Data from various stages of the analysis pipeline on coral collected sampled in the Caribbean during 2013 (Contagious coral diseases project)

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Project
» Are coral diseases contagious? (Contagious coral diseases?)

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Abstract
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Dataset Description

This dataset contains analysis pipeline files. There are 3 types of files:

1. One set has the extension “.fa”. These are the fasta files in various stages through our analysis pipeline.

2. Additionally, several chimera checks are performed. Chimera sequences are placed in chimera files e.g. "fasta.chimeras.fa."

3. One file contains a cluster for error correction and output consensus "cons.fa"

Coral disease transmission experiments were completed for dark-spot syndrome on Sidereastrea siderea and yellow-band disease on Orbicella faveolata, as described in Randall et al. 2016. Following experimentation, microbial communities were extracted from tissue samples to determine whether any potential pathogen may have transmitted from healthy to exposed corals. Microbial communities on healthy corals were compared with diseased corals to identify any potential pathogens.

Experimental diseased and healthy corals were sampled and their microbial communities were analyzed using 454 Illumina pyrosequencing of the amplified 16S rRNA gene on the V1-V3 hypervariable region.

Methods & Sampling

[Adapted from: Randall et al. 2016 *PLoS ONE* 11(1): e0147493. doi:10.1371/journal.pone.0147493]

Immediately following completion of the waterborne-transmission experiments (See Randall et al. 2016 *PLoS ONE*11(1) attached), three each, of diseased, exposed, and healthy colonies of *S. siderea* were randomly selected for bacterial-community analyses, to determine whether potential bacterial pathogens had transmitted to the exposed colonies. The nine coral colonies were placed in individual, sterile whirl-paks at -80 degrees C and then were transported on dry ice to Mote Marine Laboratory in Sarasota, Florida.

Tissue was removed from the skeleton of the preserved-coral colonies using a Paasche airbrush with 10 mL of sterile seawater. The tissue slurry was collected in a sterile 50 mL Falcon® tube and homogenized using a vortex. The tissue homogenate was then spun down into a pellet using a centrifuge set at 10,000 rpm. The pellet was re-suspended in 2 mL of solution C1 and DNA was extracted using a Powersoil DNA extraction kit (MoBIO Laboratories Inc. Lot #PS14F19). Extracted DNA was then sent to MRDNA Laboratory (www.mrdnalab.com, Shallowater, TX, USA) for Illumina sequencing (20,000 reads per assay) using the universal bacterial primers 27F/519R with a barcode on the forward primer. The 16S rRNA gene on the V1 – V3 hypervariable region was amplified by applying a 30 cycle polymerase chain reaction (PCR) with the HotStarTaq Plus Master Mix Kit (Qiagen, USA). PCR was applied using the following protocol: (1) 94 degrees C for 3 minutes, (2) 28 cycles of: 94 degrees C for 30 seconds, 53 degrees C for 40 seconds, and 72 degrees C for 1 minute, and (3) a final elongation step at 72 degrees C for 5 minutes. After amplification, PCR products were confirmed in 2% agarose gels to determine the success of amplification and the relative intensity of the bands. Multiple samples were pooled together in equal proportions based on their molecular weight and DNA concentrations. Pooled samples were purified using calibrated Ampure XP beads. Then the pooled and purified PCR product was used to prepare DNA libraries by following the Illumina TruSeq DNA library preparation protocol. Sequencing was performed using the Illumina sequencing platform at MR DNA (www.mrdnalab.com, Shallowater, TX, USA) following the manufacturer's guidelines. Sequence data were processed using a standardized analysis pipeline. Briefly, sequences were initially depleted of barcodes. Then sequences less than 150bp or with ambiguous base calls were removed. Operational taxonomic units (OTUs) were generated, and chimeras were removed using UCHIME [48]. OTUs were defined by clustering at 3% divergence (i.e., showing 97% similarity) using a de novo method. Final OTUs were taxonomically classified using BLASTn against the curated National Center for Biotechnology Information (NCBI) database and the Ribosomal Database Project (RDP).

Field collection:

Wonderland Reef, Florida (24.56028 N, 81.50127 W). Collections in July 2013.

Laboratory experimentation:

Mote Marine Laboratory, Tropical Research Laboratory, Summerland Key, Florida from 10 July – 14 August 2013.

Data Processing Description

Please see the methods described above and in Randall et al. 2016 for data processing.

Data Management Office Notes:

- Links created to direct the user to the original file generated by PI.
- Data files linked are unaltered.

