Sequence read accession (SRA) numbers and collection metadata for coral microbiome collected in Moorea, French Polynesia from Jul 2018 to Aug 2020

Website: https://www.bco-dmo.org/dataset/954262
Data Type: Other Field Results, experimental
Version: 1
Version Date: 2025-04-08

Project
» Collaborative Research: Tipping points in coral reefs and their associated microbiomes: interactive effects of herbivory, nutrient enrichment, and temperature (RECHARGE)

Contributors	Affiliation	Role
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Abstract
This dataset contains the complete sample information for the 16S rRNA gene V4 region amplicon sequencing data associated with the NCBI SRA accession from BioProject PRJNA994532. All raw sequencing data can be found at this publicly available NCBI SRA BioProject. The associated samples were collected from an in situ coral manipulative experiment in Moorea, French Polynesia between 2018-2020 from Acropora retusa, Porites lobata, and Pocillopora spp. Data collection was a multi-university collaborative effort between the Vega Thurber Laboratory, at Oregon State University during the time of the experiment, and the Burkepile Community Ecology Laboratory at UC Santa Barbara. The experiment, conducted on the fore reef on the north shore of the island, evaluated the interaction of consumer pressure level (termed "Herbivory" in the dataset and in Vompe et al., 2023) and nutrient enrichment on coral microbiome composition and host success. The experiment also captured two severe and sequential marine heatwaves in 2019 and 2020. This experiment aimed to evaluate whether managing local inputs, including water column nutrient levels and fishing regimes, interacts with heat stress to affect coral success. Coral microbiomes were sampled as these microbial communities are known to interact with host health during heat stress. The data herein correspond to the microbiomes of the sampled corals.

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Coverage

Location: Moorea, French Polynesia S17° 28.386′ W149° 49.059′ 10m depth
Spatial Extent: **Lat**:-17.4731 **Lon**:-149.81765
Temporal Extent: 2018-07 - 2020-08

Methods & Sampling

Relevant Materials and Methods from Vompe et al. (2023):

Site and in situ experiment

Our experimental study site is located on the northern forereef in Mo'orea, French Polynesia (S17° 28.386′ W149° 49.059′). Mo'orea is a tropical, volcanic high island in the Central South Pacific Ocean. A shallow, ~1 km wide lagoon and barrier reef surround the island. The forereef gradually slopes downwards toward the open ocean and is composed of coral spur and sand groove formations. At the inception of our experiment in August 2018, this reef was dominated by scleractinian corals with low abundance of fleshy macroalgae. Coral cover was 56.0 ± 1.0% (mean ± SE) and macroalgae cover was 0.8 ± 0.2% (mean ± SE).

At this site, we have an ongoing in situ experiment investigating tipping points of coral benthic and microbial ecology in response to nutrient enrichment and herbivore reduction, as in Adam et al. (2022). Briefly, our experimental platform is a factorial design at 10 m depth on the forereef, consisting of four herbivore exclosures (~1 m2 each) placed over eight natural 30-m2 reef plots. The plots are exposed to two levels of nutrient enrichment (four plots ambient/four plots enriched) and four levels of herbivory (exclosures with different size holes of 2.5 cm × 2.5 cm, 5.0 cm × 5.0 cm, 7.5 cm × 7.5 cm, or open top, with one exclosure of each herbivory condition at each plot). Nutrient enrichment was achieved in the plots via PVC tubes with Osmocote® (19-6-12, N-P-K) slow-release garden fertilizer. These tubes were wrapped in plastic mesh to contain the fertilizer. The nutrient enrichment tubes were replaced every 12–16 weeks, except for two periods during the COVID-19 pandemic when travel to Mo'orea was not possible. See Supplementary Methods (Vompe et al. 2023) for a full description of the experimental setup.

