Diversity, distribution, and temporal stability of coral 'zooxanthellae' on a Pacific reef evaluated with samples collected in Palau from 2013 to 2022

Website: https://www.bco-dmo.org/dataset/957899
Data Type: Other Field Results, experimental
Version: 1
Version Date: 2025-05-06

Project
» Collaborative Research: Stability, flexibility, and functionality of thermally tolerant coral symbioses (Thermally tolerant coral)

Contributors	Affiliation	Role
LaJeunesse, Todd Christopher	Pennsylvania State University (PSU)	Principal Investigator
Lewis, Allison M.	Pennsylvania State University (PSU)	Student
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Abstract
This data set provides information about the long-term composition of symbiont populations within individual coral colonies. Diverse coral taxa (Scleractinia) from a West Indo-Pacific fore reef (Palau) were tagged and sampled at various intervals--ranging from six months to several years--over nine years' time. Symbiont identity was examined using multiple genetic markers that resolved symbiont diversity to species and individual genotypes (i.e. clonal strains). Consistent with previous colony monitoring studies, symbiont populations in a majority of colonies were dominated by one species and one strain (based on multi-locus genotyping) over multiple years. Thus, the distribution of symbiont diversity at the genus, species and clone level, comprising specific and stable partner combinations, scale predictably to reef habitat, host taxon, and individual colony.

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Coverage

Location: Palau offshore reef: 7.2497°N, 134.2288°E
Spatial Extent: **Lat**:7.2497 **Lon**:134.2288
Temporal Extent: 2013 - 2022

Dataset Description

This data set provides information about the long-term composition of symbiont populations within individual coral colonies. Associated publication is "Lewis, A.M., Butler, C.C., Turnham, K.E. et al. The diversity,

distribution, and temporal stability of coral 'zooxanthellae' on a Pacific reef: from the scale of individual colonies to across the host community. Coral Reefs 43, 841–856 (2024). https://doi.org/10.1007/s00338-024-02503-x"

Methods & Sampling

Study location and transects

Permanent transects were established in August of 2013 with the objective of tracking symbiotic associations over time. Three twenty-five meter transects were positioned along a western north-facing barrier reef containing diverse and healthy coral assemblages typical of the equatorial West Pacific Ocean (Rebotel reef located at 7.2497°N, 134.2288°E). The transects were spaced over an area spanning approximately 100 meters of reef at a depth ranging approximately between 8 and 12 meters (at high-tide). To mark the endpoints of each transect, steel rebar stakes were driven into the carbonate substrate using a sledgehammer.

Colony tagging and temporal sampling of transect colonies

Transect tape was strung between rebar stakes to guide colony selection and sampling efforts. To ensure tagged corals were easily identifiable at later time points, selected colonies were within three meters from the central transect line. Numbered thermoplastic polyurethane tags were attached to corals using a hammer and steel nails (mounding and encrusting coral species) or by UV-stabilized nylon cable ties (branching species). Individual colonies were photographed to verify coral species. A fragment of skeleton and tissue (approximately ~2 cm^2) was removed for genetic analysis using a small chisel and hammer and placed in numbered plastic bags with seawater. Coral fragments were transported by boat to the Palau International Coral Reef Center (PICRC) where they were preserved in 20% Dimethyl sulfoxide salt (DMSO-EDTA-NaCl) buffer and stored at -20°C.

A variety of taxonomically diverse corals were selected for long-term monitoring. Coral host species were identified visually from photographs. Transect collections include 162 individual coral colonies representing 10 families and 21 genera; *Acropora* and *Isopora* (Acroporidae), *Stylophora, Seriatopora,* and *Pocillopora* (Pocilloporidae), *Symphyllia* (Lobophylliidae), *Diploastrea* (Diploastreidae), *Podabacia* (Fungiidae), *Goniastrea, Favites, Platygyra,* and *Leptoria* (Merulinidae) (Budd et al. 2012, Huang et al. 2014a, Huang et al. 2014b) as well as three additional genera, *Turbinaria* (Dendrophylliidae)*, Psammocora* (Psammocoridae), *Leptastrea* (Leotastreidae), and *Pachyseris* (Pachyseridae) (WoRMS 2024 https://www.marinespecies.org).

