Tank exposure to white band disease Acropora cervicornis 16s amplicon rDNA sequencing

Website: https://www.bco-dmo.org/dataset/997761
Version: 1
Version Date: 2026-04-30

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

Contributors	Affiliation	Role
Vollmer, Steven V.	Northeastern University	Principal Investigator, Contact
Selwyn, Jason D.	Texas A&M, Corpus Christi (TAMU-CC)	Scientist, Data Manager
Douglas, Brecia	Northeastern University	Student
Trytten, Emily	Northeastern University	Student

Table of Contents

- Coverage
- Dataset Description
- Parameters
- Project Information
- Funding

Coverage

Spatial Extent: **Lat**:0 **Lon**:0

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]