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Data Files

File	
sequences_fasta.chimeras.fa filename: 658310/sequences_fasta.chimeras.fa	(FASTA, 275 bytes) MD5:1ab6b445c3f0e0d11225c314276c986a
Fasta file from various stages through analysis pipeline. Several chimera checks were performed.	
sequences_fasta.chimeras_ref.fa filename: 658310/sequences_fasta.chimeras_ref.fa	(FASTA, 7.27 MB) MD5:922b67aa5f7f00c0420d2e55b6e8436c
Fasta file from various stages through analysis pipeline. Several chimera checks were performed.	
sequences_fasta.chimeras_ref.fas filename: 658310/sequences_fasta.chimeras_ref.fas	(Octet Stream, 7.27 MB) MD5:9c3d4fdd69c9e23dcdbee34ced3a1841
Several chimera checks were performed.	
sequences_fasta.chimeras_ref.fas.fa filename: 658310/sequences_fasta.chimeras_ref.fas.fa	(FASTA, 5.99 MB) MD5:652b8d6023364f8985fe2d22204273a2
Fasta file from various stages through analysis pipeline. Several chimera checks were performed.	
sequences_fasta.cons.fa filename: 658310/sequences_fasta.cons.fa	(FASTA, 87.60 MB) MD5:bbf6ea1b50020fd4bd8b8574698009f9
Fasta file from various stages through analysis pipeline. Clustered for error correction and output consensus.	
sequences_fasta.db.fa filename: 658310/sequences_fasta.db.fa	(FASTA, 8.23 MB) MD5:98d5c6760a7c593c2a5f361b3b6006fe
Fasta file from various stages through analysis pipeline.	

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Related Publications

Randall, C. J., Jordán-Garza, A. G., Muller, E. M., & van Woesik, R. (2016). Does Dark-Spot Syndrome Experimentally Transmit among Caribbean Corals? PLOS ONE, 11(1), e0147493. doi:10.1371/journal.pone.0147493
General

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	Paasche airbrush
Generic Instrument Name	Airbrush
Dataset-specific Description	Tissue was removed from the skeleton of the preserved-coral colonies using a Paasche airbrush with 10 mL of sterile seawater
Generic Instrument Description	Device for spraying liquid by means of compressed air.

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Deployments

vanWoesik_2012

Website	https://www.bco-dmo.org/deployment/562802
Platform	Caribbean_nearshore
Start Date	2012-06-01
End Date	2016-05-31
Description	First, we will use a hierarchical sampling design to test whether coral diseases follow a contagious-disease model over two spatial scales in the Caribbean. We will also undertake this study in locations with and without a recent history of frequent thermal stress to test the alternate hypothesis that coral diseases are not infectious and contagious but are instead the result of compromised coral hosts that have undergone thermal stress. Second, we will undertake transmission experiments to examine whether coral diseases are indeed transmissible. Study Locations: (1) Mahahual, Mexico (latitude 18"42'N, longitude 87"42'W) and (2) Tuxpan, Mexico (latitude 21"01'N, longitude 97"11'W), (3) Robet van (latitude 9"12'N, longitude 82"09'W), (4) St. John, United States Virgin Islands (USVI) (latitude 18"18'N, longitude 64"45'W), and (5) Wonderland Reef, Florida (latitude 24.56028 N, longitude 81.50127 W). **Methods & Sampling** Wonderland Reef, Florida 24.56028 N, 81.50127 W Collections in July 2013 Laboratory experimentation: Mote Marine Laboratory, Tropical Research Laboratory, Summerland Key, Florida 10 July – 14 August 2013

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Project Information

Are coral diseases contagious? (Contagious coral diseases?)

Coverage: Caribbean

Diseases are one of the greatest threats to corals in the Caribbean. Yet, very little is known about marine diseases in general and coral diseases in particular. Although some pathogens have been acknowledged, identifying coral pathogens has proven difficult and evasive. Presently, coral diseases are assumed to be both infectious and contagious, suggesting that infection is caused by pathogens being passed from colony to colony through a vector. However, few studies have tested this assumption. Spatial epidemiology, or disease mapping, can provide insight into whether diseases cluster and follow a contagious-disease model. In this study we will take a two tiered approach. First, we will use a hierarchical sampling design to test whether coral diseases follow a contagious-disease model over two spatial scales in the Caribbean. We will also undertake this study in locations with and without a recent history of frequent thermal stress to test the alternate hypothesis that coral diseases are not infectious and contagious but are instead the result of compromised coral hosts that have undergone thermal stress. Second, we will undertake transmission experiments to examine whether coral diseases are indeed transmissible.

The research will take place in the Caribbean, at four locations: (1) Mahahual, Mexico (latitude 18"42'N, longitude 87"42'W) and (2) Tuxpan, Mexico (latitude 21"01'N, longitude 97"11'W), (3) Bocas del Toro, Panama (latitude 9"12'N, longitude 82"09'W) and (4) St. John, United States Virgin Islands (USVI) (latitude 18"18'N, longitude 64"45'W).

Intellectual merit

There is a certain urgency to identify coral diseases, predict their prevalence, and determine whether they are infectious and contagious or non-communicable. By understanding the etiology of coral diseases, we can determine whether human intervention will help reduce their prevalence. Without understanding these processes, we will merely continue to measure disease, continue to look for pathogens that may not exist, and watch coral populations continue to deteriorate. Although microbes play a role in disease infection, many coral diseases might not be transmissible. Therefore, we may need to incorporate environmental threshold parameters, which may be more likely the underlying mechanisms driving coral-disease dynamics. The results will have important implications for modeling diseases and predicting contemporary and future coral disease outbreaks.

Broader Impact

The underlying assumption of most disease models is contagion, which is the transmission of pathogens from infected to susceptible hosts. This study will examine this basic assumption. If it turns out that coral diseases are a consequence of a two-step process, and the corals that are tolerant to temperature stress are also resistant to diseases, then making predictions based on temperature trends will be transformational, especially in rapidly warming, yet heterogeneous, oceans. The study will train students in the field of spatial epidemiology of coral diseases.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1219804

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