Colony sizes and morphometric assessments of Acropora cervicornis genotypes sampled July 2020 for fecundity analysis at Mote Marine Laboratory

Website: https://www.bco-dmo.org/dataset/843028
Data Type: Other Field Results
Version: 1
Version Date: 2021-03-23

Project
» CAREER: Applying phenotypic variability to identify resilient Acropora cervicornis genotypes in the Florida Keys (Resilient Acerv)

Contributors	Affiliation	Role
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Abstract
Fecundity was assessed for Acropora cervicornis corals with known disease susceptibility. This dataset presents morphometric assessments and information on colony sizes of 10 replicate adult colonies from 12 genets held in Mote Marine Lab's spawning nurseries.

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Coverage

Spatial Extent: **N**:24.56257 **E**:-81.40009 **S**:24.45782 **W**:-81.88595
Temporal Extent: 2020-07-02 - 2020-08-03

Dataset Description

This dataset is part of a larger study of *Acropora cervicornis* (staghorn) corals studied at Mote Marine Lab's Elizabeth Moore International Center for Coral Reef Research and Restoration. The different analyses are listed here, and links to other data from this study can be found in the Related Datasets section below.

Analyses undertaken include:

1. Total Population (**this dataset** of Colony size)
2. Morphometric Assessment (**this dataset** of Colony size)
3. Primary Fecundity Analysis (**this dataset's population subset**, plus Polyps dataset)
4. Dissections (Oocyte number dataset, Oocyte size dataset)
5. Secondary Fecundity Analysis (Gamete bundle dataset)

See Related Datasets section below for links to above mentioned datasets.

Methods & Sampling

Sampling of *Acropora cervicornis* coral genotypes took place at Mote Marine Lab's spawning nurseries at Sand Key (24.45782, -81.88595) and Looe Key (24.56257, -81.40009). Ten replicate adult colonies from 12 genets were assessed for colony size and fecundity.

Colony Size (this dataset) sampling details:
Total Population
12 genets with 10 replicate adult colonies each (N=120 colonies), Sand Key location.
White-band disease resistant genets: 3, 7; White-band disease susceptible genets: 1, 13, 31, 34, 41, 44, 47, 50, 62, 63, according to Muller *et al.* 2018 eLife (see Disease Susceptibility table below in Supplemental Files).

Genets 62 and 63 were later determined to be clonal so data were combined for analysis.

Morphometric Assessment
On July 2, 2020, the dimensions of length, width, and height (L x W x H) in centimeters were measured. Health condition was assessed and recorded for all 120 colonies, with the following rankings:
1 = completely healthy
2 = partial mortality
3 = not expected to survive
4 = dead or missing.

The size of colonies was calculated using the volume formula for an ellipsoid where EV=4/3*pi*L*W*H (Kiel thesis, 2012)
The corrected volume was calculated using a modified formula based on Kiel et al. (2012) where EV= 4/3*pi*L/2*H/2*W/2.

***Population Subset*:**
A subset of 5 colonies from each genet that were healthy (condition '1') and similar in size were selected to be sampled (on July 3, 2020) for the Primary Fecundity analysis. Sampled colonies have a date of sampling listed. Those without dates were not sampled.

Problem report:
***Genet 31*:** In the time between when the parental colonies were morphometrically assessed/sampled in the Sand Key nursery for the primary fecundity analysis and brought into the lab for spawning/sampled for the secondary fecundity analysis, the entire tree for genet 31 snapped off from its anchor and went missing. As such, 5 colonies of genet 31 were brought in from a different spawning nursery and location (Looe Key Nursery: 24.56257, -81.40009). Thus, the fecundity data obtained from the fragments and gamete bundles come from different subpopulations (fragments from Sand Key and gamete bundles from Looe Key).

