Genetic sequence accessions, collection information, and methodology for raw sequences from ezRAD libraries of Pocillopora spp. collected in Moorea, French Polynesia in 2019

Website: https://www.bco-dmo.org/dataset/881853
Data Type: Other Field Results
Version: 1
Version Date: 2022-10-04

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

Contributors	Affiliation	Role
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Abstract
This dataset contains genetic sequence accessions, collection information, and methodology for raw sequences from ezRAD libraries of Pocillopora spp. collected in 2019. Samples were collected between 5 and 20m on the fore reef in Moorea, French Polynesia. Sequence accessions are for holdings in the Sequence Read Archive (SRA) at the National Center for Biotechnology Information (NCBI). All sequence and biosample accessions can be found under BioProject PRJNA852278 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA852278).

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Coverage

Spatial Extent: **N**:-17.472 **E**:-149.762 **S**:-17.583 **W**:-149.924
Temporal Extent: 2019-08

Methods & Sampling

Tissue samples from 44 Pocillopora colonies were collected using SCUBA in August 2019 from six sites (LTER 1 – 6) and three depths (5, 10, and 20 m) around Mo'orea, French Polynesia. Tissue samples were stored in salt-saturated DMSO (dimethyl sulfoxide) buffer until DNA was extracted. Genomic DNA was extracted from tissue using the OMEGA (BIO-TEK) E.Z.N.A. Tissue DNA Kit. Extractions were quantified using the Qubit dsDNA HS Assay Kit with the Qubit Fluorometer. ezRAD libraries were generated by digesting samples with the isoschizomer restriction enzymes MboI and Sau3AI (New England BioLab), which cleave at GATC cut sites, and libraries were generated with the KAPA HyperPrep Kit (Roche) using TruSeq DNA indexes (Illumina). Libraries were size selected at 350 – 700 bp and sequenced on the MiSeq platform as paired-end 300 bp runs at Florida State University.

Data Processing Description

BCO-DMO Data manager processing notes:
* Imported file SraRunTable.txt which was generated by submitter using the NCBI run selector.
* subset columns from the run selector results

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Data Files

File
pocillopora_sequences.csv (Comma Separated Values (.csv), 13.75 KB) MD5:53a07dcc6ad68595ab8ff45e654caa97 Primary data file for dataset ID 881853

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Related Publications

Johnston, E. C., Cunning, R., & Burgess, S. C. (2022). Cophylogeny and specificity between cryptic coral species (Pocillopora spp.) at Mo′orea and their symbionts (Symbiodiniaceae). Molecular Ecology, 31(20), 5368–5385. Portico. https://doi.org/10.1111/mec.16654
Results

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Related Datasets

IsRelatedTo

Florida State University (2022). Cophylogeny between Pocillopora spp. and Symbiodiniaceae at Moorea. NCBI:BioProject: PRJNA852278. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA852278.

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Parameters

Parameter	Description	Units
BioProject	NCBI SRA BioProject ID	unitless
BioSample	NCBI SRA BioSample ID	unitless
geo_loc_name	Location where sample was collected	unitless
Collection_Date	Year and month of collection in format (YYYY-MM)	unitless
lat	Latitude of site where sample collected	decimal degrees
lon	Longitude of site where sample collected	decimal degrees
Depth	Depth of coral from which sample was taken	meters (m)
Experiment	NCBI SRA Experiment ID	unitless
Run	SRA Run ID	unitless
Sample_ID	Unique ID of the sample	unitless
Sample_Name	Sample name	unitless
SRA_Study	NCBI SRA Study ID	unitless
Organism	Genus of organism	unitless
Isolate	Isolate (Coral)	unitless
dev_stage	Developmental stage of the coral	unitless
Tissue	Tissue sampled	unitless
Assay_Type	Type of genomic library	unitless
AvgSpotLen	Average spot length	unitless
Bases	Size of genomic library	unitless
BioSampleModel	BioSample model	unitless
Bytes	Filesize in bytes for datastore file	unitless
DATASTORE_filetype	Type of file	unitless
Instrument	Sequencing instrument used to create library	unitless
Isolation_Source	Coral reef habitat type where sample was collected	unitless
Library_Name	Coral reef habitat type where sample was collected	unitless
LibraryLayout	Paired end read samples	unitless
LibrarySelection	Library selection (Reduced Representation)	unitless
LibrarySource	Within cell subunit	unitless
mtORF_haplotype	mitochondrial Open Reading Frame haplotype name	unitless
Platform	Platform (Illumina)	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
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.

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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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