Return visits to resample colonies referenced waterproof site maps showing the relative position of each colony, along with colony photos, and tag number that verified their identity. The position of the sample along the surface of the colony was randomized with each sampling. Sampling times were dependent on travel and were varied, initially occurring at approximately six month to one-year intervals. Sampling was conducted at nine independent time points, spanning a total observation period of nine years for several colonies.

Spatial sampling of transect colonies

Intra-colony diversity was investigated by spatial collections. In July 2016, two (paired) samples were collected from each tagged colony. The first sample was obtained from the left side of the colony when facing the colony with the reef slope behind it. The location of the second sample was randomized along the top axis of the colony using a percent distance method. When viewed from above, the colony was visually segmented into ten equal-sized partitions, each representing 10% of the colony's transverse axis. Next, a random number was generated to assign the numbered partitions between paired samples ($^{\#}1$–$^{\#}10$). Using this method, the distance between paired samples ranged from samples taken adjacent to each other to samples collected at the opposite end of the colony. Skeletal fragments were individually placed into separate pre-labeled collection bags and preserved following the methods described above.

DNA extraction and analysis of diversity using conventional genetic markers

DNA extractions were performed on 5x5 mm skeletal fragments containing animal tissue with associated symbionts using a modified Promega Wizard genomic DNA extraction protocol described by LaJeunesse et al. (2003). Samples were analyzed by denaturing gradient gel electrophoresis (DGGE) profiling of the ribosomal internal transcribed spacer 2 (ITS2). Prominent and discrete bands in DGGE of diagnostic profile fingerprints were excised in a sub-set of samples and directly sequenced as described by LaJeunesse (2002). Thus, by targeting only the prominent bands through direct sequencing, we isolated the numerically dominant ITS2 rDNA sequence in the nuclear genomes of resident symbionts. DGGE-fingerprinting was also used to identify

samples containing a mixed population of two or more symbionts when present at greater than 10% of the total population (Thornhill et al. 2006). For additional verification of symbiont species identity, the nuclear large-subunit ribosomal DNA (*LSU*) was amplified following conditions specified by Zardoya et al. (1995). All sequencing was conducted on an Applied Biosciences sequencer (Applied Biosciences, Foster City, CA) at the Pennsylvania State University Genomics Core facility.

High-resolution genotyping of the symbiont population

Microsatellite loci were used to resolve multilocus genotypes of clone-dominated symbiont populations (i.e. synonymous with resolving individual strains, or clones). A total of 10 microsatellite loci developed for *Cladocopium* spp. were used including 9 loci (Sgr 34, SgrSpl 13, SgrSpl 22, SgrSpl 24, SgrSpl 25, SgrSpl 26, SgrSpl 78, Spl 1, and Spl 16) described by Wham et al. (2014) and 1 locus (C1.05) described by Bay et al. (2009). Genotyping was applied to those colonies harboring *Cladocopium madreporum*, *Cladocopium patulum*, *Cladocopium* C21 and *Cladocopium* $C^{Stylophora}$. These loci are unlinked and using 10 provides sufficient variability to unambiguously identify distinct clonal cell lines. Each locus was amplified in reaction volumes of 10 µl each comprised of 1 µl of 10 mM dNTPs (deoxynucleotide triphosphates), 1 µL 25 mM MgCl2, 0.2 U Taq DNA Polymerase, and 1 µl of standard Taq Buffer (New England Biolabs, Ipswich, MA), 1 µL of forward and reverse primers at 10 µM and 1 µL of 100-50 ng DNA template). PCR amplifications were performed according to the specifications given by Wham et al. (2014) and Bay et al. (2009). Microsatellites were analyzed on an ABI 3730 Genetic Analyzer (Applied Biosystems) using a 500-bp standard (LIZ-labeled) at the Penn State University Nucleic Acid Facility. Fragments sizes were scored visually using Geneious (Geneious version 6.1.8 created by Biomatters, Newark, NJ, USA).