Coral sampling for microbiome analysis

To investigate how the microbiomes of different coral species respond to environmental stress, samples of *Acropora retusa*, *Porites lobata* species complex, and *Pocillopora* spp. were collected over 2 years (July 2018–August 2020), 3× a year, in March, July or August, and November. Corals in the *P. lobata* species complex will be referred to as *P. lobata* below for brevity. However, we acknowledge there may be cryptic diversity in our samples (Brown et al., 2021). A nonmetric multidimensional scaling (NMDS) ordination of Bray–Curtis distances between *P. lobata* sample microbiomes from July 2018 suggests that the possible presence of cryptic members of the *P. lobata* species complex in our dataset was unlikely to affect *P. lobata* microbiome variation, as there are no obvious sample microbiome composition clusters. The taxonomic name *Pocillopora* spp. is used for this study because *Pocillopora* species have high cryptic diversity (Johnston et al., 2022), which makes it difficult to visually delineate among species. We selected *Pocillopora* spp. specimens that had consistent phenotypes similar to those now defined as *Pocillopora meandrina* or Haplotype 8a as described in Figure 1 of Johnston et al. (2022). Different coral species, even genotypes, tend to have distinct microbiomes (Bourne et al., 2016; Dunphy et al., 2019; Rosales et al., 2019). A NMDS ordination of Bray–Curtis distances between *Pocillopora* spp. sample microbiomes from July 2018 suggests that the possible presence of cryptic *Pocillopora* species in our dataset was unlikely to affect *Pocillopora* spp. microbiome variation, as there are no obvious sample microbiome composition clusters.

All colonies of each coral species appeared healthy when initially selected for microbiome sampling. Live tissue on these focal colonies was repeatedly sampled throughout the study regardless of subsequent visual phenotype, as long as live tissue remained. Live tissue was sampled at haphazardly chosen locations on the colonies at each time point. For *A. retusa* and *Pocillopora* spp., haphazardly chosen live branch tips were sampled. For *P. lobata*, live tissue was sampled from haphazardly chosen locations around the center of the colony. Coral samples were collected in July 2018, November 2018, March 2019, August 2019, November 2019, March 2020, and August 2020, covering a 28-month period. Additional coral colonies were sampled in November 2018, March 2019, and August 2019 to increase sample sizes and to account for initial focal colony mortality. Colonies of each species were also added to the dataset in March 2020 and August 2020 to restore sample size due to colony mortality. Bleaching and mortality data for coral colonies added to the microbiome sampling effort after the start of the experiment were collected retroactively. This was possible because these corals were already present in the exclosures and data could be collected from our photomosaic time series

from before they were added to the microbiome sampling effort.

During each sampling event, coral fragments <1 cm3 were snipped from each of the focal colonies using bone cutters that were flame-sterilized with 95% ethanol at the surface. Corals were sampled between 08:00 and 14:00 h to help minimize diel microbiome variation. Fragments were immediately placed in sterile 207 mL Whirl-Paks. This volume of sample is sufficient to produce accurate microbiome data without significantly damaging the focal colony (Zaneveld et al., 2016). Upon surfacing, Whirl-paks were placed on ice and transported to shore (~15 min) then transferred to Qiagen DNeasy PowerSoil lysis matrix tubes, containing a guanidinium thiocyanate preservative, using 95% ethanol flame-sterilized forceps. Tubes were stored at −40°C prior to transport on Techni Ice to Oregon State University where they were stored at −80°C until further processing.

Microbiome analyses

The V4 region of the 16S rRNA gene was amplified using 515F and 806RB primers from total DNA, then barcoded, purified, and sequenced (Apprill et al., 2015; Parada et al., 2016). Microbiome sequence library generation, sequence processing, and quality control were done as in Williams et al. (2022) with some modifications. See the Supplementary Methods (Vompe et al. 2023) for full protocols and conditions. All microbiome analyses were performed in R v4.2.2, using functions from base R and “tidyverse” (Wickham et al., 2019), as well as functions from a suite of packages developed for microbiome analyses, including “phyloseq” (McMurdie & Holmes, 2013), “vegan” (Oksanen et al., 2022), and Analysis of Compositions of Microbiomes with Bias Correction (ANCOM-BC) in the “ANCOMBC” package (Lin & Peddada, 2020; Vompe et al., 2023).

BCO-DMO Processing Description

- Import "complete sample data.xlsx" into BCO-DMO system
- Split lat_lon field into Latitude and Longitude, with negative values for S and W
- Remove original lat_lon field
- Export file "954262_v1_microbiome_accession_info.csv"

Taxonomic names checked using the World Register of Marine Species Taxa Match tool on 2025-04-15. All names matched a known name exactly.