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Additional sampling details (Related datasets)
(Please refer to the Related Datasets section below for links to datasets related to Sampling for Primary Fecundity Analyses, Dissections, and Sampling for Secondary Fecundity Analyses. The Sampling details are listed below, but please see the individual dataset pages for additional information):

***Sampling for Primary Fecundity Analysis*:** On July 3, 2020, from 5 colonies of every genet, 3 linear branches (~10 cm in length) were sampled using bone cutters from the central portion of each colony (N=180 branches). Using a ruler, the number of polyps per one square centimeter was recorded from every branch near the base of the fragment (Polyps per Area dataset, https://www.bco-dmo.org/dataset/868308). The top ~2 cm (sterile zone) of every branch was removed before placing into a 50 mL falcon tube with 10% formalin to fix tissues. After 2 days, the formalin solutions were replaced with a 5% HCl solution, with every branch and tube triple rinsed with DI water in between to remove excess formalin. After 3 days, the 5% HCl solution in every tube was replaced with 10% HCl and subsequently refreshed every 2-3 days until branches were completely decalcified. Once decalcified, samples were triple rinsed in DI water and returned to their tubes with 70% EtOH for storage until dissection.

***Dissections*:** Under a dissecting microscope, every coral fragment was dissected using a scalpel and forceps to haphazardly select 5 polyps per fragment (N = 900 polyps) to count the total number of oocytes within each polyp (Oocyte Number dataset, https://www.bco-dmo.org/dataset/867314). From those, 5 oocytes were randomly selected to measure their size under a compound microscope using an ocular micrometer to record the maximum diameter (length, d1) and its perpendicular diameter (width, d2). The volume of oocytes was calculated using the formula for a prolate ellipsoid: V= (4/3)*pi*((d1)/2)*((d2)/2)^2. Oocytes were measured using a 10x ocular micrometer and 4x objective (total 40x) and a calibration factor was applied using the formula: V=(4/3)*pi*((d1/2)*250)*((d2/2)*250)^2

and converted to the units of cubed millimeters (mm3) for final values. (see Oocyte Size Dataset, https://www.bco-dmo.org/dataset/843067and Oocyte Number dataset, https://www.bco-dmo.org/dataset/867314).

Sampling for Secondary Fecundity Analysis: As a secondary assessment of fecundity, 5 replicate colonies of every genet were brought back to the lab on July 31, 2020 for spawning and ex situ assisted sexual reproduction. From every genet that spawned during August 4-10, 2020 (all of them), 40 random gamete bundles were collected during spawning using a transfer pipet and 50 mL falcon tube. Each bundle was immediately placed into a 2 mL glass vial with 10% formalin for fixation and inverted several times to break up the bundle in each vial. Then, the total number of oocytes and sperm per bundle were counted. Eggs were counted by eye by 2 independent observers. Replicate sperm counts were recorded using a hemocytometer. (Gamete Bundle Dataset, https://www.bco-dmo.org/dataset/868493)

Data Processing Description

Data were compiled into Excel (Microsoft Office) and analyzed using R version 4.0.3 (2020-10-10) -- "Bunny-Wunnies Freak Out". Nonparametric statistical and correlation analyses were conducted.

BCO-DMO Processing:
- separated Latitude and Longitude into separate columns
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions

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Data Files

File
colony_size.csv (Comma Separated Values (.csv), 12.68 KB) MD5:a934de0a56a44433b74561a95af88339 Primary data file for dataset ID 843028

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Supplemental Files

File
Disease_Susceptibility_Table filename: Disease_Susceptibility_Table.pdf (Portable Document Format (.pdf), 64.24 KB) MD5:b155930985bd0c9e954a1f0eeacc78a1 Acropora cervicornis genotypes and susceptibility to white-band disease

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Related Publications

Borger, J. L., & Colley, S. (2010). The effects of a coral disease on the reproductive output of Montastraea faveolata (Scleractinia: Faviidae). Revista de biologia tropical, 58 Suppl 3, 99–110.
Related Research

Foster, N., Box, S., & Mumby, P. (2008). Competitive effects of macroalgae on the fecundity of the reef-building coral Montastraea annularis. Marine Ecology Progress Series, 367, 143–152. https://doi.org/10.3354/meps07594
Related Research

Graham, J. E., & van Woesik, R. (2013). The effects of partial mortality on the fecundity of three common Caribbean

corals. Marine Biology, 160(10), 2561–2565. doi:10.1007/s00227-013-2248-y
Related Research