The number of alleles amplified at each locus identified samples homogeneous for only one genotype as opposed to a mixed population. Two alleles at each locus, expected for *Cladocopium*, represent a single genotype (Wham et al. 2014, Wham and LaJeunesse 2016), while three or more alleles may be indicative of a combination of multiple co-occurring genotypes or non-target (i.e. non-specific) PCR amplifications. Distinctive symbiont genotypes characterized for each symbiont species (i.e., unique multi-locus genotypes or MLGs) were assigned a number designation (**T**able S2 from Lewis et al., 2024). Matching symbiont clones were identified when alleles were identical across all microsatellite loci.

While genotypes of mixed populations in a colony could not be characterized for some colonies, there were instances when both mixed and pure single genotypes were observed at different time points for a particular colony. Thus, over the course of temporal and spatial sampling, in instances when a sample was homogeneous for one, the MLG for each was deduced.

Use of high resolution **psbA^{ncr}** *sequences to verify clone identity*

The non-coding region of the *psbA* minicircle (*psbA*^{ncr}) was amplified and sequenced according to the conditions described by Moore et al. (2003). Data from these hyper-variable nucleotide sequences was used to verify symbiont species identity, further assess intra-species genotype identity (i.e. clone), and display this clone diversity on a phylogeny (LaJeunesse and Thornhill 2011). Sequences were aligned using the internet version of ClustalOmega followed by manual editing.

Sea surface temperatures

We obtained average monthly surface seawater temperatures from HOBO temperature loggers deployed at Ulong Rock near the offshore reef site (7.29042° N; 134.24105° E) provided from the Coral Reef Research Foundation. Additional temperatures were obtained from the Daily 5-km Satellite Coral Bleaching Thermal Stress Monitoring Product Suite data from the National Oceanic and Atmospheric Administration's Coral Reef Watch website. Daily surface seawater temperatures (SST) for Palau were determined by calculating the average of the daily low (SST_MIN) and high (SST_MAX) SST between July 2013 and July 2022 (NOAA Coral Reef Watch). Both surface seawater measurements were plotted for the period of observation to evaluate seasonality and identify potential anomalous temperature events (see Figure 4b in Lewis et al., 2024). The temperature data is presented in the Supplemental file below titled 'palau_hobo_temps_offshore_2013_2022.csv'.

Data Processing Description

Phylogenetic Analysis

PAUP v4.0a169 was used to create an unrooted maximum parsimony phylogeny based on a heuristic search

(Swofford 2014). Because each phylogeny was congruent, they were concatenated, and a phylogenetic tree created with gaps (and insertions) treated as a 5th character and scored as one change. Bootstrap values based on 1,000 iterations were evaluated to statistically assess branch support.

BCO-DMO Processing Description

- Imported data from source file "Table_2_Palau_Transect_Microsats.xlsx" sheet name "C.madreporum" into the BCO-DMO data system.
- Imported data from source file "Table_2_Palau_Transect_Microsats.xlsx" sheet name "C.patulum"
- Imported data from source file "Table_2_Palau_Transect_Microsats.xlsx" sheet name "Cladocopium C21"
- Imported data from source file "Table_2_Palau_Transect_Microsats.xlsx" sheet name "Cladocopium _stylophora"
- Combine all data into a single table, adding a new column for 'Symbiont' based on sheet name
- Modified parameter (column) names to conform with BCO-DMO naming conventions. The only allowed characters are A-Z,a-z,0-9, and underscores.
-Taxonomic names in the dataset were checked using the World Register of Marine Species (WoRMS) taxa match tool.

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Data Files

File	
957899_v1_palau_transect_microsats.csv	(Comma Separated Values (.csv), 28.60 KB) MD5:6b3f9318b85623e52d767ecfe2685dca
Primary data file for dataset ID 957899, version 1. Multilocus genotypes from tagged colonies. Microsatellite loci are listed across the top with the corresponding allele sizes below. Genotype profiles are listed for a coral colony over its 35-month observation period which includes all alleles recovered in a single sample. In contrast, single multilocus genotypes represent alleles originating from only one symbiont clone. Single multilocus genotypes were deduced and then extracted (based on alleles found in isolation) from the genotype profiles and are provided below.	

