ITS2 amplicon sequences from Acropora hyacinthus samples collected at mutliple timepoints in Moorea, French Polynesia after the mass bleaching event of 2019

Website: https://www.bco-dmo.org/dataset/876564
Data Type: Other Field Results
Version: 1
Version Date: 2022-06-29

Project
» RAPID: Collaborative Research: Studies of recovery from bleaching in Acropora hyacinthus: epigenetic shifts, impacts on reproductive biology and carry-over effects (Moorea coral bleaching)

Contributors	Affiliation	Role
Strader, Marie	Auburn University	Principal Investigator, Contact
Hofmann, Gretchen E.	University of California-Santa Barbara (UCSB-MSI)	Co-Principal Investigator
Heyl, Taylor	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset represents ITS2 amplicon sequences from Acropora hyacinthus samples collected at mutliple timepoints in Moorea, French Polynesia after the mass bleaching event of 2019.

Table of Contents

Coverage

Spatial Extent: **N**:-14.4751 **E**:-149.817 **S**:-17.4731 **W**:-149.818
Temporal Extent: 2019-05-19 - 2019-10-09

Methods & Sampling

To assess in hospite symbiont community dynamics in a major reef-building coral, *Acropora hyacinthus*, during a mass bleaching event we sampled small pieces of tissue from each colony and performed ITS2 amplicon sequencing. Samples were collected at the height of the bleaching event (May 2019), 3 months after (August 2019) and 5 months later (October 2019). Samples were collected at 3 different reef zones, backreef (~1 meter depth), shallow forereef (~5 meter depth), and deeper forereef (~14 meter depth).

Raw sequence data have been deposited in the NCBI Sequence Read Archive (SRA) under BioProject number PRJNA833391. This dataset also includes relevant metadata for each sample.

Data Processing Description

BCO-DMO Processing Description:
- Converted date columns to format YYYY-MM-DD
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Converted latitude and longitude from South and West to North and East and split columns
- Added a conventional header with dataset name, PI names, version date

[table of contents | back to top]

Data Files

File
amplicon_sequencing.csv(Comma Separated Values (.csv), 22.65 KB) MD5:60c88de32f57df18e82fd80974767bec Primary data file for dataset ID 876564

[table of contents | back to top]

Related Publications

Leinbach, S. E., Speare, K. E., & Strader, M. E. (2022). Reef habitats structure symbiotic microalgal assemblages in corals and contribute to differential heat stress responses. Coral Reefs. https://doi.org/10.1007/s00338-022-02316-w
Results

[table of contents | back to top]

Related Datasets

IsRelatedTo

Auburn University. In hospite Symbiodiniaceae ITS2 Targeted loci environmental. 2022/04. 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/PRJNA833391. NCBI:BioProject: PRJNA833391.

[table of contents | back to top]

Parameters

Parameter	Description	Units
Accession	NCBI accession number	unitless
Sample_Name	name of individual sample	unitless
BioSample	NCBI BioSample number	unitless
Details	description of colony and location of coral reef	unitless
Host	species identification of coral host	unitless
Location	location of sample site	unitless
Date	date of sample collection in format YYYY-MM-DD	unitless
Depth	water depth of sample site	meters (m)
Latitude	latitude North of sample site	decimal degrees
Longitude	longitude East of sample site	decimal degrees

[table of contents | back to top]

Project Information

RAPID: Collaborative Research: Studies of recovery from bleaching in Acropora hyacinthus: epigenetic shifts, impacts on reproductive biology and carry-over effects (Moorea coral bleaching)

Coverage: Moorea, French Polynesia; Auburn University; University of California, Santa Barbara

NSF Award Abstract:

Coral reefs provide strong economic and ecological benefits, yet they are declining worldwide largely due to extreme heat events that cause bleaching, a disturbance of the essential relationship between the algae that live inside the coral and the coral. There is currently a mass coral bleaching event in Moorea, French Polynesia where up to 90% of corals show some level of bleaching in response to heat stress. This location is ideal to study adaptation and acclimation thanks to the facilities and sampling of the Moorea Coral Reef (MCR) Long Term Ecological Research (LTER) site. This project explores how strong natural disaster events shape genetic differences in populations through time. By using historical environmental data it may be possible to identify modifications of the genome linked to past bleaching events. This knowledge will help establish models to predict reef recovery after disturbance and will be useful for choosing colonies with the best chance of survival in restoration efforts. This project also investigates how the bleaching history of the parents impacts characteristics of the next generations, such as reproductive output, larval, survival and heat tolerance. This project will provide training and involvement in research for three senior PhD students and at least five undergraduates. Coral restoration efforts rely on understanding how corals might adapt to environmental

stress.

The mass coral bleaching event currently occurring in French Polynesia (April 2019) offers an opportunity to test hypotheses regarding mechanisms of rapid response to large scale disturbances. This project investigates potential epigenetic and genetic mechanisms involved in either resisting stress or recovering from bleaching. The research leverages the Moorea Coral Reef (MCR) LTER, which integrates the high resolution oceanographic metrics and data on long-term community dynamics into the study of rapid adaptation of Acropora hyacinthus. Genetic and epigenetic signatures of a natural selection event (bleaching) are tracked in the field to test the impact of bleaching history on reproductive and carry-over effects in larval and juvenile corals. Both physiological and molecular methods, such as 2bRAD genotyping and reduced representation bisulfite sequencing, are employed to investigate correlations between phenotypes and genetic and epigenetic differences in the genome. This work explores associations between selection on genetic variation and epigenetic variation as well as the potential role of DNA methylation in phenotypic change across a generation in association with coral bleaching. In this era of global change, there is mounting evidence that rapid evolutionary processes are occurring at time scales relevant to ecological processes. Therefore, capitalizing on a system with rich long-term ecological data, such as that associated with the MCR LTER, is ideal to investigate mechanisms of rapid adaptation.

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.

[table of contents | back to top]

Funding

Funding Source	**Award**
NSF Division of Ocean Sciences (NSF OCE)	OCE-1935308
NSF Division of Ocean Sciences (NSF OCE)	OCE-1935305

[table of contents | back to top]