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Data Files

File	
954262_v1_microbiome_accession_info.csv	(Comma Separated Values (.csv), 498.65 KB) MD5:7dd8d3d8ca6c1ae594c0e6d5913e863a
Primary data file for dataset ID 954262, version 1	

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Supplemental Files

File	
Supporting Information filename: gcb17088-sup-0001-datas1.pdf	(Portable Document Format (.pdf), 3.53 MB) MD5:7a0e20ad5f034647d1c6233790734638
The supporting information from Vompe et al. (2023), referenced in the submission. This file contains further details about data collection and analyses.	

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Related Publications

Adam, T. C., Holbrook, S. J., Burkepile, D. E., Speare, K. E., Brooks, A. J., Ladd, M. C., Shantz, A. A., Vega Thurber, R., & Schmitt, R. J. (2022). Priority effects in coral–macroalgae interactions can drive alternate community paths in the absence of top-down control. Ecology, 103(12). Portico. https://doi.org/10.1002/ecy.3831
Methods

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

Bourne, D. G., Morrow, K. M., & Webster, N. S. (2016). Insights into the Coral Microbiome: Underpinning the Health and Resilience of Reef Ecosystems. Annual Review of Microbiology, 70(1), 317–340. https://doi.org/10.1146/annurev-micro-102215-095440
Methods

Brown, A. L., Hamman, E. A., Shima, J. S., Wares, J. P., & Osenberg, C. W. (2021). Extended phenotypes on coral reefs: cryptic phenotypes modulate coral-vermetid interactions. Ecology, 102(2). Portico. https://doi.org/10.1002/ecy.3215
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

Cleveland, W. S., & Devlin, S. J. (1988). Locally Weighted Regression: An Approach to Regression Analysis by Local Fitting. Journal of the American Statistical Association, 83(403), 596–610. https://doi.org/10.1080/01621459.1988.10478639
Methods

Dunphy, C. M., Gouhier, T. C., Chu, N. D., & Vollmer, S. V. (2019). Structure and stability of the coral microbiome in space and time. Scientific Reports, 9(1). doi:10.1038/s41598-019-43268-6
Methods

Edgar, R. C. (2004). MUSCLE: multiple sequence alignment with high accuracy and high throughput. Nucleic Acids Research, 32(5), 1792–1797. doi:10.1093/nar/gkh340
Methods

Johnston, E. C., Wyatt, A. S. J., Leichter, J. J., & Burgess, S. C. (2022). Niche differences in co-occurring cryptic coral species (Pocillopora spp.). Coral Reefs. doi:10.1007/s00338-021-02107-9
Methods

Lin, H., & Peddada, S. D. (2020). Analysis of compositions of microbiomes with bias correction. Nature Communications, 11(1). https://doi.org/10.1038/s41467-020-17041-7
Methods

Liu, G., Strong, A. E., & Skirving, W. (2003). Remote sensing of sea surface temperatures during 2002 Barrier Reef coral bleaching. Eos, Transactions American Geophysical Union, 84(15), 137–141. Portico. https://doi.org/10.1029/2003eo150001 https://doi.org/10.1029/2003EO150001
Methods

Lozada-Misa, Paula et al. (2017). Analysis of benthic survey images via CoralNet : a summary of standard operating procedures and guidelines. http://doi.org/10.7289/V5/AR-PIFSC-H-17-02
Software

McMurdie, P. J., & Holmes, S. (2013). phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. PLoS ONE, 8(4), e61217. doi:10.1371/journal.pone.0061217
Software

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2016). 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., McCowan, D., Maynard, J. A., & Heron, S. F. (2013). Changes in Bleaching Susceptibility among Corals Subject to Ocean Warming and Recurrent Bleaching in Moorea, French Polynesia. PLoS ONE, 8(7),

e70443. https://doi.org/10.1371/journal.pone.0070443
Methods

Price, M. N., Dehal, P. S., & Arkin, A. P. (2010). FastTree 2 – Approximately Maximum-Likelihood Trees for Large Alignments. PLoS ONE, 5(3), e9490. https://doi.org/10.1371/journal.pone.0009490
Software

R Core Team (2022). R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org/. R version 4.2.2 (2022-10-31)
Software

