Microbiome Host Bleaching and Mortality Data for coral hosts collected in Moorea, French Polynesia from Jul 2018 to Aug 2020

Website: https://www.bco-dmo.org/dataset/954197
Data Type: Other Field Results, experimental
Version: 1
Version Date: 2025-03-19

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

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Abstract
This dataset contains bleaching and mortality levels for the coral hosts associated with the 16S rRNA gene V4 region amplicon sequencing data, NCBI SRA accession from BioProject PRJNA994532. Orthorectified photomosaics were assembled from photos taken of experimental plots from an in situ coral manipulative experiment in Moorea, French Polynesia between 2018-2020. Partial bleaching and mortality was assigned from these photomosaics to Acropora retusa, Porites lobata, and Pocillopora spp. coral colonies associated with the microbiome sampling described above, whenever possible. 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 bleaching and mortality. 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 colony partial bleaching and partial mortality data were collected for hosts sampled for microbiome analyses, because we aimed to correlate microbiome changes to changes in host phenotypes.

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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

The relevant methods as described in 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.

Coral bleaching and mortality data collection and analyses

At each microbiome sample collection point, except during March 2020, ~64 high-resolution digital photographs were taken of each plot using an Olympus TG camera. The digital photographs were then used to generate orthorectified photomosaics using Agisoft Metashape (AgiSoft PhotoScan Professional, 2024) software. These high-resolution photomosaics allowed identification of benthic organisms to a low taxonomic resolution. Percent cover of benthic organisms was quantified using 225 random points per m2 plot using CoralNet software (Lozada-Misa at al., 2017) in manual annotation mode. Photomosaics were also used to create digital maps of the plots in which each focal coral was identified and circled. For each focal colony, we recorded whether coral bleaching or mortality was present (prevalence) and, if so, estimated the percentage of the colony surface area (to the nearest 5%) that was bleached or dead (severity). Because corals undergo natural, seasonal variation in Symbiodiniaceae density that can affect their coloration, we defined bleached tissue only as tissue that had lost all pigmentation.

Mortality and bleaching were tracked for focal corals at all time points, except March 2020. Comparisons between average per colony bleaching and mortality levels were assessed across coral species and time points using one-way analysis of variance (ANOVA) with TukeyHSD (honestly significant difference) post hoc tests. In March 2020, samples for microbiome analysis were collected, but the photomosaics were not conducted due to the interrupted field season resulting from the COVID-19 shutdown. However, qualitative notes on bleaching and health status during coral microbiome sample collection were recorded for focal colonies. Additionally, coral bleaching and mortality data were gathered for *A. retusa* and *Pocillopora* spp. during the peak of the 2019 heatwave in May, as described above; however, these data were collected from individual photos of coral plots taken from the top, not photomosaics. In this study, we only analyzed correlations between microbiome dynamics and host bleaching and mortality for months during microbiome sample collection so that phenotypic and microbiome data for each coral colony could be paired.

BCO-DMO Processing Description

- Imported "bleaching mortality data.xlsx" into BCO-DMO system
- Converted dates to YYYY-MM format
- Changed "ID" field to Colony to prevent confusion with the sample ID
- Exported file as "954197_v1_host_bleaching_mort.csv"

Problem Description

While microbiome data were collected in March 2020, bleaching and mortality data were not collected for this time point due to COVID-19 travel restrictions and lockdowns.

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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

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

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

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	Associated sample taken for microbiome analyses	unitless
Date	Month of data collection as YYYY-MM	unitless
Coral	Code for the coral species evaluated (Aret = Acropora retusa, Plob = Porites lobata, Poc = Pocillopora)	unitless
Herbivory	Consumer pressure level created by the experimental exclosures (1x1, 2x2, 3x3, or 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
Run	Associated microbiome analysis sequencing run	unitless
Colony	Unique coral colony ID in the photomosaics	unitless
percent_bleached	Partial colony bleaching percentage	percent
percent_dead	Partial colony mortality percentage	percent

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Instruments

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	Olympus TG camera
Generic Instrument Name	Camera
Dataset-specific Description	At each microbiome sample collection point, except during March 2020, ~64 high-resolution digital photographs were taken of each plot using an Olympus TG camera.
Generic Instrument Description	All types of photographic equipment including stills, video, film and digital systems.

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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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