

# Estimates of bleaching mortality and colony size for different *Pocillopora* haplotypes at Moorea in 2019

**Website:** <https://www.bco-dmo.org/dataset/856424>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2021-07-23

## Project

» [Collaborative research: Coral community resilience: testing the role of hidden diversity in pocilloporid corals at Moorea](#) (Pocilloporid Coral Diversity)

Contributors	Affiliation	Role
<a href="#">Burgess, Scott</a>	Florida State University (FSU)	Principal Investigator
<a href="#">Edmunds, Peter J.</a>	California State University Northridge (CSUN)	Co-Principal Investigator
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## Abstract

This dataset includes estimates of bleaching mortality and colony size for different *Pocillopora* haplotypes at Moorea in 2019. These data have been published in Figure 5, Figure 6, and Table 1 of Burgess et al. (2021).

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## Coverage

**Spatial Extent:** Lat:-17.5333 Lon:-149.8333

**Temporal Extent:** 2019-02 - 2019-02

## Methods & Sampling

Tissue was collected in February 2019 from a total of 68 colonies from Sites 1 (n = 7), 2 (n = 30), 3 (n = 19), and 5 (n = 12). Of these 68 colonies, 51 colonies were tracked between February 2019 (before the bleaching) and August 2019 (after the bleaching). Tissue was collected in August from a total of 394 colonies from Sites 1 (n = 65), 2 (n = 69), 3 (n = 42), 4 (n = 83), 5 (n = 68), and 6 (n = 67).

The mitochondrial Open Reading Frame (mtORF) marker, using the FATP6.1 and RORF primers found in Flot et al. (2008), was used to haplotype individuals. *P. meandrina* and *P. eydouxi* were differentiated using a restriction fragment length polymorphism (RFLP) gel-based assay following Johnston et al. (2018). Samples were identified to haplotype based on previously published sequences of mtORF haplotypes, using the naming conventions in Pinzón and Lajeunesse (2011), Pinzón et al. (2013), Forsman et al. (2013), Edmunds et al. (2016), and Johnston et al. (2017).

## Data Processing Description

Data were processed using R 3.6.3. These data have been published in Figure 5, Figure 6, and Table 1 of Burgess et al. (2021).

### BCO-DMO Processing:

- renamed fields (columns) to conform with BCO-DMO naming conventions;
- replaced "NA" with "nd" to indicate "no data".

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## Data Files

File
<b>haplotypes_2019.csv</b> (Comma Separated Values (.csv), 17.14 KB) MD5:43482d084d9962730eccd10dc1c420c1 Primary data file for dataset ID 856424

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## Supplemental Files

File
<b>Figure_5_Make.R</b> (Octet Stream, 10.33 KB) MD5:2833188b77deec4d0e8e5ceaa458949e R code to produce Figure 5, and the accompanying analyses presented in the text, in: Burgess SC, Johnston EC, Wyatt ASJ, Leichter JJ, Edmunds PJ (2021) Response diversity in corals: hidden differences in bleaching mortality among cryptic Pocillopora species. Ecology. Uses 'Data on Haplotypes 2019.csv'
<b>Figure_6_Make.R</b> (Octet Stream, 7.97 KB) MD5:6ab813dc383b6d39829e6abb2d3e7d2a R code to produce Figure 6, and the accompanying analyses presented in the text, in: Burgess SC, Johnston EC, Wyatt ASJ, Leichter JJ, Edmunds PJ (2021) Response diversity in corals: hidden differences in bleaching mortality among cryptic Pocillopora species. Ecology. Uses 'Data on Haplotypes 2019.csv'

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## Related Publications

Burgess, S. C., Johnston, E. C., Wyatt, A. S. J., Leichter, J. J., & Edmunds, P. J. (2021). Response diversity in corals: hidden differences in bleaching mortality among cryptic Pocillopora species. Ecology, 102(6).

doi:[10.1002/ecy.3324](https://doi.org/10.1002/ecy.3324)

*Results*

Edmunds, P., & Riegl, B. (2020). Urgent need for coral demography in a world where corals are disappearing. Marine Ecology Progress Series, 635, 233–242. doi:[10.3354/meps13205](https://doi.org/10.3354/meps13205)

*Methods*

Flot, J.-F., Magalon, H., Cruaud, C., Couloux, A., & Tillier, S. (2008). Patterns of genetic structure among Hawaiian corals of the genus Pocillopora yield clusters of individuals that are compatible with morphology. Comptes Rendus Biologies, 331(3), 239–247. doi:[10.1016/j.crv.2007.12.003](https://doi.org/10.1016/j.crv.2007.12.003)

*Methods*

Forsman, Z., Johnston, E., Brooks, A., Adam, T., & Toonen, R. (2013). Genetic Evidence for Regional Isolation of Pocillopora Corals from Moorea. *Oceanography*, 26(3), 153–155. doi:[10.5670/oceanog.2013.58](https://doi.org/10.5670/oceanog.2013.58)

*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](https://doi.org/10.7717/peerj.4355)

*Methods*

Johnston, E. C., Forsman, Z. H., Flot, J.-F., Schmidt-Roach, S., Pinzón, J. H., Knapp, I. S. S., & Toonen, R. J. (2017). A genomic glance through the fog of plasticity and diversification in Pocillopora. *Scientific Reports*, 7(1).

doi:[10.1038/s41598-017-06085-3](https://doi.org/10.1038/s41598-017-06085-3)