Rosales, S. M., Miller, M. W., Williams, D. E., Traylor-Knowles, N., Young, B., & Serrano, X. M. (2019). Microbiome differences in disease-resistant vs. susceptible Acropora corals subjected to disease challenge assays. Scientific Reports, 9(1). https://doi.org/10.1038/s41598-019-54855-y
Methods

Speare, K. E., Adam, T. C., Winslow, E. M., Lenihan, H. S., & Burkepile, D. E. (2021). Size-dependent mortality of corals during marine heatwave erodes recovery capacity of a coral reef. Global Change Biology, 28(4), 1342–1358. Portico. https://doi.org/10.1111/gcb.16000
Methods

Vompe, A. D., Epstein, H. E., Speare, K. E., Schmeltzer, E. R., Adam, T. C., Burkepile, D. E., Sharpton, T. J., & Vega Thurber, R. (2023). Microbiome ecological memory and responses to repeated marine heatwaves clarify variation in coral bleaching and mortality. Global Change Biology, 30(1). Portico. https://doi.org/10.1111/gcb.17088
Results

Wickham, H., Averick, M., Bryan, J., Chang, W., McGowan, L., François, R., Grolemund, G., Hayes, A., Henry, L., Hester, J., Kuhn, M., Pedersen, T., Miller, E., Bache, S., Müller, K., Ooms, J., Robinson, D., Seidel, D., Spinu, V., … Yutani, H. (2019). Welcome to the Tidyverse. Journal of Open Source Software, 4(43), 1686. https://doi.org/10.21105/joss.01686
Software

Williams, S. D., Klinges, J. G., Zinman, S., Clark, A. S., Bartels, E., Villoch Diaz Maurino, M., & Muller, E. M. (2022). Geographically driven differences in microbiomes of Acropora cervicornis originating from different regions of Florida's Coral Reef. PeerJ, 10, e13574. Portico. https://doi.org/10.7717/peerj.13574
Methods

Zaneveld, J. R., Burkepile, D. E., Shantz, A. A., Pritchard, C. E., McMinds, R., Payet, J. P., … Thurber, R. V. (2016). Overfishing and nutrient pollution interact with temperature to disrupt coral reefs down to microbial scales. Nature Communications, 7(1). doi:10.1038/ncomms11833
Methods

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Related Datasets

Software

AgiSoft PhotoScan Professional (Version 2.2) (Software). (2024*). Retrieved from https://www.agisoft.com/downloads/installer/

Oksanen, J., Simpson, G. L., Blanchet, F. G., Kindt, R., Legendre, P., Minchin, P. R., O'Hara, R. B., Solymos, P., Stevens, M. H. H., Szoecs, E., Wagner, H., Barbour, M., Bedward, M., Bolker, B., Borcard, D., Carvalho, G., Chirico, M., De Caceres, M., Durand, S., … Borman, T. (2001). vegan: Community Ecology Package [dataset]. In CRAN: Contributed Packages. The R Foundation. https://doi.org/10.32614/cran.package.vegan https://doi.org/10.32614/CRAN.package.vegan

alexvompe. (2023). *alexvompe/recharge_microbiology_2018_2020: Recharge microbiology 2018 - 2020 data and code release* (Version v1.0) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.10151103

References

Moorea Coral Reef LTER, & Edmunds, P. (2020). *MCR LTER: Coral Reef: Long-term Population and Community Dynamics: Corals, ongoing since 2005* [Data set]. Environmental Data Initiative. https://doi.org/10.6073/PASTA/10EE808A046CB63C0B8E3BC3C9799806

https://doi.org/10.6073/pasta/10ee808a046cb63c0b8e3bc3c9799806

Oregon State University. Interactive effects of herbivory, nutrient enrichment, and temperature on coral reefs and their microbiomes in Moorea, French Polynesia. 2023/07. 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/PRJNA994532. NCBI:BioProject: PRJNA994532.

