Coral colony genetic sequence accession numbers for samples collected from the lagoon environment of Ofu Island, American Samoa between 2011 and 2015.

Website: https://www.bco-dmo.org/dataset/762497
Data Type: Other Field Results
Version: 1
Version Date: 2019-03-18

Project
» Ecological, evolutionary and physiological responses of corals to a mass bleaching event in American Samoa (Bleaching American Samoa)

Contributors	Affiliation	Role
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Abstract
Coral colony genetic sequence accessions for samples collected from the lagoon environment of Ofu Island in the National Park of American Samoa between 2011 and 2015.

Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Related Publications
- Related Datasets
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Coverage

Spatial Extent: **N**:-14.1795 **E**:-169.65462 **S**:-14.17977 **W**:-169.655
Temporal Extent: 2011-04 - 2015-12

Dataset Description

Coral colony genetic sequence accessions for samples collected from the lagoon environment of Ofu Island in the National Park of American Samoa between 2011 and 2015. All data and samples were collected at depths less than 3.0m.

This dataset includes all sequence data accession numbers for the publication Thomas & Palumbi (2017) housed at The National Center for Biotechnology Information under BioProject PRJNA522016 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA522016).

Methods & Sampling

Seven colonies of A. hyacinthus from the back-reef environment of Ofu Island were tagged, sampled, and monitored at five time-points spanning the bleaching event: before bleaching representing baseline expression levels (August 2011), and then two months (April 2015), six months (August 2015), 10 months (December 2015) and 12 months (February 2016) after initial bleaching was observed in February 2015. Coral nubbins of approximately 24 cm in size were collected from colonies within 3 h of high-tide using garden clippers and preserved in RNAlater. All colonies occurred at depths of approximately 0.51.0 m and were within a 2500 m2area of back-reef. Total RNA was extracted from tissue samples using Qiagen's RNAeasy Plus Kit, and 35 cDNA libraries (seven colonies for five dates) were generated using the Illumina TruSeq RNA Library Prep Kit v2 with Protoscript II Reverse Transcriptase. The 35 libraries were multiplexed and sequenced across three lanes on a Hiseq2500 at the University of Utah Microarray and Genomic Analysis Core Facility.

Location: Ofu Island, American Samoa. All data and samples were collected from the lagoon environment in the National Park of American Samoa at depths less than 3.0m.

Data Processing Description

BCO-DMO Data Manager Processing Notes:

* added a conventional header with dataset name, PI name, version date

* modified parameter names to conform with BCO-DMO naming conventions
* added lat/lons and species name for each coral colony from information provided with a previous data submission for coral colony water temps: https://www.bco-dmo.org/dataset/676132
* added a data column for direct links to NCBI accession numbers

[table of contents | back to top]

Data Files

File
recovery.csv (Comma Separated Values (.csv), 4.42 KB) MD5:8bb3c990e6282366f793038d919c04e4 Primary data file for dataset ID 762497

[table of contents | back to top]

Related Publications

Barshis, D. J., Ladner, J. T., Oliver, T. A., Seneca, F. O., Traylor-Knowles, N., & Palumbi, S. R. (2013). Genomic basis for coral resilience to climate change. Proceedings of the National Academy of Sciences, 110(4), 1387–1392. doi:10.1073/pnas.1210224110
Methods

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature Methods, 9(4), 357–359. doi:10.1038/nmeth.1923
Software

Li, H., Handsaker, B., Wysoker, A., Fennell, T., Ruan, J., … Homer, N. (2009). The Sequence Alignment/Map format and SAMtools. Bioinformatics, 25(16), 2078–2079. doi:10.1093/bioinformatics/btp352
Methods

Love, M. I., Huber, W., & Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15(12). doi:10.1186/s13059-014-0550-8
Methods

Thomas, L., & Palumbi, S. R. (2017). The genomics of recovery from coral bleaching. Proceedings of the Royal Society B: Biological Sciences, 284(1865), 20171790. doi:10.1098/rspb.2017.1790

Results

[table of contents | back to top]

Related Datasets

Different Version

Thomas, L., & Palumbi, S. R. (2017). *Data from: The genomics of recovery from coral bleaching* (Version 1) [Data set]. Dryad Digital Repository. https://doi.org/10.5061/dryad.3444s

[table of contents | back to top]

Parameters

Parameter	Description	Units
sample	Sequence file (corresponds to NCBI library "Name" field for SRA sample)	unitless
date	Year and Month the colony was collected in format yyyy-mm	unitless
colony	colony label	unitless
bleaching_status	Bleaching score (0-100% bleached)	percent (%)
accession	SRA Accession number at The National Center for Biotechnology Information	unitless
latitude	Latitude of colony	decimal degrees
longitude	Longitude of colony	decimal degrees
species	Coral species (Genus species)	unitless
accession_link	SRA Accession link to The National Center for Biotechnology Information	untiless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2500
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.

[table of contents | back to top]

Deployments

Palumbi_AmSamoa_2013-2015

Website	https://www.bco-dmo.org/deployment/676237
Platform	American_Samoa
Start Date	2013-01-04
End Date	2015-08-21
Description	Coral colony samples, temperature, DNA/RNA, bleaching metrics.

[table of contents | back to top]

Project Information

Ecological, evolutionary and physiological responses of corals to a mass bleaching event in American Samoa (Bleaching American Samoa)

Coverage: American Samoa

Description from NSF award abstract:
The strongest coral bleaching event in nearly 20 years began in American Samoa in January 2015. Coral bleaching occurs when ocean water temperatures exceed a coral's normal heat tolerance. But bleaching events usually show an unexplained pattern - colonies next to one another can show very different levels of bleaching - from pure white to the normal tan color of a healthy coral. The investigators have observed this pattern among 280 corals on reefs in American Samoa that have been studied for years. This system will be used to test four major hypotheses about what causes some corals to bleach and some not: differences in 1) species, 2) the temperature the corals experienced, 3) the symbiont they harbor, and 4) the genotype of the coral host. In addition, the investigators will return to American Samoa at regular intervals to measure the rate of recovery of each coral colony and conduct the same tests as above for recovery rate. The stark-white reefscapes left behind by bleaching events are one of the most common signals of increased ocean warming. This work will take advantage of years of prior study and the advent of a coral bleaching event to understand the rules for survival on reefs.

The reefs of American Samoa began showing a major bleaching event starting in January 2015, including 62 corals that have been intensively studied for coral thermal resistance, field temperatures, and symbiont type. In April 2015 the investigators monitored bleaching status of these and additional corals, totaling 280 corals from four species, and uncovered marked variation in bleaching extent within and between species and within and between reef regions. The team will test the relative importance of microclimate to bleaching state by examining records of approximately 50 temperature loggers in place since before the bleaching event. They will test the influence of symbiont type and host gene expression profiles by examining samples of 60 colonies taken at four time points after bleaching. The investigators will also examine the full suite of 280 corals for genetic variation to estimate the relationship between bleaching state, recovery rate and genetic polymorphism. These data will be used to test micro-climate, symbiont, and coral genetics as determinants of bleaching and bleaching recovery. Because the investigators have samples from these 280 colonies before bleaching mortality, this study will provide the first estimate for the evolutionary impact of a bleaching event on coral populations.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1547921

[table of contents | back to top]