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Supplemental Files

File
Aligned sequenced data used to produce phylogeny of species diversity from long-term monitoring filename: Palau_LSU_cob_Clade_C_transect_diversity.nex (Plain Text, 159.35 KB) MD5:741f06415f14167ad9d71bb6e1654af7 Nexus file for maximum parsimony phylogeny reconstruction showing the symbiodiniacean diversity found in colonies representing 21 genera and ~50 species from all three transects. The phylogenic reconstruction was based on of the mitochondrial cob, ITS2, and partial LSU gene sequences (combined alignments representing ~1959 bases).
palau_hobo_temps_offshore_2013_2022.csv (Comma Separated Values (.csv), 268.87 KB) MD5:2399d08f496b4978c36d7f1604600839 Temperature Data for 2013–2022. HOBO temperature logger was from Ulong Rock location. NOAA satellite temperature data obtained from: https://coralreefwatch.noaa.gov/product/vs/gauges/palau.php.
table_s1_host_symbiont_tagged_colonies.csv (Comma Separated Values (.csv), 6.52 KB) MD5:870c6d0fd3b1dcbd42491553dd308ad3 Table S1. Host and symbiont identities among tagged colonies from three transects first sampled in August 2013. Host identification based on morphology while symbiont was based on a combination of partial ITS2-DGGE profiling as well as LSU and psbAncr sequencing. The presence of a second co-dominant symbiont is indicated when observed.
Table_S1_host_symbiont_tagged_colonies.pdf (Portable Document Format (.pdf), 261.00 KB) MD5:2418a1385c1195fb2d966fe52dacf9ce PDF version of Table S1. Host and symbiont identities among tagged colonies from three transects first sampled in August 2013. Host identification based on morphology while symbiont was based on a combination of partial ITS2-DGGE profiling as well as LSU and psbAncr sequencing. The presence of a second co-dominant symbiont is indicated when observed.

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Related Publications

Bay, L. K., Howells, E. J., & van Oppen, M. J. H. (2009). Isolation, characterisation and cross amplification of thirteen microsatellite loci for coral endo-symbiotic dinoflagellates (Symbiodinium clade C). Conservation Genetics Resources, 1(1), 199–203. https://doi.org/10.1007/s12686-009-9048-1
Related Research

Budd, A.F., Fukami, H., Smith, N.D., and Knowlton, N. (2012).Taxonomic classification of the reef coral family Mussidae (Cnidaria: Anthozoa: Scleractinia). Zoological Journal of the Linnean Society, 166(3), 465–529. doi:10.1111/j.1096-3642.2012.00855.x
Related Research

Geneious | Bioinformatics Software for sequence data analysis. (n.d.). Retrieved from https://www.geneious.com/
Software

Huang, D., Benzoni, F., Arrigoni, R., Baird, A. H., Berumen, M. L., Bouwmeester, J., Chou, L. M., Fukami, H., Licuanan, W. Y., Lovell, E. R., Meier, R., Todd, P. A., & Budd, A. F. (2014). Towards a phylogenetic classification of reef corals: theIndo-Pacific generaMerulina,GoniastreaandScapophyllia(Scleractinia,Merulinidae). Zoologica Scripta, 43(5), 531–548. Portico. https://doi.org/10.1111/zsc.12061
Related Research

Huang, D., Benzoni, F., Fukami, H., Knowlton, N., Smith, N. D., & Budd, A. F. (2014). Taxonomic classification of the reef coral families Merulinidae, Montastraeidae, and Diploastraeidae (Cnidaria: Anthozoa: Scleractinia). Zoological Journal of the Linnean Society, 171(2), 277–355. https://doi.org/10.1111/zoj.12140
Related Research

LaJeunesse, T. C.(2002). Diversity and community structure of symbiotic dinoflagellates from Caribbean coral reefs. Marine Biology, 141(2), 387–400. https://doi.org/10.1007/s00227-002-0829-2
Methods