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Parameters

Parameter	Description	Units
Sample	Unique sample name, containing the Illumina MiSeq lane, placeholder sample number, the Nextera barcode sequences, and the unique sample number	unitless
Date_MonthYear	Collection date given as the month and year	unitless
Coral_Code	Code for the host coral species sampled (Aret = Acropora retusa, Plob = Porites lobata, Poc = Pocillopora)	unitless
Herbivory	Consumer pressure level generated by the experimental exclosures (1x1, 2x2, 3x3, open)	unitless
Nutrients	Enrichment condition in the exclosures (Nutrient or Ambient)	unitless
Plot	Unique plot containing a set of coral exclosures (A1, A2, B3, B4, C1, C3, D2, or D4)	unitless
Tag	Unique colony identifier (numeric)	unitless
Batch	Identifier of Illumina MiSeq run (R1, R2, or R3)	unitless
Run	NCBI SRA SRR identifier	unitless
AssayType	Type of DNA sequencing performed	unitless
AvgSpotLen	Total across paired reads	unitless
Bases	Number of bases in the sample	unitless
BioProject	NCBI SRA BioProject containing the sequences from these samples	unitless

BioSample	SAMN identifier for each sample	unitless
BioSampleModel	Type of metagenomic survey	unitless
Bytes	Total size of the sequencing data files	bytes
CenterName	Institution where sequencing was conducted	unitless
Collection_Date	Collection date given as [year]-[month]	unitless
Consent	Availability of the data	unitless
DATASTORE_filetype	Available file types for downloading the raw sequencing data	unitless
DATASTORE_provider	Organizations linked to this repository	unitless
DATASTORE_region	Data storage region	unitless
env_broad_scale	General description of the sampling environment	unitless
env_local_scale	Specific description of the sampling environment at the local scale	unitless
env_medium	Medium from which DNA was isolated (Coral Tissue or PCR water)	unitless
Experiment	NCBI SRA SRX identifier	unitless
geo_loc_name_country	Region where sample was collected	unitless
geo_loc_name_country_continent	Continent where sample was collected	unitless
geo_loc_name	Specific name of sampling environment	unitless
Host	Most accurate possible host taxonomy	unitless
Instrument	Instrument for DNA sequencing	unitless
Latitude	Latitude of collection, South is negative	decimal degrees

Longitude	Longitude of collection, West is negative	decimal degrees
LibraryName	Equivalent to 'Sample'	unitless
LibraryLayout	Type of amplicon sequencing performed	unitless
LibrarySelection	Selection to perform amplicon sequencing	unitless
LibrarySource	DNA source type	unitless
Organism	Organism type (coral reef metagenome or indoor metagenome)	unitless
Platform	Platform for sequencing	unitless
ReleaseDate	Public release date for the raw sequencing data	unitless
create_date	Date the dataset was initially uploaded to the NCBI SRA	unitless
version	Version of the public dataset	unitless
SRA_Study	SRA study Identifier	unitless
unique_sample_identifier	A unique number identifying each sample	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq System
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	The V4 region of the 16S rRNA gene was amplified using 515F and 806RB primers from total DNA, then barcoded, purified, and sequenced (Apprill et al., 2015; Parada et al., 2016). Microbiome sequence library generation, sequence processing, and quality control were done as in Williams et al. (2022) with some modifications.
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	During each sampling event, coral fragments less than 1 cm3 were snipped from each of the focal colonies using bone cutters that were flame-sterilized with 95% ethanol at the surface.
Generic Instrument Description	A bone cutter is a surgical instrument used to cut bones or coral fragments.

Dataset-specific Instrument Name	Eppendorf Benchtop Centrifuge 5430
Generic Instrument Name	Centrifuge
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	Thermo Fisher Scientific Owl A3-1 Large-Gel Electrophoresis System
Generic Instrument Name	Electrophoresis Chamber
Dataset-specific Description	Thermo Fisher Scientific Owl A3-1 Large-Gel Electrophoresis System. A Gel Transilluminator was also used.
Generic Instrument Description	General term for an apparatus used in clinical and research laboratories to separate charged colloidal particles (or molecules) of varying size through a medium by applying an electric field.

Dataset-specific Instrument Name	Invitrogen Qubit 4 Fluorometer
Generic Instrument Name	Qubit fluorometer
Dataset-specific Description	Invitrogen Qubit 4 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	Vortex
Generic Instrument Name	Shaker
Dataset-specific Description	Used with Qiagen Bead Beater Vortex Attachment
Generic Instrument Description	A Shaker is a piece of lab equipment used to mix, blend, or to agitate substances in tube(s) or flask(s) by shaking them, which is mainly used in the fields of chemistry and biology. A shaker contains an oscillating board which is used to place the flasks, beakers, test tubes, etc.

