Acropora cervicornis genomic/trancriptomic sequence accessions with associated data on tank exposure to white band disease and survival outcomes with corals collected from Florida, USA and Bocas del Toro, Panama in 2021

Website: https://www.bco-dmo.org/dataset/922006
Data Type: experimental
Version: 1
Version Date: 2024-03-12

Project
» Multi-omic bases of coral disease resistance (coral disease resistance)

Contributors	Affiliation	Role
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Abstract
Genomic data was collected from 96 Acropora cervicornis samples, 48 of which were collected from the Coral restoration foundation nursery in Florida in June 2021 and the other 48 were collected from Bocas del Toro Panama in November 2021. All samples were sequenced using illumina short read sequencing to create whole genome sequencing profiles of the DNA with one of the Florida samples, the K2 genotype, being sequenced using additional Nanopore long reads to assemble and annotate an A. cervicornis genome. All genotypes were used in a disease exposure assay to assess individual genotype disease resistance with a further, 16 colonies from Florida being sequenced at two timepoints across disease exposed and healthy colonies (total 48 sequences) using RNAseq to identify patterns in differential gene expression based on disease resistance. This dataset includes sample metadata, treatment information, and disease state for corals in the exposure experiment. Sample metadata and accession identifiers for sequences at The National Center for Biotechnology Information (NCBI) are included as a supplemental file.

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Coverage

Location: Florida samples collected from the Coral Restoration Foundation Nursery in the Florida Keys (24.73 N, 81.04 W). Panama samples collected from near the Smithsonian Tropical Research Institute Station in Bocas del Toro, Panama (9.35 N, 82.26 W).
Spatial Extent: **N**:24.73 **E**:-81.04 **S**:9.35 **W**:-82.26

Temporal Extent: 2021-06-19 - 2021-11-12

Dataset Description

Related NCBI BioProjects containing genomic/transcriptomic data from this study (see Supplemental Files for accession metadata):

mRNA sequencing from 48 A. cervicornis colonies differentially exposed to white band disease at multiple time points: NCBI BioProject PRJNA949884 (https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA949884)

Whole genome sequencing of DNA from 96 A. cervicornis colonies: NCBI BioProject PRJNA950067 (https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA950067)

Short and long read data and Genome Assembly for the Coral Restoration Foundation K2 genotype of A. cervicornis: NCBI BioProject PRJNA948411 (https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA948411)

Methods & Sampling

Putative genotypes were collected on SCUBA from either the Coral Restoration Foundation nursery habitat (Florida) or from five natural reefs (Panama). Florida sampling took place in June 2021 and Panama sampling occurred in November 2021. At each location, ten replicate fragments from each putative genotype were spread across one of ten 18-liter recirculating tanks held at ambient seawater temperatures at each location's flow-thru seawater system. Each fragment was experimentally lesioned with a waterpik to facilitate transmission (Gignoux-Wolfsohn et al. 2012). Five tanks were exposed to 50ml of disease slurry produced from 10 WBD infected coral fragments and five tanks were exposed to 50ml of healthy slurry from 10 healthy fragments. Slurries were produced by waterpiking disease or healthy coral tissue off the sampled corals in filtered seawater (FSW) and normalizing the slurry doses to a standard ocular density of 0.6 at 600nm. Exposed coral tanks were censused for disease twice daily at 6am and 6pm (local time, EST) for up to 7 days and disease coral fragments were pulled from tanks at the first signs of disease to prevent amplifying pathogen spread within each tank.

High molecular weight genomic DNA was extracted from all samples using the Zymo Quick-DNA 96 kit. Whole genome sequencing was produced for all putative genotypes using Illumina DNA Prep kit on two 150bp paired-end NovaSeq S4 runs. For the K2 genotype three libraries were prepared using Oxford Nanopore Technologies (ONT) kit SQK-LSK112. Two libraries were not size selected while the third included 20+kb PippenPrep size-selection. All ONT prepared libraries were sequenced separately on three Minion flow cells (FLO-MIN112). High-quality base-calling was performed using Guppy v6.1.7 (Oxford Nanopore Technologies). An additional four Illumina PCR-Free shotgun libraries were constructed using the DISCOVAR protocol to produce libraries with fragments between 400 and 600 bp (Love et al. 2016). KAPA PCR-free library kits were leveraged with the addition of a second round of 0.7x Agencourt AmPure XP SPRI bead cleanup post adapter ligation. Libraries were multiplexed and sequenced on a single rapid-run HiSeq 2500 flowcell with 250 bp paired-end sequencing. Finally, mRNA sequence data was obtained for 48 samples (including the K2 genotype) using NEBs unidirectional mRNA library preparations sequenced on an Illumina NEXTSEQ 550 platform.