LaJeunesse, T. C., & Thornhill, D. J. (2011). Improved Resolution of Reef-Coral Endosymbiont (Symbiodinium) Species Diversity, Ecology, and Evolution through psbA Non-Coding Region Genotyping. PLoS ONE, 6(12), e29013. https://doi.org/10.1371/journal.pone.0029013
Related Research

LaJeunesse, T. C., Lee, S. Y., Gil-Agudelo, D. L., Knowlton, N., & Jeong, H. J. (2015). Symbiodinium necroappetenssp. nov. (Dinophyceae): an opportunist 'zooxanthella' found in bleached and diseased tissues of Caribbean reef corals. European Journal of Phycology, 50(2), 223–238. https://doi.org/10.1080/09670262.2015.1025857
Methods

LaJeunesse, T. C., Loh, W. K. W., van Woesik, R., Hoegh-Guldberg, O., Schmidt, G. W., & Fitt, W. K. (2003). Low symbiont diversity in southern Great Barrier Reef corals, relative to those of the Caribbean. Limnology and Oceanography, 48(5), 2046–2054. Portico. https://doi.org/10.4319/lo.2003.48.5.2046
Methods

Lewis, A. M., Butler, C. C., Turnham, K. E., Wham, D. F., Hoadley, K. D., Smith, R. T., Kemp, D. W., Warner, M. E., & LaJeunesse, T. C. (2024). The diversity, distribution, and temporal stability of coral 'zooxanthellae' on a pacific reef: from the scale of individual colonies to across the host community. Coral Reefs, 43(4), 841–856. https://doi.org/10.1007/s00338-024-02503-x
Results

Moore, R. B. (2003). Highly organized structure in the non-coding region of the psbA minicircle from clade C Symbiodinium. INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY, 53(6), 1725–1734. https://doi.org/10.1099/ijs.0.02594-0
Related Research

NOAA Coral Reef Watch. 2022, updated daily. NOAA Coral Reef Watch Version 3.1 Daily 5km Satellite Regional Virtual Station Time Series Data for Palau, July 1, 2013 to July 31, 2022. College Park, Maryland, USA: NOAA Coral Reef Watch. Data set accessed at https://coralreefwatch.noaa.gov/product/vs/gauges/palau.php.
Related Research

Sievers, F., & Higgins, D. G. (2017). Clustal Omega for making accurate alignments of many protein sequences. Protein Science, 27(1), 135–145. Portico. https://doi.org/10.1002/pro.3290
Software

Swofford, D. L. 2014. PAUP* Phylogenetic analysis using parsimony (*and other methods). 4.0d146 ed. Sinauer Associates, Sunderland, MA
Software

Thornhill, D. J., LaJeunesse, T. C., Kemp, D. W., Fitt, W. K., & Schmidt, G. W. (2005). Multi-year, seasonal genotypic surveys of coral-algal symbioses reveal prevalent stability or post-bleaching reversion. Marine Biology, 148(4), 711–722. https://doi.org/10.1007/s00227-005-0114-2
Related Research

Wham, D. C., & LaJeunesse, T. C. (2016). Symbiodinium population genetics: testing for species boundaries and analysing samples with mixed genotypes. Molecular Ecology, 25(12), 2699–2712. Portico. https://doi.org/10.1111/mec.13623
Related Research

Wham, D., Carmichael, M., & LaJeunesse, T. (2014). Microsatellite loci for Symbiodinium goreaui and other Clade C Symbiodinium. Conservation Genetics Resources, 6, 127–129.
Related Research

Zardoya, R., Costas, E., Lopez-Rodas, V., Garrido-Pertierra, A., & Bautista, J. (1995). Revised dinoflagellate phylogeny inferred from molecular analysis of large-subunit ribosomal RNA gene sequences. Journal of Molecular Evolution, 41(5). https://doi.org/10.1007/bf00175822 https://doi.org/10.1007/BF00175822
Methods

