Phenotypic information collected from white plague disease exposure in a controlled environment at The University of the Virgin Islands Center for Marine and Environmental Studies in June of 2017

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Project
» Immunity to Community: Can Quantifying Immune Traits Inform Reef Community Structure? (Coral Immune Traits)

Contributors	Affiliation	Role
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Abstract
Phenotypic information collected from white plague disease exposure in a controlled environment at The University of the Virgin Islands Center for Marine and Environmental Studies in June of 2017.

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Coverage

Spatial Extent: **Lat**:18.34403 **Lon**:-64.98435
Temporal Extent: 2017-06

Methods & Sampling

Location: Brewer’s Bay (18.34403, -64.98435), St. Thomas, The U.S. Virgin Islands

Disease prevalence was recorded as the percentage of individuals infected by the end of the seven-day study. Disease prevalence among species was compared using a Fisher’s Exact Test in R. A photograph and timestamp was captured upon appearance of lesions and then immediately before each fragment was culled around 30% tissue loss. Disease severity was measured by calculating the rate of lesion progression across the coral fragment as the amount of tissue lost between the appearance of the lesion to the time it was culled

divided by that time period. Time to infection was measured by the number of days it took for each coral fragment to show lesions throughout the seven-day study and visualized with a survival plot through a Kaplan-Meier estimate of the survivorship by using the *survfit* function in the R package *survival* (Therneau, 2020). The relative risk of each species was also calculated as: “Relative risk (RR) = Risk in exposed / Risk in non-exposed” where the *risk in exposed* individuals was calculated as the prevalence (diseased/total population) of those exposed to disease and *risk in non-exposed* individuals was calculated as the prevalence (diseased/total population) of those not exposed to disease.

Disease transmission and phenotypic sampling matched the methods from this published study “Species-specific susceptibility to white plague disease in three common Caribbean corals” Williams et al. (2020). Dr. Marilyn Brandt was the lead PI in that investigation and a CO-PI in the investigation being submitted.

Instruments:
Band Saw to fragment colonies. Camera and ruler to take photographs. Hammer and chisel to take samples of culled coral. Samples flash frozen in liquid nitrogen, stored in -80˚C until shipped via dry shipper to The University of Texas at Arlington for molecular work.

Data Processing Description

Lesion progression rate and percent tissue loss was calculated from photographs processed through ImageJ. Relative Risk was calculated using this equation: “Relative risk (RR) = Risk in exposed / Risk in non-exposed” which uses Markov Chain Monte Carlo simulations with Gibbs Sampling in OpenBUGS (OpenBUGS (MRC Biostatistics Unit, Cambridge, UK). Days to infections was visualized with a survival plot through a Kaplan-Meier estimate of the survivorship by using the survfit function in the R package survival (Therneau, 2020). Statistical significance comparisons and visualizations were processed in R v3.5.1 (Rstudio v1.2.5033).

BCO-DMO Data Manager Processing Notes:
* Extracted data submitted in Excel file "EAGER_PhenotypeDATA_BCODMO_Submission.xlsx" to csv
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions: only A-Za-z0-9 and underscore allowed. Can not start with a number. (spaces, +, and - changed to underscores).
* Rounded Time frame (hours) and (days) to three decimal places.
* removed percent symbol from values in percent_lost,percent_lost_per_min,percent_lost_per_hour,percent_lost_per_day so they could be typed correctly as numeric. Units provided in parameter information.
* Provided species names checked using the World Register of Marine Species taxa match tool. Corrected species name in the dataset Sidereastrea siderea -> Siderastrea siderea
http://www.marinespecies.org/aphia.php?p=taxdetails&id=207516
* Species list with exact match to AphiaID taxonomic identifiers added to supplemental documents.

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Data Files

File	
coral_pheno.csv	(Comma Separated Values (.csv), 6.18 KB) MD5:a02cf87b6126443f6b49094f980124cb
Primary data file for dataset ID 829113	

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Supplemental Files

File
Species list and identifiers filename: species_list.csv (Comma Separated Values (.csv), 219 bytes) MD5:a9685f29c346ef03a257404657578731 Coral scientific name (Genus species) and AphiaID (taxonomic identifier).

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Related Publications

R Core Team (2019). R: A language and environment for statistical computing. R v3.5.1. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Therneau T (2020). A Package for Survival Analysis in R. R package version 3.1-12, https://CRAN.R-project.org/package=survival
Software

Williams, L., Smith, T. B., Burge, C. A., & Brandt, M. E. (2019). Species-specific susceptibility to white plague disease in three common Caribbean corals. Coral Reefs, 39(1), 27–31. doi:10.1007/s00338-019-01867-9
Methods

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Related Datasets

References

Mydlarz, L., Brandt, M. (2021) **Coral 16s rRNA sequence accession, sample, and experimental treatment information from white plague disease exposed corals at Brewer's Bay, St. Thomas, The U.S. Virgin Islands in June of 2017.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-17 http://lod.bco-dmo.org/id/dataset/841008 [view at BCO-DMO]
Relationship Description: The same coral samples used.