Organism identifier (LSID):
Acropora cervicornis (urn:lsid:marinespecies.org:taxname:206989)

BCO-DMO Processing Description

* Submitted file "exposure_experiment.csv" was imported into the BCO-DMO data system for this dataset.
* Column names adjusted to conform to BCO-DMO naming conventions designed to support broad re-use by a variety of research tools and scripting languages. [Only numbers, letters, and underscores. Can not start with a number]

Problem Description

Samples from the experimental tanks H1 in Panama, and H2 and H3 in Florida were removed due to complete

colony collapse independent of experimental treatment.

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Data Files

File
922006_v1_whiteband-exposure-survival.csv (Comma Separated Values (.csv), 39.92 KB) MD5:db4a7e5b4fb7a2574db5110193b53fc9
Primary data file for dataset ID 922006, version 1. This table includes the disease state for corals in the exposure experiment. See related Supplemental File (sample_metadata.csv) which contains additional metadata and sequence accessions at NCBI.

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Supplemental Files

File
Metadata & accession numbers for sequences at NCBI filename: sample_metadata.csv (Comma Separated Values (.csv), 8.16 KB) MD5:d67ab4b1a670bb25aee4f9363725d6d2 Metadata & accession numbers for sequences at The National Center for Biotechnology Information (NCBI) under BioProject PRJNA950067. Columns in this data table are: ID, Fully descriptive colony ID genotype, Putative Genotype location, Region of origin (Florida or Panama) reef, Reef of origin (of initial genotype in Florida) lat, Latitude, decimal degrees lon, Longitude, decimal degrees longread_accession, NCBI Accession number for long reads used in genome assembly WGS_accession, NCBI Accession number for short reads used in whole genome sequencing T[37]_[HD]_RNA_accession, NCBI Accession number for RNAseq reads from Time point 3 or 7 (T3/T7) in either health (H) or disease (D) exposed treatments.

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Related Publications

Gignoux-Wolfsohn, S. A., Marks, C. J., & Vollmer, S. V. (2012). White Band Disease transmission in the threatened coral, Acropora cervicornis. Scientific Reports, 2(1). https://doi.org/10.1038/srep00804
Methods

Love, R. R., Weisenfeld, N. I., Jaffe, D. B., Besansky, N. J., & Neafsey, D. E. (2016). Evaluation of DISCOVAR de novo using a mosquito sample for cost-effective short-read genome assembly. BMC Genomics, 17(1). https://doi.org/10.1186/s12864-016-2531-7
Methods

Selwyn, J. D., & Vollmer, S. V. (2023). Whole genome assembly and annotation of the endangered Caribbean coral Acropora cervicornis. G3: Genes, Genomes, Genetics, 13(12). https://doi.org/10.1093/g3journal/jkad232
Results

Vollmer, S. V., Selwyn, J. D., Despard, B. A., & Roesel, C. L. (2023). Genomic Signatures of Disease Resistance in Endangered Staghorn Corals [Data set]. Zenodo. https://doi.org/10.5281/ZENODO.8095056 https://doi.org/10.5281/zenodo.8095056
Software

Vollmer, S. V., Selwyn, J. D., Despard, B. A., & Roesel, C. L. (2023). Genomic signatures of disease resistance in endangered staghorn corals. Science, 381(6665), 1451–1454. https://doi.org/10.1126/science.adi3601
Results

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Related Datasets

IsRelatedTo

Northeastern University (2023). Acropora cervicornis genomic basis of disease resistance. 2023/03. NCBI:BioProject: PRJNA950067. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA950067.

Northeastern University (2023). Acropora cervicornis isolate:K2 Genome sequencing and assembly. 2023/10. In: NCBI:BioProject: PRJNA948411 [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA948411.

Northeastern University (2023). Differential gene expression Acropora cervicornis. 2023/03. In: NCBI:BioProject: PRJNA949884. [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA949884.

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Parameters

Parameter	Description	Units
Tank	Experimental tank (H1-5 or D1-5)	untiless
Treatment	Experimental exposure (H - healthy exposure, D - disease exposure)	untiless
Location	Region of origin (Florida or Panama)	untiless
Genotype	Putative Genotype	untiless
Day_1_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 1 in the AM (Eastern Time Zone).	untiless
Day_1_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 1 in the PM (Eastern Time Zone).	untiless
Day_2_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 2 in the AM (Eastern Time Zone).	untiless
Day_2_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 2 in the PM (Eastern Time Zone).	untiless
Day_3_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 3 in the AM (Eastern Time Zone).	untiless
Day_3_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 3 in the PM (Eastern Time Zone).	untiless
Day_4_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 4 in the AM (Eastern Time Zone).	untiless
Day_4_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 4 in the PM (Eastern Time Zone).	untiless
Day_5_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 5 in the AM (Eastern Time Zone).	untiless
Day_5_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 5 in the PM (Eastern Time Zone).	untiless
Day_6_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 6 in the AM (Eastern Time Zone).	untiless
Day_6_PM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 6 in the PM (Eastern Time Zone).	untiless
Day_7_AM	Disease state (healthy = 0, diseased = 1) of the coral colony in the exposure experiment on Day 7 in the AM (Eastern Time Zone).	untiless

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Instruments

Dataset-specific Instrument Name	NovaSeq S4
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.

