primers for general bacteria 967F and 1046R (Sogin et al., 2006; Chen et al., 2011; Shiu et al., 2020). Standard curves (for *V. coralliilyticus* and general bacteria) were made from a *Vibrio coralliilyticus*culture (AS008) isolated from corals collected in the Flower Garden Banks National Marine Sanctuary (northwest Gulf of Mexico). Sequencing of the full-length 16S gene region of bacterial DNA with primers 8F and 1513R resulted in 97.5% percent identity with *V. coralliilyticus* strain U2 (accession MK999891.1) with 100% query cover. The primers vcpARTR and vcpARTF were used to amplify metalloprotease genes and the amplicon was then cleaned using a genejet PCR purification kit (Thermo Fisher, MA); resultant DNA concentrations were acquired using Qubit (Thermo Fisher, MA). A standard curve was made using serial dilutions from 109 to 100 gene copies per µl template; the standard curve for *V. coralliiyticus* primers vcpARTR and vcpARTF had an efficiency of 106.2%; the standard curve for general bacteria primers 967F and 1046R had an efficiency of 92.3%. Sanger sequencing of gene fragments amplified using vcpARTF and vcpARTR primers from DNA extracted from *C. striatus* feces resulted in a top hit against a *V. coralliilyticus* strain P4 metalloprotease gene (accession JQ345042.1) with an e-value of 3x10-12 (query cover 58%, percent identity 85%).

Data Processing Description

Analysis of 16S rRNA gene amplicons

Bacterial 16-S reads were processed in RStudio (version 1.1.456) through the DADA2 pipeline (version 1.11.0, Callahan et al., 2016) and using phyloseq (v1.38). The DADA2 pipeline generated a table of amplicon sequence variants (ASVs), and bacteria taxonomy was assigned using the SILVA rRNA database (version 132, Quast et al., 2012). Non-target (*e.g.*, mitochondrial, chloroplast) reads and singletons were removed. A total of 865

potential contaminant ASVs were identified and removed with the decontam package (v. 1.10.0) using the prevalence method (Davis et al., 2018). A total of 160 samples with >1,000 reads remained after these initial quality control and filtering steps (excluding negatives and mock communities), with a mean of 15,263 reads per sample. All analyses outlined below were conducted based on this dataset, but additional ASV and sample filtering steps were included for several of the approaches. Raw sequencing data are deposited on the SRA (BioProject PRJNA935035).

Quantitative PCR of *Vibrio coralliilyticus* genes in fish feces

Amplification of the *V. coralliilyticus* target gene at <30 cycles was counted as a positive detection, which roughly corresponded to amplification of the 102 gene copies µl-1 standard (Ct=30.4). Delta cycle threshold (dCT) values were calculated by subtracting the cycle threshold at which the signal from general bacteria primers was detected from the cycle threshold at which *V. coralliilyticus* was detected. Higher dCT values indicate lower relative abundances of *V. coralliilyticus*.

BCO-DMO Processing Description

- Imported "qPCR data.CSV", "taxon_identifiers.csv", and "BCODMO_List_SRA.xlsx" into the BCO-DMO system
- Worked with submitter to determine corrections to identifiers, changing "Sample.Name" values in "qPCR data.CSV" from "CTSI1" to "CTST9" and from "ZESC8" (where the "dCT" value was "17.473") to "ZESC9"
- Joined "qPCR data.CSV" and "BCODMO_List_SRA.xlsx" on the sample identifiers by creating a temporary column that removed the "20" from the beginning of "Sample Name", adding all columns from "BCODMO_List_SRA.xlsx" and "dCT" from "qPCR data.CSV"
- Included "diet" field information from "qPCR data.CSV" where the isolated "species" column matched the species indicated in the "Sample Name" of "BCODMO_List_SRA.xlsx"
- Added month of collection to the "*collection_date" column in "BCODMO_List_SRA.xlsx" as it was referenced in the methods section
- Added a lat and lon for all rows to indicate the subject reef's general location by creating the fields "isolation_lat" and "isolation_lon"
- Checked all scientific names referenced in methods section and the methods section of related dataset using World Register of Marine Species (WoRMS) Taxon Match. All scientific names referenced are valid and accepted names as of 2024-09-23
- Included "Identification_in_methods", "matched_AphiaID", "LSID", "AphiaID_accepted", and "ScientificName_accepted" in "taxon_identifiers.csv" supplemental file
- Removed "sp." and spp." from "host" field values in "BCODMO_List_SRA.xlsx"
- Joined "taxon_identifiers.csv" and "BCODMO_List_SRA.xlsx", using "host" field values from "BCODMO_List_SRA.xlsx" and "ScientificName_accepted" from "taxon_identifiers.csv"
- Renamed fields to comply with system requirements by removing special characters and spaces and to indicate which fields specifically applied to the host organism or medium by adding "host_" to the field names
- Saved final file as "935908_v1_bact_vibrio_coralliilyticus_rdna_accessions.csv"

Problem Description

A total of 40 samples failed 16-S rDNA sequencing. Final N=142 out of 182 collected samples.