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Parameters

Parameter	Description	Units
Species	Species (scientific name in format Genus species).	unitless
Treatment	Treatment type (Disease or Control).	unitless
Colony	Originating colony that fragment came from. Each colony was fragmented in two to have one fragment exposed to a white plague infected O.franksi and the other to remain as a paired control and exposed to a healthy O. franksi.	unitless
Bucket	Aquaria identifier. "C" for controls, "D" for disease-exposed. Numbers are identifiers that do not have a broader meaning.	unitless

Parent_ID	Coral colony genotype identifier. Two coral fragments came from the same parent colony. One fragment went to a control bucket, another to the disease-exposed bucket.	unitless
ID	Colony identifier, pairing coral fragments to their origin parent ID.	unitless
Rate_type	An anecdotal categorization for the progression rate of that fragment. This metric is not applied in any calculation in the publication. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	unitless
Days_to_infection	The days it took for a particular fragment to be exposed to white plague disease to show signs of lesion presence. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	days
cm2_lost	Area of tissue lost as a result of lesion progression. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	square centimeters (cm^2)
Time_frame_min	Time frame (minutes) from the initial observation of lesion presence to when the fragment was culled from the experiment. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	minutes
Time_frame_hours	Time frame (hours) from the initial observation of lesion presence to when the fragment was culled from the experiment. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	hours
Time_frame_days	Time frame (days) from the initial observation of lesion presence to when the fragment was culled from the experiment. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	days
cm2_per_min	lesion progression rate in centimeters squared per minute	cm^2/min
cm2_per_day	lesion progression rate in centimeters squared per day	cm^2/day
percent_lost	Total percent tissue loss as a result of white plague lesion progression. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	percent (%)
percent_lost_per_min	Total percent tissue loss per minute as a result of white plague lesion progression. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	percent per minute (%/min)

percent_lost_per_hour	Total percent tissue loss per hour as a result of white plague lesion progression. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	percent per hour (%/hr)
percent_lost_per_day	Total percent tissue loss per day as a result of white plague lesion progression. A zero "0" indicates that sample did not have any lesion growth, even if exposed to the disese as part of its treatment.	percent per day (%/d)

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Project Information

Immunity to Community: Can Quantifying Immune Traits Inform Reef Community Structure? (Coral Immune Traits)

Coverage: US Virgin Islands

NSF abstract:

Coral diseases have increased significantly throughout the past 30 years. Climate change and other detrimental environment factors are likely to blame. Unhealthy coral reefs cannot support the fish and other life that make the reef a vibrant and diverse ecosystem. Corals reefs in the Caribbean Sea are disease hotspots and many reefs have experienced population collapses due to outbreaks of disease. Importantly, coral species vary in their susceptible to disease, but the reasons behind this variation are unknown. This project will quantify coral susceptibility to disease by examining coral immunity using several novel approaches and experiments. Seven species of coral that differ in disease susceptibility, growth rates, growth form and reproductive strategies will be used. Immune responses of each species of coral will be measured by exposing the corals to bacterial immune stimulators. Susceptibility to white plague disease, a prevalent disease affecting many species of corals, will also be measured by exposing the corals to active white plague disease and calculating disease transmission rates. The immune response and disease transmission data for each coral species will be used to develop a predictive model to determine how different coral communities will respond to disease threats under climate change scenarios. This project will support graduate students at University of Texas, Arlington (Hispanic-serving Institution) and University of Virgin Islands (Historically Black University) and many undergraduate students at all three institutions (Mote Marine Laboratory). This research will be highlighted at outreach events at all three institutions which take place regularly and include Earth Day Texas in Dallas, TX, Mote's Living Reef Exhibit and Aquarium in Sarasota, FL and "Reef Fest" and Agricultural fairs in the U.S. Virgin Islands.

Environmental changes, such as ocean warming, have led to an increase in the prevalence of coral diseases, causing region-wide population collapses in some locations. However, not all coral species, or even populations within species, are affected by disease equally. Some species are host to many different types of diseases, but have limited mortality. Other species suffer significant disease-related mortality. How and why disease susceptibility differs among species and the effects of this differential susceptibility on reef community structure and composition are currently unknown. This project will use immune-challenge experiments that will quantify novel components of the innate immune system of corals, coupled with the application of a trait-based model, to fulfill three goals: 1) Determine variability of coral immune traits in seven common coral species found on Caribbean reefs, 2) Determine the variability in resistance to white plague disease transmission in the same coral species 3) Develop a predictive model of coral community assemblage that incorporates immune traits. Quantification of coral immunity will also incorporate unique approaches, such as combining full transcriptome sequencing with protein activity assays for a gene-to-phenotype analysis. Data will be mapped onto immune pathways for comprehensive pathway evaluation between coral species and these will serve as trait inputs into a "traitspace" model. These traits will provide continuous data within the model, which will create a probability density function (PDF) for the trait distributions of each species. These PDFs will then be used to determine the probability of species under different disease exposure scenarios. Model analyses will determine which traits influence community structure and characterize how disease exposure and the immune response will predict community assemblages through space and time. The completion and application of a trait-base model that incorporates extensive immunity parameters (none of which have been applied to trait

models within coral ecosystems) is a distinct product from this project.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712134
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712240
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712540

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