Staghorn coral health following experimental treatment with and without antibiotics

Website: https://www.bco-dmo.org/dataset/816316

Data Type: experimental

Version: 1

Version Date: 2020-06-25

Project

» Coral-microbial interactions as determinants of disease dynamics (Coral-microbial interactions)

Contributors	Affiliation	Role
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Abstract

This dataset reports results from a priority experiment with staghorn corals fragments from 10 genotypes. Antibiotic-treated and untreated tanks were sampled for DNA and exposed to disease or healthy slurries at two time points. Corals that developed disease were sampled and sacrificed. Health status of the coral fragments was scored every 12hrs.

Table of Contents

- Coverage
- Dataset Description
 - Methods & Sampling
 - Data Processing Description
- Data Files
- Related Datasets
- <u>Parameters</u>
- Project Information
- Funding

Coverage

Spatial Extent: **Lat**:9.3513 **Lon**:-82.2565 **Temporal Extent**: 2015-06 - 2015-06

Dataset Description

This dataset reports results from a priority experiment with staghorn corals fragments from 10 genotypes. Antibiotic-treated and untreated tanks were sampled for DNA and exposed to disease or healthy slurries at two time points. Corals that developed disease were sampled and sacrificed. Health status of the coral fragments was scored every 12hrs.

Methods & Sampling

Priority experiment was conducted in 24 recirculating tanks at the Smithsonian stations in Bocas del Toro, Panama. Replicate staghorn corals fragments from 10 genotypes were placed into the tanks containing 12 liters of UV sterilized seawater. Twelve tanks were then exposed to an antibiotic cocktail of Kanamycin, Ampicillan, Tetracycline and Choloramphenicol (100mg/ml each) twice over a 48hr period, and the corals from the antibiotic treated and untreated tanks were sampled for DNA (T0 sample point) and lesioned with an airbrush. Half of the antibiotic- treated and untreated tanks were then exposed to 30ml of disease slurry (D) or healthy slurry (H) for the first exposure. 24hrs later a second dose of disease or healthy slurry was applied to

complete the priority experiment treatments of healthy_healthy (h_h), disease_disease (d_d), healthy_disease (h_d), and disease_healthy (d_h). DNA for the microbial analyses were sampled 18hrs later (T2) and then disease was monitored over the course of the experiment. Corals that developed disease were sampled (T3) and sacrificed. All of corals were sampled (T3) timepoint on day 7.

Health status of the coral fragments was scored every 12hrs. 2-3 coral polyps were sampled using sterilized tweezers and placed into 200 ul of CHAOs DNA extraction buffer for downstream DNA analyses. Corals that developed disease were removed from tanks during the experiment.

Data Processing Description

BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date

[table of contents | back to top]

Data Files

File

coral_priority.csv(Comma Separated Values (.csv), 124.89 KB)
MD5:e21766630bf308de67946698c08545f8

Primary data file for dataset ID 816316

[table of contents | back to top]

Related Datasets

IsRelatedTo

Gouhier, T. C., Vollmer, S. V. (2021) **Microbial 16S OTU annotation information from staghorn coral health experiments with treatment with and without antibiotics.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-06-26 doi:10.26008/1912/bco-dmo.816367.1 [view at BCO-DMO]

Gouhier, T. C., Vollmer, S. V. (2021) **Microbial 16S OTU count data from staghorn coral health experiments with treatment with and without antibiotics.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-06-25 doi:10.26008/1912/bco-dmo.816379.1 [view at BCO-DMO]

[table of contents | back to top]

Parameters

Parameter	Description	Units
Tank	Tank ID/label	unitless
Antibiotic	Experimental antibiotic treatment. Factor with levels Anti or No_Anti	unitless
firstDose	First experimental exposure to microbes from healthy or diseased corals. Factor: levels Healthy or Disease	unitless
secondDose	Second experimental exposure to microbes from healthy or diseased corals. Factor: levels healthy or disease	unitless
Genotype	Coral host genotype. Factor with levels represented by labels corresponding to different colors	unitless
time	Time since antibiotic treatment was administered	hours
outcome	Health status of coral host. Factor with levels $0 = \text{Healthy}$; $1 = \text{Disease}$; $2 = \text{On way to}$ White Band Disease (WBD); $3 = \text{Tank Death}$	unitless

[table of contents | back to top]

Project Information

Coral-microbial interactions as determinants of disease dynamics (Coral-microbial interactions)

Coverage: Panama, Bocas del Toro Archipelago

Description from NSF award abstract:

The health of numerous animal and plant hosts depends on the composition of their microbiome. Although the health of hosts is often linked to environmental factors that favor the growth of pathogenic microbes, the diversity of animal and plant microbiomes suggests that competition plays an important role in determining the frequency and severity of disease outbreaks. This project uses the endangered Caribbean staghorn coral as a model system to understand how the environment and microbial interactions controls the spread of White Band Disease (WBD), a bacterial disease that has decimated nearly 95% of Caribbean staghorn coral populations. A combination of manipulative experiments, field surveys and mathematical modeling will be used to determine how water temperature, microbial movement between- and microbial competition within coral hosts influence WBD incidence. By identifying the environmental and microbial drivers of WBD, this project will allow managers to (i) predict hotspots of vulnerability to WBD in space and time, and (ii) identify optimal strategies for restoring these once prominent members of Caribbean coral reef communities. This research will address important societal needs by cross-training graduate students in coral biology, microbial genetics, bioinformatics, mathematical modeling, computer programming and statistics. Results of this project will be integrated into undergraduate courses in genetics, ecological modeling and biostatistics in order to emphasize the importance of quantitative and interdisciplinary STEM training for addressing important questions in biology. Finally, a series of interactive web modules will be created to disseminate the results of this project beyond academic circles, including to Northeastern University's Marine Science Center K-12 outreach programs and the Smithsonian Tropical Research Institute's outreach programs in Panama.

There is growing recognition that the processes that structure microbial communities may scale up to explain disease outbreaks in their hosts. Despite the complexity of microbial communities, most studies to date have focused on resolving the direct relationship between the environment, the occurrence of pathogenic microbes,

and the incidence of disease. However, the effects of microbial species interactions and dispersal on the emergence of host diseases remain largely unknown. This project will combine microbial genetics and mathematical modeling to understand the relative influence of the environment, species interactions and dispersal on the structure of microbial communities and the dynamics of disease in their coral hosts. This research uses the endangered Caribbean staghorn coral (Acropora cervicornis) and White Band Disease (WBD) as a model host-pathogen system. This once dominant, reef-building coral was decimated by WBD, prompting its listing as an endangered species. Recent work in this system suggests that (i) bacteria are the cause of WBD, (ii) the microbial community living within the host can produce antibiotic compounds that suppress pathogenic bacteria, and (iii) temperature increase promotes infection and reduces the production of antibiotic compounds. These findings suggest that the interplay between the environment and host-associated microbial species determines the structure of the microbial community and the health of the coral host. To disentangle these processes, a multi-factorial transmission experiment will be conducted to understand the direct and indirect effects of temperature, pathogen exposure, and microbial community complexity on disease dynamics. To determine how these results scale up to natural coral reefs, a spatial coral-microbial model will be fitted to field survey data. This fitted model will elucidate how seasonal temperature variation and microbial dispersal jointly influence coral disease outbreaks and the structure of coral-microbial communities across spatial scales. The proposed research will integrate research with teaching and training of undergraduate students.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1458158

[table of contents | back to top]