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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
Methods

Burkepile, D. E., Shantz, A. A., Adam, T. C., Munsterman, K. S., Speare, K. E., Ladd, M. C., Rice, M. M., Ezzat, L., McIlroy, S., Wong, J. C. Y., Baker, D. M., Brooks, A. J., Schmitt, R. J., & Holbrook, S. J. (2019). Nitrogen Identity Drives Differential Impacts of Nutrients on Coral Bleaching and Mortality. Ecosystems, 23(4), 798–811.

https://doi.org/10.1007/s10021-019-00433-2
Methods

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 13(7), 581–583. doi:10.1038/nmeth.3869
Software

Chen, C.-P., Tseng, C.-H., Chen, C. A., & Tang, S.-L. (2010). The dynamics of microbial partnerships in the coral Isopora palifera. The ISME Journal, 5(4), 728–740. https://doi.org/10.1038/ismej.2010.151
Methods

Davis, N. M., Proctor, D. M., Holmes, S. P., Relman, D. A., & Callahan, B. J. (2018). Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome, 6(1). doi:10.1186/s40168-018-0605-2
Methods

Ezzat, L., Lamy, T., Maher, R. L., Munsterman, K. S., Landfield, K. M., Schmeltzer, E. R., Clements, C. S., Vega Thurber, R. L., & Burkepile, D. E. (2020). Parrotfish predation drives distinct microbial communities in reef-building corals. Animal Microbiome, 2(1). https://doi.org/10.1186/s42523-020-0024-0
Methods

Forsman, Z. H., Barshis, D. J., Hunter, C. L., & Toonen, R. J. (2009). Shape-shifting corals: Molecular markers show morphology is evolutionarily plastic in Porites. BMC Evolutionary Biology, 9(1), 45. https://doi.org/10.1186/1471-2148-9-45
Methods

Forsman, Z., Wellington, G. M., Fox, G. E., & Toonen, R. J. (2015). Clues to unraveling the coral species problem: distinguishing species from geographic variation inPoritesacross the Pacific with molecular markers and microskeletal traits. PeerJ, 3, e751. https://doi.org/10.7717/peerj.751
Methods

Grupstra, C. G. B., Howe-Kerr, L. I., van der Meulen, J. A., Veglia, A. J., Coy, S. R., & Correa, A. M. S. (2023). Consumer feces impact coral health in guild-specific ways. Frontiers in Marine Science, 10. https://doi.org/10.3389/fmars.2023.1110346
Results

Grupstra, C. G. B., Rabbitt, K. M., Howe-Kerr, L. I., & Correa, A. M. S. (2020). Fish predation on corals promotes the dispersal of coral symbionts. doi:10.1101/2020.08.10.243857
Methods

Gélin, P., Postaire, B., Fauvelot, C., & Magalon, H. (2017). Reevaluating species number, distribution and endemism of the coral genus Pocillopora Lamarck, 1816 using species delimitation methods and microsatellites. Molecular Phylogenetics and Evolution, 109, 430–446. https://doi.org/10.1016/j.ympev.2017.01.018
Methods

Harmelin-Vivien, M. L., & Bouchon-Navaro, Y. (1983). Feeding diets and significance of coral feeding among Chaetodontid fishes in Moorea (French Polynesia). Coral Reefs, 2(2), 119–127. https://doi.org/10.1007/bf02395282 https://doi.org/10.1007/BF02395282
Methods

Johnston, E. C., Forsman, Z. H., & Toonen, R. J. (2018). A simple molecular technique for distinguishing species reveals frequent misidentification of Hawaiian corals in the genus Pocillopora. PeerJ, 6, e4355. doi:10.7717/peerj.4355
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
Methods

Pratchett, M. S., Berumen, M. L., & Kapoor, B. G. (Eds.). (2013). “Chapter 6: Feeding preferences and dietary specialisation among obligate coral-feeding butterflyfishes,” Biology of Butterflyfishes. https://doi.org/10.1201/b15458
Methods

Quast, C., Pruesse, E., Yilmaz, P., Gerken, J., Schweer, T., Yarza, P., Peplies, J., Glöckner, F. O. (2012). The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids

Research, 41(D1), D590–D596. doi:10.1093/nar/gks1219
Methods

Rotjan, R., & Lewis, S. (2008). Impact of coral predators on tropical reefs. Marine Ecology Progress Series, 367, 73–91. https://doi.org/10.3354/meps07531
Methods

