mtORF haplotype of each Pocillopora colony sampled at a given site and depth at Moorea, French Polynesia in August 2019

Website: https://www.bco-dmo.org/dataset/857058
Data Type: Other Field Results
Version: 1
Version Date: 2021-08-03

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

Contributors	Affiliation	Role
Burgess, Scott	Florida State University (FSU)	Principal Investigator
Edmunds, Peter J.	California State University Northridge (CSUN)	Co-Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset reports the mtORF haplotype of each Pocillopora colony sampled at a given site and depth at Moorea in August 2019. These data are published in Figures 2, 3, and 4 of Johnston et al., 2021 (doi: 10.1007/s00338-021-02107-9). The attached Supplemental File "Pocillopora_mtORF.fasta" contains the mtORF haplotype sequence (855bp) for each coral colony as identified by the 'Tube_ID' column.

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Coverage

Spatial Extent: **Lat**:-17.5333 **Lon**:-149.8333
Temporal Extent: 2019-08 - 2019-08

Methods & Sampling

In August 2019, *Pocillopora* colonies were sampled from three depths (5, 10, and 20 m) at each of four sites (sites 1, 2, 4, and 5) on the fore reef of Mo'orea. Site locations and names correspond to that used by the Mo'orea Coral Reef Long-Term Ecological Research (MCR-LTER) program. At each depth at each site, 10-15 50x50 cm quadrats were randomly placed on the reef along the target depth contour until approximately 50 colonies had been sampled. Tissue from all *Pocillopora* colonies within the quadrat was sampled. Tissue (~ 5 mm diameter) was collected using small bone clippers, stored in salt-saturated dimethyl sulfoxide DMSO buffer. Genomic DNA was extracted from tissues using Chelex 100 (Bio-Rad, USA). DNA was then used for PCR amplification using the mitochondrial Open Reading Frame (mtORF) marker (Flot & Tillier, 2007). A restriction fragment length polymorphism (RFLP) gel-based assay was used to distinguish *P. meandrina* and *P. eydouxi*. In GENEIOUS v.9.1.8 (Biomatters), forward mtORF sequences (855bp) were aligned and samples were identified to haplotype based on previously published sequences of mtORF haplotypes (see the attached Supplemental

File 'Pocillopora_mtORF.fasta').

Data Processing Description

These data are published in Figures 2, 3, and 4 of Johnston et al. (2021). The R scripts and data used to perform analyses and prepare figures are available from Dryad (doi: 10.5061/dryad.kwh70rz3p).

BCO-DMO Processing:
- renamed fields (columns) to conform with BCO-DMO naming conventions.

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Data Files

File
haplotypes_moorea.csv (Comma Separated Values (.csv), 15.81 KB) MD5:9136b5bc5eebba89aa08a0ff60dc84a5 Primary data file for dataset ID 857058

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Supplemental Files

File
Pocillopora_mtORF.fasta (Octet Stream, 567.75 KB) MD5:b9b83031af5e78ee5a60e1a41073c455 Mitochondrial Open Reading Frame (mtORF) sequences (855bp) for each coral colony as identified by 'Tube_ID' in the "Pocillopora haplotypes at Moorea by site and depth" dataset (Dataset ID 857058).

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Related Publications

Flot, J.-F., & Tillier, S. (2007). The mitochondrial genome of Pocillopora (Cnidaria: Scleractinia) contains two variable regions: The putative D-loop and a novel ORF of unknown function. Gene, 401(1-2), 80–87. doi:10.1016/j.gene.2007.07.006
Methods

Johnston, E. C., Wyatt, A. S. J., Leichter, J. J., & Burgess, S. C. (2021). Niche differences in co-occurring cryptic coral species (Pocillopora spp.). Coral Reefs. doi:10.1007/s00338-021-02107-9
Results

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Related Datasets

Different Version

Johnston, E., Wyatt, A., Leichter, J., & Burgess, S. (2021). Niche differences in co-occurring cryptic coral species (Pocillopora spp.) (Version 2) [Data set]. Dryad. https://doi.org/10.5061/DRYAD.KWH70RZ3P
https://doi.org/10.5061/dryad.kwh70rz3p

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Parameters

Parameter	Description	Units
Depth_m	Sampling depth in meters	meters (m)
Site	Sampling site, label corresponds to the site used in the Moorea Coral Reef Long-Term Ecological Research (MCR-LTER) program	unitless
Tube_ID	Coral colony identifier	unitless
Species_haplotype	mtORF haplotype ID	unitless

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Instruments

Dataset-specific Instrument Name	PCR amplification
Generic Instrument Name	Thermal Cycler
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: 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
NSF Division of Ocean Sciences (NSF OCE)	OCE-1829867

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