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Parameters

Parameter	Description	Units
Symbiont_species	Symbiont species	unitless

Colony_and_Month	Sample ID with first 4 characters representing transect number, middle characters representing colony number, and final grouping representing number of months after the start of monitoring	unitless
Host_Genera	Genus of host organism	unitless
Host_Species	Species of host organism	unitless
Genotype	Designation of a unique/distinct multi-locus genotype which corresponds to a symbiont species	unitless
C1_22_allele_1	Size (base pairs) of first allele at C1-22 microsatellite locus	base pairs (number of nucleotides)
C1_22_allele_2	Size (base pairs) of second allele at C1-22 microsatellite locus	base pairs (number of nucleotides)
C1_25_allele_1	Size (base pairs) of first allele at C1-25 microsatellite locus	base pairs (number of nucleotides)
C1_25_allele_2	Size (base pairs) of second allele at C1-25 microsatellite locus	base pairs (number of nucleotides)
C1_24_allele_1	Size (base pairs) of first allele at C1-24 microsatellite locus	base pairs (number of nucleotides)
C1_24_allele_2	Size (base pairs) of second allele at C1-24 microsatellite locus	base pairs (number of nucleotides)
C1_05_allele_1	Size (base pairs) of first allele at C1-05 microsatellite locus	base pairs (number of nucleotides)
C1_05_allele_2	Size (base pairs) of second allele at C1-05 microsatellite locus	base pairs (number of nucleotides)
Zoa_33_allele_1	Size (base pairs) of first allele at Zoa_33 microsatellite locus	base pairs (number of nucleotides)
Zoa_33_allele_2	Size (base pairs) of second allele at Zoa_33 microsatellite locus	base pairs (number of nucleotides)
C1_16_allele_1	Size (base pairs) of first allele at C1-16 microsatellite locus	base pairs (number of nucleotides)
C1_16_allele_2	Size (base pairs) of second allele at C1-16 microsatellite locus	base pairs (number of nucleotides)
Z1_Spl_1_allele_1	Size (base pairs) of first allele at Z1_spl_1 microsatellite locus	base pairs (number of nucleotides)

Z1_Spl_1_allele_2	Size (base pairs) of second allele at Z1_spl_1 microsatellite locus	base pairs (number of nucleotides)
C1_34_allele_1	Size (base pairs) of first allele at C1-34 microsatellite locus	base pairs (number of nucleotides)
C1_34_allele_2	Size (base pairs) of second allele at C1-34 microsatellite locus	base pairs (number of nucleotides)
z78_allele_1	Size (base pairs) of first allele at z78 microsatellite locus	base pairs (number of nucleotides)
z78_allele_2	Size (base pairs) of second allele at z78 microsatellite locus	base pairs (number of nucleotides)

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Instruments

Dataset-specific Instrument Name	Applied Biosciences Sequencer at Penn State University Genomics Core Facility
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Successful PCR amplicons of each genetic marker were Sanger sequenced with sequences analyzed at the Penn State University Genomics Core Facility on an Applied Biosciences Sequencer. (Possibly the Applied Biosystems 3730XL)
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	ABI 3730 Genetic Analyzer (Applied Biosystems)
Generic Instrument Name	Gene Analyzer
Dataset-specific Description	Fragment analysis was performed on an ABI 3730 Genetic Analyzer (Applied Biosystems) using a 500-bp standard (LIZ-labeled) at the Penn State University Nucleic Acid Facility.
Generic Instrument Description	An automated analyzer designed for a wide range of sequencing and fragment analysis applications with the ability to perform comparative sequencing, linkage analysis, STR analysis, SNP detection, discovery and validation, mutation detection, and many other applications.

Dataset-specific Instrument Name	hammer and chisel
Generic Instrument Name	Manual Biota Sampler
Dataset-specific Description	A fragment of skeleton and tissue was removed for genetic analysis using a small chisel and hammer.
Generic Instrument Description	"Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool.