Dataset-specific Instrument Name	Minion flow cells (FLO-MIN112)
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.

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.

Dataset-specific Instrument Name	Illumina NEXTSEQ 550
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.

Dataset-specific Instrument Name	
Generic Instrument Name	DNA Extractor
Dataset-specific Description	Zymo Quick-DNA 96 kit Oxford Nanopore Technologies (ONT) kit SQK-LSK112 DNA Prep kit KAPA PCR-free library kits
Generic Instrument Description	A device that is used to isolate and collect DNA for subsequent molecular analysis.

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Project Information

Multi-omic bases of coral disease resistance (coral disease resistance)

Coverage: Bocas del Toro, Panama and Coral Restoration Nursery, Marathon, Florida, US

NSF Award Abstract:

Coral disease outbreaks have radically altered the structure and function of tropical coral reefs worldwide. As progress has been made towards understanding the basic cause of many coral diseases, significant gaps remain in our knowledge of how corals respond to and resist disease infection, even as calls are being made for science to assist in coral evolution by selecting thermal or disease tolerant coral species or genotypes - often called "super corals". This project uses the endangered Caribbean staghorn coral Acropora cervicornis and White Band Disease (WBD) as a host-pathogen system to study the genetics of coral disease resistance. WBD epidemics decimated this key shallow-water Caribbean coral and led to its endangered listing. While the recovery of staghorn corals has been slow, data indicate that up to 15% or more of staghorn corals are highly disease resistant. This project uses modern genomic tools to identify genetic markers for staghorn coral disease resistance. The identification of genetic markers for disease resistance (i) provides needed information on the efficacy of "assisted evolution" for coral resiliency (ii) helps predict how well staghorn coral can resist future disease outbreaks, (iii) assists conservation efforts aimed at identifying and selecting corals with high disease resistance, and (iv) spurs the development of molecular assays for coral disease resistance. This research provides graduate and undergraduate training in the STEM fields of microbiology, genetics, and computational biology. The project is as a platform to develop outreach curricula to teach students about coral diseases and reef health, which are disseminated via Northeastern University's K-12 outreach program and the Smithsonian Tropical Research Institute's outreach program in Panama. This project is co-funded by the Biological Oceanography Program in the Division of Ocean Sciences and the Symbiosis, Defense, and Self-recognition Program in the Division of Integrative Organismal Systems.

It is increasingly becoming clear that the future of coral reefs depends on the resilience of reef-building corals to adapt or acclimate to their changing environment, which in turn requires that key traits like thermal

tolerance and disease resistance are genetically heritable, identifiable, and quantifiable. Using staghorn corals and WBD as a model host-pathogen system, this project identifies the genetic underpinnings of disease resistance in Caribbean staghorn corals using state-of-the-art, multi-omic approaches linking patterns of variation across the staghorn coral genome, transcriptome and proteome. For Aim 1, genome-wide SNP variation from 200 staghorn coral genotypes from two populations [100 Florida; 100 Panama] is used to identify genomic regions associated with disease resistance using genome-wide association (GWA) analyses. For Aim 2, tank-based transmission experiments are used to profile key differences in the transcriptomic (mRNA and miRNA) and proteomic response of resistant versus susceptible staghorn corals during disease exposure. Mulit-omic data are analyzed using: (1) eQTL to link SNPs to mRNA expression, (2) miRNA-mRNA interactions and correlation networks to test for post-transcriptional gene regulation, and (3) network-based approaches. For Aim 3, 16s rDNA amplicon sequencing are used to identify changes in the staghorn coral microbiome due to disease resistance and exposure using microbial DNA from the resistant and susceptible corals used in the tank-based experiment (Aim 2). In addition to identify genetic markers associated with coral disease resistance, this study produces (1) the most complete multi-omic analysis of coral immunity and disease resistance to date, and (2) the first functional analyses of miRNA post-translational gene regulation in a cnidarian host-pathogen system. Data on the genetics of coral disease resistance provide valuable information on the efficacy of "assisted evolution" for coral resiliency. By using nursery raised staghorn corals from Florida, this project directly identifies highly disease resistant corals that can be used in the large-scale out planting efforts.

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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1924145

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