*Methods*

PINZÓN, J. H., & LAJEUNESSE, T. C. (2010). Species delimitation of common reef corals in the genus Pocillopora using nucleotide sequence phylogenies, population genetics and symbiosis ecology. *Molecular Ecology*, 20(2), 311–325. doi:10.1111/j.1365-294x.2010.04939.x <https://doi.org/10.1111/j.1365-294X.2010.04939.x>

*Methods*

Pinzón, J. H., Sampayo, E., Cox, E., Chauka, L. J., Chen, C. A., Voolstra, C. R., & Lajeunesse, T. C. (2013). Blind to morphology: genetics identifies several widespread ecologically common species and few endemics among Indo-Pacific cauliflower corals (Pocillopora, Scleractinia). *Journal of Biogeography*, 40(8), 1595–1608.

doi:[10.1111/jbi.12110](https://doi.org/10.1111/jbi.12110)

*Methods*

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## Related Datasets

### Different Version

Burgess, S., Johnston, E., Wyatt, A., Leichter, J., & Edmunds, P. (2021). Response diversity in corals: hidden differences in bleaching mortality among cryptic Pocillopora species (Version 3) [Data set]. Dryad.

<https://doi.org/10.5061/DRYAD.FQZ612JS0> <https://doi.org/10.5061/dryad.fqz612js0>

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## Parameters

Parameter	Description	Units
Trip	1 = February 2019; 2= August 2019	unitless
Site	Sampling site; label corresponds to the site used in the Moorea Coral Reef Long-Term Ecological Research (MCR-LTER) program	unitless
Species_haplotype	mtORF haplotype identifier	unitless
Photos_max_length_cm	Longest diameter (in centimeters) along the longest axis of the coral in planar view from the photoquadrat images taken in February (for Trip 1) or August (for Trip 2) 2019	centimeters (cm)
Mortality	0 = alive in August 2019; 1 = dead in August 2019	unitless
Species	The taxon name ascribed to the mtORF haplotype	unitless

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## Project Information

**Collaborative research: Coral community resilience: testing the role of hidden diversity in pocilloporid corals at Moorea (Pocilloporid Coral Diversity)**

## Coverage: Moorea, French Polynesia

### *NSF Award Abstract:*

While most coral reefs in the world are threatened by multiple disturbances that are driving coral cover downward, the coral reefs at Mo'orea, French Polynesia, provide a striking exception. However, it is not yet clear what makes the coral communities of Mo'orea an exception to the trend of global decline in coral cover, and what drives spatial variation in recovery patterns around the island. The most recent wave of recovery on the outer reefs is dominated by corals in the genus *Pocillopora* (the cauliflower coral). While the colonies of this coral all look similar to one another, they actually represent multiple 'hidden' species that are genetically divergent but visibly indistinguishable. The morphological similarity makes it hard to identify species in the field, and this often forces researchers to pool these corals into a single group, which has impeded a full understanding of coral recovery. The ecological differences among these hidden species remain poorly understood, but they may be a crucial factor keeping the ecosystem in a coral-dominated state. This project is studying how 'hidden diversity' provides a form of 'ecological insurance' that provides reef-building coral communities around this island with ecological and evolutionary options that buffer reefs from unpredictable and unfavorable environmental conditions. If multiple cryptic species exhibit a diversity of responses to disturbance and stress, then it increases the ability of the community to recover and re-organize after impacts compared to that if all the species responded the same way. By studying the reefs at Mo'orea, this project provides unique, important, and transferable knowledge to better understand fundamental mechanism driving coral community recovery following catastrophic damage, and will provide much-needed information to better manage coral reefs and favor them remaining in a coral-dominated state. A PhD student and a postdoctoral researcher at Florida State University (FSU) are being supported and mentored during the project, and a program of professional growth is being provided for a technician who will work on the project. The investigators are working with science educators from Florida schools to introduce marine biology clubs that will provide outreach opportunities for FSU and California State University Northridge participants to engage high school students and teachers in the research themes at the core of this project.

This project will test the hypothesis that the presence of morphologically similar yet genetically divergent lineages of corals in the genus *Pocillopora* drives rapid recovery of coral communities dominated by *Pocillopora* on the outer reefs of Mo'orea, French Polynesia. By creating a diverse portfolio in the capacity of the *Pocillopora* community to recover and reorganize after disturbance, hidden ecological differences among coral lineages in their response to disturbance is expected to promote community resilience. A well-studied genetic marker will be used to distinguish coral colonies among different lineages. Field-based projects, co-located with Moorea Coral Reef-Long-Term Ecological Research (MCR-LTER) sites, will determine how pocilloporid lineages differ in their distribution and abundance, spatial and temporal patterns of annual recruitment, symbiont composition, and post-settlement growth and survival. These data will be used to build Integral Projection Models (IPMs) to compare population differences among lineages in their sensitivity to size-dependent perturbations, and their capacity for population growth following disturbance. Results from the field projects and IPMs will be synthesized to estimate response diversity as the multivariate dispersion of lineage dissimilarity, and to assess the extent to which it predicts variation among sites in the recovery rate of pocilloporid percent cover, estimated empirically from the MCR-LTER time series. The intellectual merits of this project lie in developing new and transferable understanding of: i) the ecological differences within an ecologically important coral genus, ii) why pocilloporids at Mo'orea are an exception to the global trend of declining coral cover, and iii) the potential for hidden response diversity to act as a fundamental mechanism determining the capacity for coral communities to reestablish and reorganize following disturbances.

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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1829898</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1829867</a>

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