Dataset-specific Instrument Name	SCUBA
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	Samples of Scleractinia from various families were sampled by SCUBA with a hammer and chisel throughout various sites across the Indo-Pacific
Generic Instrument Description	The self-contained underwater breathing apparatus or scuba diving system is the result of technological developments and innovations that began almost 300 years ago. Scuba diving is the most extensively used system for breathing underwater by recreational divers throughout the world and in various forms is also widely used to perform underwater work for military, scientific, and commercial purposes. Reference: https://oceanexplorer.noaa.gov/technology/technical/technical.html

Dataset-specific Instrument Name	camera
Generic Instrument Name	Underwater Camera
Dataset-specific Description	Individual colonies were photographed to verify coral species.
Generic Instrument Description	All types of photographic equipment that may be deployed underwater including stills, video, film and digital systems.

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Project Information

Collaborative Research: Stability, flexibility, and functionality of thermally tolerant coral symbioses (Thermally tolerant coral)

Coverage: Coral Reefs of Palau, Micronesia

NSF abstract:

All reef-building corals require large numbers of internal symbiotic microalgae (called Symbiodinium) for their survival and growth. These mutualisms have shown considerable sensitivity to changes in the environment in recent decades, especially due to global increases in ocean temperatures. When exposed to severe thermal

stress, corals loose their symbionts and often die. However, recent experiments show that some symbionts may be more stress-tolerant. Corals with these heat-resistant symbionts continue to receive high amounts of algal derived nutrients and grow under elevated temperatures. If the global trend in seawater warming continues to increase, these heat-resistant symbioses may become more ecologically prevalent on reef systems around the world and could play a critical role in maintaining healthy and productive coral communities. This project will examine the ecological and physiological attributes of stress-tolerant symbioses from the Indo Pacific where coral communities are the largest, most diverse, and productive in the world. The researchers will conduct a series of experiments to (1) evaluate host and symbiont attributes that contribute to thermal tolerance and (2) characterize the relative flexibility and functionality of various corals and symbionts exposed to typical ambient and stressful temperatures. Broader impacts of the project include the training of several Ph.D. students, undergraduates, and high school students in the disciplines of physiology and ecology. The researchers will partner with Global Ocean Exploration, Inc. to communicate this research to the general public through short documentary videos, editorials, and podcasts. An interactive K-5 program, "Invertebrates on the Road," will introduce elementary students in Pennsylvania to marine invertebrate diversity. Research results will also be disseminated to the public at the University of Delaware via educational seminars, as well as through hands-on research displays and demonstrations presented at the annual open house "Coast Day" festival in each year of the project.

This project will examine several attributes important to the functional ecology of coral-dinoflagellate symbioses. Specifically, the research team seeks to understand the interplay between coral and symbiont physiologies under different environmental conditions and determine the relative influence of biotic factors crucial to the performance of stress tolerant symbioses. Results from recent experiments on Indo-west Pacific corals found that Clade D (S. trenchii) symbionts are stress-tolerant. These symbionts are able to maintain function and provide nutrients to their hosts under high temperatures that typically elicit the breakdown of symbioses involving many other species of symbiont. A number of questions arise about how enhanced thermal tolerance symbioses may be aided by a combination of factors; for example: Are symbionts physiologically hardier in corals that are routinely feeding? Do host genotypes that are adapted to high temperatures affect the physiology of their symbionts in ways that make the partnership more stress-tolerant? A series of experiments over three years will examine the functionality of different coral-symbiont pairings exposed to ambient and high temperatures. Reciprocal transplants between inshore (stress-tolerant) and offshore (stress-susceptible) reef sites will be used to produce specific host-symbiont parings. Controlled experiments will test the relative importance of coral trophic status (nutrient content) while holding symbiont type constant and how changes in both coral trophic status and symbiont species identity of the resident affect thermal tolerance. Tank experiments on shore will track rates of photosynthesis as well as carbon translocation and assimilation from symbiont to host tissues and skeletons. Long-term growth rates via skeletal density, linear extension, and biomass gain will also be measured. This project will help elucidate how biochemical, physiological and ecological differences among host-symbiont pairings may respond to rising ocean temperatures and enhance the future viability of coral reefs.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1636022
NSF Division of Integrative Organismal Systems (NSF IOS)	IOS-1258058

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