

# Microbial communities of corals analyzed using 454 Illumina pyrosequencing from Wonderland Reef, Florida in 2013

**Website:** <https://www.bco-dmo.org/dataset/657866>

**Data Type:** experimental

**Version:** 1

**Version Date:** 2016-08-30

## Project

» [Are coral diseases contagious?](#) (Contagious coral diseases?)

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## Abstract

Microbial communities of corals analyzed using 454 Illumina pyrosequencing from Wonderland Reef, Florida in 2013

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## Coverage

**Temporal Extent:** 2013-07 - 2013-08

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## Dataset Description

Coral disease transmission experiments were completed for dark-spot syndrome on *Siderea 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]

Immediately following completion of the waterborne-transmission experiments (See Randall et al. 2016), 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](http://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](http://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:**

1. Tabs were converted to commas for ease of processing.
2. A column was created titled "taxon\_level" and existing first column was named "taxon". This was to reflect the information described in the original file names.
3. Extra delimiter was removed from the end of each row.
4. Percent values were truncated to include 5 numbers after the decimal.

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#### **Data Files**

File
<b>analysis.csv</b> (Comma Separated Values (.csv), 777.68 KB) MD5:6a7130fb83a5275df9261f861e66863f
Primary data file for dataset ID 657866

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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](https://doi.org/10.1371/journal.pone.0147493)

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## **Parameters**

Parameter	Description	Units
organism	the category of organism which the analysis was organised by	unitless
measurement	indication of whether percentage or count of specific taxonomy found on coral is described	unitless
taxon_level	taxonomic level for which percentages and counts are described	unitless
taxon	taxonomy for which percentages and counts are described	unitless
D4U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = healthy	percent or count
D13U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = healthy	percent or count
D27U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = healthy	percent or count
Y11U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = healthy	percent or count
Y26U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = healthy	percent or count
Y27U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = healthy	percent or count
D1L	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = exposed to dark-spot syndrome	percent or count
D3L	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = exposed to dark-spot syndrome	percent or count
D22L	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = exposed to dark-spot syndrome	percent or count
Y4L	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = exposed to yellow-band disease	percent or count
Y23L	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = exposed to yellow-band disease	percent or count
Y9L	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = exposed to yellow-band disease	percent or count
D1U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = diseased with dark-spot syndrome	percent or count
D3U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = diseased with dark-spot syndrome	percent or count
D22U	percent or count found on sample; coral species = <i>Siderastrea siderea</i> ; health status = diseased with dark-spot syndrome	percent or count
Y4U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = diseased with yellow-band disease	percent or count
Y23U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = diseased with yellow-band disease	percent or count
Y9U	percent or count found on sample; coral species = <i>Orbicella faveolata</i> ; health status = diseased with yellow-band disease	percent or count

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## Instruments

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

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## Deployments

### vanWoesik\_2012

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/562802">https://www.bco-dmo.org/deployment/562802</a>
<b>Platform</b>	Caribbean_nearshore
<b>Start Date</b>	2012-06-01
<b>End Date</b>	2016-05-31
<b>Description</b>	<p>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).</p> <p><b>Methods &amp; Sampling</b> Wonderland Reef, Florida 24.56028 N, 81.50127 W</p>

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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**

<b>Funding Source</b>	<b>Award</b>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1219804</a>

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