Shiu, J.-H., Yu, S.-P., Fong, C.-L., Ding, J.-Y., Tan, C.-J., Fan, T.-Y., Lu, C.-Y., & Tang, S.-L. (2020). Shifting in the Dominant Bacterial Group Endozoicomonas Is Independent of the Dissociation With Coral Symbiont Algae. Frontiers in Microbiology, 11. https://doi.org/10.3389/fmicb.2020.01791
Methods

Sogin, M. L., Morrison, H. G., Huber, J. A., Welch, D. M., Huse, S. M., Neal, P. R., Arrieta, J. M., & Herndl, G. J. (2006). Microbial diversity in the deep sea and the underexplored "rare biosphere." Proceedings of the National Academy of Sciences, 103(32), 12115–12120. https://doi.org/10.1073/pnas.0605127103
Methods

Viviani, J., Moritz, C., Parravicini, V., Lecchini, D., Siu, G., Galzin, R., & Viriot, L. (2019). Synchrony patterns reveal different degrees of trophic guild vulnerability after disturbances in a coral reef fish community. Diversity and Distributions, 25(8), 1210–1221. Portico. https://doi.org/10.1111/ddi.12931
Methods

Walters, W., Hyde, E. R., Berg-Lyons, D., Ackermann, G., Humphrey, G., Parada, A., … Knight, R. (2015). Improved Bacterial 16S rRNA Gene (V4 and V4-5) and Fungal Internal Transcribed Spacer Marker Gene Primers for Microbial Community Surveys. mSystems, 1(1). doi:10.1128/msystems.00009-15 https://doi.org/10.1128/mSystems.00009-15
Methods

Wilson, B., Muirhead, A., Bazanella, M., Huete-Stauffer, C., Vezzulli, L., & Bourne, D. G. (2013). An Improved Detection and Quantification Method for the Coral Pathogen Vibrio coralliilyticus. PLoS ONE, 8(12), e81800. https://doi.org/10.1371/journal.pone.0081800
Methods

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Related Datasets

IsRelatedTo

Correa, A. M.S., Grupstra, C. (2024) **Lesion frequencies and sizes after fish feces treatment on coral samples collected on the north shore of Mo'orea, French Polynesia, Oct 2020 to Jun 2021.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-09-24 http://lod.bco-dmo.org/id/dataset/933832 [view at BCO-DMO]
Relationship Description: Related dataset includes results of experiment to measure coral lesion frequencies and sizes after fish feces treatment.

References

Rice University. Consumer feces impact coral health in guild-specific ways. 2023/02. 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/PRJNA935035. NCBI:BioProject: PRJNA935035.

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Parameters

Parameter	Description	Units

sample_name	Biological sample name, contains year ("20"), species abbreviation, and sample number; abbreviations represent species or medium from which sample was derived; Obligate corallivores: Chaetodon ornatissimus, "CHOR"; Chaetodon lunulatus, “CHLU”; Chaetodon reticulatus, “CHRE”; Amanses scopas, “AMSC”. Facultative corallivores: Chaetodon citrinellus, “CHCI”; Chaetodon pelewensis, “CHPE”; Chlorurus spilurus, “CHSP”. Grazer/detritivores: Ctenochaetus flavicauda, “CTFL”; Ctenochaetus striatus, "CTST"; Zebrasoma scopas, “ZESC”. Corals: Acropora hyacinthus “ACR”; Pocillopora species complex, “POC”; Porites lobata species complex, “POR”. Algae: mixed communities of turf algae, “Turf”; Asparagopsis, “Asp”; Dictyota, “Dict”; Lobophora, “Lob”; Sargassum, “Sarg”; Turbinaria, “Turb". Environmental: Sediment, “SED”' water, “WAT”	unitless
SRA	NCBI SRA sample accession ID	unitless
BioSample	NCBI Biosample accession ID	unitless
organism	Organism type	unitless
strain	Type of strains in community; mixed community, mock community	unitless
isolation_source	General description of isolation location type	unitless
isolation_lat	Latitude of reef on the north shore of Mo'orea, French Polynesia where coral was sampled, south is negative	decimal degrees
isolation_lon	Longitude of reef on the north shore of Mo'orea, French Polynesia where coral was sampled, west is negative	decimal degrees
collection_date	Year and month of sample collection	unitless
geo_loc_name	Geographic location of sampling	unitless
depth	Sampling depth range	meters (m)
env_broad_scale	Broad-scale environmental context	unitless
host_description	Host organism or medium description; water, sediment, coral species, fish species	unitless
host_tissue_sampled	Sample type; feces, coral, algae, water, or sediment	unitless