Kiel, C. (2012). Acropora cervicornis metrics for quantifying the size and total amount of branching coral. University of Miami, M.S. Thesis. 26 pp.
https://scholarship.miami.edu/discovery/delivery/01UOML_INST:ResearchRepository/12355422660002976?l#13355515660002976
Methods

Kiel, C., Huntington, B., & Miller, M. (2012). Tractable field metrics for restoration and recovery monitoring of staghorn coral Acropora cervicornis. Endangered Species Research, 19(2), 171–176. https://doi.org/10.3354/esr00474
Methods

Muller, E. M., Bartels, E., & Baums, I. B. (2018). Bleaching causes loss of disease resistance within the threatened coral species Acropora cervicornis. eLife, 7. doi:10.7554/elife.35066 https://doi.org/10.7554/eLife.35066
Methods

Okubo, N., Motokawa, T., & Omori, M. (2006). When fragmented coral spawn? Effect of size and timing on survivorship and fecundity of fragmentation in Acropora formosa. Marine Biology, 151(1), 353–363. doi:10.1007/s00227-006-0490-2
Related Research

Pratchett, M. S., Hoey, A. S., Tan, C.-H., Kuo, C.-Y., Bauman, A. G., Kumaraswamy, R., & Baird, A. H. (2019). Spatial and Temporal Variation in Fecundity of Acropora spp. in the Northern Great Barrier Reef. Diversity, 11(4), 60. doi:10.3390/d11040060
Related Research

R Core Team (2020). R: A language and environment for statistical computing. R v4.0.3. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Smith, L.E., & Hughes, T.P. (1999). An experimental assessment of survival, re-attachment and fecundity of coral fragments. Journal of Experimental Marine Biology and Ecology, 235(1), 147–164. doi:10.1016/s0022-0981(98)00178-6 https://doi.org/10.1016/S0022-0981(98)00178-6
Related Research

Teo, A., Guest, J. R., Neo, M. L., Vicentuan, K., & Todd, P. A. (2016). Quantification of coral sperm collected during a synchronous spawning event. PeerJ, 4, e2180. doi:10.7717/peerj.2180
Related Research

Vargas-Ángel, B., Colley, S. B., Hoke, S. M., & Thomas, J. D. (2005). The reproductive seasonality and gametogenic cycle of Acropora cervicornis off Broward County, Florida, USA. Coral Reefs, 25(1), 110–122. doi:10.1007/s00338-005-0070-9
Related Research

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Related Datasets

IsRelatedTo

Koch, H., Azu, Y., Bartels, E., Muller, E. (2022) **Fecundity and number of oocytes from Acropora cervicornis genotypes measured July 2020 at Mote Marine Lab.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-03-14 doi:10.26008/1912/bco-dmo.867314.1 [view at BCO-DMO]

Koch, H., Azu, Y., Bartels, E., Muller, E. (2022) **Fecundity and oocyte sizes of Acropora cervicornis genotypes measured July 2020 at Mote Marine Lab.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-03-23 doi:10.26008/1912/bco-dmo.843067.1 [view at BCO-DMO]
Relationship Description: Oocyte sizes were determined on a population subset (fragment sampled for fecundity) of the Colony Size dataset

Koch, H., Azu, Y., Bartels, E., Muller, E. (2022) **Fecundity assessment of Acropora cervicornis colonies from spawning observations and gamete bundle analysis in August 2020 at Mote Marine Laboratory.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-03-15 doi:10.26008/1912/bco-dmo.868493.1 [view at BCO-DMO]