Dataset-specific Instrument Name	Thermocycler
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	The V4 region of the 16S rRNA gene was amplified using 515F and 806RB primers from total DNA, then barcoded, purified, and sequenced (Apprill et al., 2015; Parada et al., 2016).
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)

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Project Information

Collaborative Research: Tipping points in coral reefs and their associated microbiomes: interactive effects of herbivory, nutrient enrichment, and temperature (RECHARGE)

Coverage: Mo'orea, French Polynesia

NSF Award Abstract:
Coral reefs are some of the most diverse, yet most imperiled, ecosystems on the planet. Global change has driven the decline of corals worldwide with many reefs now lacking corals and being overrun by macroalgae. This research examines the impacts of several factors of thermal stress, overfishing of important herbivorous fishes, and nutrient pollution on the health of corals and their ability to recover after large coral-killing disturbances. Importantly, the investigators address the impacts of global change on the coral microbiome, the microbes that associate with corals and impact coral health. The overarching hypothesis is that factors such as overfishing and nutrient pollution impact coral health via impacts to their microbes. This 6-year experiment on the coral reefs of Mo'orea, French Polynesia examines what levels of herbivory, mostly by parrotfishes and surgeonfishes, are needed to provide resistance and resilience of corals and their microbiomes when reefs are exposed to elevated nutrients and ocean temperatures. Notably, the team tests how local stressors (overfishing, nutrient pollution) potentially interact with global stressors (climate change and rising ocean temperatures) to impact coral reef health. This research may yield insight into how to manage local factors (reducing fishing, mitigating nutrient pollution) to help corals survive the global stress of climate

change. The field experiment provides a realistic platform to test questions about how local management of fisheries can alter reef health and provides data about the recoverability of reefs should new water quality management be put into place. This interdisciplinary work trains a new generation of both marine ecologists and microbiologists, including one postdoctoral researcher, two graduate students, as well as numerous undergraduates. The main international outreach effort is to map the microbiome of the island of Mo'orea. Mo'orea is approximately 130 square-kilometers in area and has five major watersheds that transport sediment and nutrients to the nearshore coral reef ecosystems. Thus poor stewardship of these watersheds likely contributes to the local phase shifts currently occurring in several areas of the lagoon. Therefore the team has engaged the local community to help collect microbiome samples from 50 terrestrial, 50 stream, 25 coastal sites, and 25 offshore sites around the island. The sampling effort is generating an island-wide map of the microbial communities associated with the soils, streams, and coastal waters that can be linked to adjacent coral reef health - The Moorea Microbiome! As part of this outreach effort, the team also collaborates with filmmakers to make a trilingual (English, French, and Tahitian) film about the project to serve as local engagement and teaching tool to help educate school groups and different stakeholders about both the seen and unseen connections between land and sea on their island.

On the island of Mo'orea, French Polynesia, coral communities have exhibited strikingly different trajectories, with some reefs recovering from disturbances and others undergoing protracted coral decline, accompanied by an increase in macroalgae. This diversity in coral community dynamics makes Mo'orea an excellent model system for testing why some reefs are resilient and return to abundant coral while others are not and undergo persistent phase shifts to macroalgal dominance. This 6-year experiment will measure the dynamics of benthic communities, coral demography, and the coral microbiome across seasonal change in ocean temperature, allowing the team to (1) link changes in coral microbiomes (e.g., a rise in pathogenic bacteria) to the trajectories of coral decline or recovery and (2) link nutrients, herbivory, and temperature to phase shifts in both benthic communities and coral microbiomes. Importantly, the team is testing the resistance of phase shifts of benthic communities and coral microbiomes by measuring their changes after removing the nutrient enrichment treatment at the end of year 3 and tracking recovery of the system for 3 more years. Thus, this project begins to answer whether reef and microbial community phase shifts can be easily reversed once they occur. Many studies have focused on the factors that disassemble coral reef communities, but this is the first to examine how reef communities can be reassembled from the microbiome upwards.

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-2023701
NSF Division of Ocean Sciences (NSF OCE)	OCE-2023424

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