host_diet	Diet of the host organism; Obligate corallivore, Facultative corallivore, or Grazer/detritivore	unitless
host_feces_dCT	Delta cycle threshold; calculated by subtracting the cycle threshold at which the general bacteria assay amplified from the cycle threshold at which the Vibrio coralliilyticus assay amplified	cycles
host_AphiaID	ID in the World Register of Marine Species that pairs to the scientificName	unitless
host_ScientificName	Scientific name matched to the World Register of Marine Species	unitless
host_LSID	Identifier for the scientific name in lowest level taxonomic rank matched to the World Register of Marine Species	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	DNA was extracted from all samples using the ZymoBIOMICS DNA/RNA Miniprep kit (Zymo Research, CA) according to the manufacturer's instructions, but with a 1hr proteinase K incubation (35°C) before the lysis buffer step. Library preparation and sequencing was conducted at the Genomics Core Lab at the Institute of Arctic Biology of the University of Alaska Fairbanks. All samples were sequenced using the 16S rRNA gene V4 primers 515f (GTGYCAGCMGCCGCGGTAA) and 806rB (GGACTACNVGGGTWTCTAAT) on Illumina MiSeq using v3 2x300bp chemistry.
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	Qubit (Thermo Fisher, MA)
Generic Instrument Name	Fluorometer
Dataset-specific Description	The primers vcpARTR and vcpARTF were used to amplify metalloprotease genes and the amplicon was then cleaned using a genejet PCR purification kit (Thermo Fisher, MA); resultant DNA concentrations were acquired using Qubit (Thermo Fisher, MA). A standard curve was made using serial dilutions from 109 to 100 gene copies per µl template; the standard curve for V. coralliiyticus primers vcpARTR and vcpARTF had an efficiency of 106.2%; the standard curve for general bacteria primers 967F and 1046R had an efficiency of 92.3%.
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

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Project Information

CAREER: Testing the effects of predator-derived feces on host symbiont acquisition and health (Fish transmit microbes)

NSF Award Abstract:
Climate change and local-scale anthropogenic stressors are degrading coral reefs across the globe. When conditions become too stressful on reefs, corals can lose beneficial microbial symbionts (e.g., dinoflagellates in the family Symbiodiniaceae) that live in their tissues via a process called “bleaching”. Although Symbiodiniaceae play key roles in the health of coral colonies, we know little about the processes that make symbionts available in the environment to prospective host corals. This research test the extent to which coral-eating fish feces, which contain live Symbiodiniaceae, facilitate symbiont acquisition by corals in their early life stages. It will generate seminal knowledge on how corallivore feces impact coral symbioses and health, and will assess the ecological importance of corallivorous fishes as drivers of coral symbiont assemblages. This research also test the extent to which corallivore feces are a source of food and nutrients that impact coral health; this has particular relevance to the survival and recovery of bleached adult corals. This research can ultimately inform intervention strategies to support reef resilience and mitigate reef degradation. Results from this project will be communicated widely in scientific arenas, in undergraduate education programs, and to the public via multimedia content and outreach. The Houston Independent School District (HISD, Houston, TX) is the nation’s 7th largest public school system. This work will enrich environmental science curricula for underrepresented minority students at under-resourced HISD high schools. This work will also support economically disadvantaged and first-generation undergraduate students in pursuing STEM majors and careers through multi-year research experiences.

Symbioses between foundation species (e.g., corals, sponges, trees) and microbiota (e.g., microeukaryotes, bacteria) underpin the biodiversity, productivity, and stability of ecosystems. Consumers, such as predators and herbivores, shape communities of these foundation species through trophic interactions. For instance, grazers contribute to the maintenance of coral dominance on reefs via consumption of macroalgal competitors. However, the indirect effects of other consumers on foundation species are rarely examined. Few studies have tested how consumers affect microbiota assembly in corals, even though coral symbionts (e.g., dinoflagellates in the family Symbiodiniaceae) play key roles in reef function and persistence. Corallivorous (coral-eating) fishes were recently demonstrated to egest large quantities of live Symbiodiniaceae cells as they swim across reefs. This research is testing the hypothesis that corallivore feces promote coral dominance on reefs by supporting coral acquisition of key symbionts and nutrients. The following research objectives will be accomplished: (1) to quantify the contribution of corallivorous fish feces to coral symbiont acquisition; and (2) to test the extent to which corallivorous fish feces influence coral health and recovery from thermal stress.

Reefs are being degraded globally due to climate-change induced bleaching and associated mortality. This project is teasing apart the extent to which nutrients and/or live symbionts associated with corallivore feces contribute to the resilience of bleached corals under ambient and heat stress conditions. The research is tightly integrated with two education objectives: (1) to organize a Research Experience for Teachers (RET) program in which rigorous learning modules that high school teachers can incorporate into their Environmental Systems course offerings are developed and tested; and (2) to provide undergraduate students with a multi-year research experience through a partnership with the Rice Emerging Scholars Program (RESP).

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-1635798
NSF Division of Ocean Sciences (NSF OCE)	OCE-2145472

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