Koch, H., Muller, E., Azu, Y., Bartels, E. (2022) **Assessment of polyps per area of Acropora cervicornis genotypes sampled July 2020 for fecundity analysis at Mote Marine Laboratory.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-03-16 doi:10.26008/1912/bco-dmo.868308.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Location	Sampling location of Mote Marine Lab's offshore nursery	unitless
Latitude	Latitude of sampling	decimal degrees
Longitude	Longitude of sampling (west is negative)	decimal degrees
Date_size_measured	Date colony sizes were collected in situ (yyyy-mm-dd) in local time	unitless
Genotype	Genotype of disease susceptibility	unitless
Phenotype	Phenotype of sample (S=white band disease susceptible, R=white band disease resistant)	unitless
Replicate_Colony	Number of colony replicate	unitless
Length	Colony Length	centimeters (cm)
Width	Colony Width	centimeters (cm)
Height	Colony Height	centimeters (cm)
Volume	Volume of colony approximating ellipsoid (4/3*pi*L*W*H)	centimeters cubed (cm3)
Volume_Corrected	Volume of colony where EV= 4/3*pi*L/2*H/2*W/2 (after Kiel et al. 2012)	centimeters cubed (cm3)
Health_Condition	Health condition (1=completely healthy, 2=partial mortality, 3=not expected to survive, 4=dead/missing)	unitless
Date_FF_sampled	Date fragments were sampled for fecundity analysis (yyyy-mm-dd) in local time	unitless
Date_GBF_sampled	Date gamete bundles were collected for secondary fecundity analysis (yyyy-mm-dd) in local time	unitless

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Instruments

Dataset-specific Instrument Name	Calcutta metal pliers
Generic Instrument Name	bone cutter
Dataset-specific Description	Each ramet was cut from the donor colony using metal pliers (Calcutta bone cutters).
Generic Instrument Description	A bone cutter is a surgical instrument used to cut bones or coral fragments.

Dataset-specific Instrument Name	ruler
Generic Instrument Name	ruler
Dataset-specific Description	the dimensions of length, width, and height (L x W x H) in centimeters were measured.
Generic Instrument Description	A device used for measuring or for drawing straight lines, consisting of an elongated piece of rigid or semi-rigid material marked with units for measurement. Device that allows one or more physical dimensions of a sample or specimen to be determined by visible comparison against marked graduations in units of measurement of dimension length.

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Project Information

CAREER: Applying phenotypic variability to identify resilient Acropora cervicornis genotypes in the Florida Keys (Resilient Acerv)

Coverage: Florida Keys, Summerland Key, FL 24.563595°, -81.278572°

NSF Award Abstract:
Caribbean staghorn coral was one of the most common corals within reefs of the Florida Keys several decades ago. Over the last 40 years disease, bleaching, overfishing and habitat degradation caused a 95% reduction of the population. Staghorn coral is now listed as threatened under the U.S. Endangered Species Act of 1973. Within the past few years, millions of dollars have been invested for the purpose of restoring the population of staghorn coral within Florida and the U.S. Virgin Islands. Significant effort has been placed on maintaining and propagating corals of known genotypes within coral nurseries for the purpose of outplanting. However, little is known about the individual genotypes that are currently being outplanted from nurseries onto coral reefs. Are the genotypes being used for outplanting resilient enough to survive the three major stressors affecting the population in the Florida Keys: disease, high water temperatures, and ocean acidification? The research within the present study will be the first step in answering this critically important question. The funded project will additionally develop a research-based afterschool program with K-12 students in the Florida Keys and U.S. Virgin Islands that emphasizes an inquiry-based curriculum, STEM research activities, and peer-to-peer mentoring. The information from the present study will help scientists predict the likelihood of species persistence within the lower Florida Keys under future climate-change and ocean-acidification scenarios. Results of this research will also help guide restoration efforts throughout Florida and the Caribbean, and lead to more informative, science-based restoration activities.

Acropora cervicornis dominated shallow-water reefs within the Florida Keys for at least the last half a million years, but the population has recently declined due to multiple stressors. Understanding the current population level of resilience to three major threats - disease outbreaks, high water temperatures, and ocean acidification conditions - is critical for the preservation of this threatened species. Results from the present study will answer the primary research question: will representative genotypes from the lower Florida Keys provide enough phenotypic variation for this threatened species to survive in the future? The present proposal will couple controlled laboratory challenge experiments with field data and modeling applications, and collaborate with local educators to fulfill five objectives: 1) identify *A. cervicornis* genotypes resistant to disease, 2) identify *A. cervicornis* genotypes resilient to high water temperature and ocean acidification conditions, 3) quantify how high water temperature and ocean acidification conditions impact disease dynamics on *A. cervicornis*; 4) determine tradeoffs in life-history traits because of resilience factors; and 5) apply a trait-based model, which will predict genotypic structure of a population under different environmental scenarios.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1452538

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