GenBank accession links of the invertebrates collected from Autonomous Reef Monitoring Structures (ARMS) from shallow fringing reefs near Dobu and Upa Upasina, Milne Bay Province, Papua New Guinea in 2014

Website: https://www.bco-dmo.org/dataset/874478
Data Type: Other Field Results
Version: 1
Version Date: 2022-05-21

Project
» Investigating Structural Changes In Reef-Associated Biodiversity Along A Natural Gradient In Ocean Acidification (OA_Gradient_Biodiversity)

Contributors	Affiliation	Role
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Abstract
This dataset contains GenBank accession links of the invertebrates collected in April and November of 2014 from Autonomous Reef Monitoring Structures (ARMS) on the acidification gradient from shallow fringing reefs near Dobu and Upa Upasina, Milne Bay Province, Papua New Guinea.

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Coverage

Spatial Extent: **Lat**:-9.824167 **Lon**:150.817667
Temporal Extent: 2014-04 - 2014-11

Methods & Sampling

Sampling Devices
This study was conducted in Milne Bay Province, Papua New Guinea at two shallow-water fringing reef localities near Dobu and Upa Upasina (9° 49.45’ S, 150° 49.06’ E) at a depth of 3 meters where almost pure CO2 gas seeps through the seafloor and into the water, changing the water carbonate chemistry and creating sharp gradients in seawater carbonate chemistry parameters within a short distance. Autonomous Reef Monitoring Structures (ARMS) were deployed along the fringing coral reefs at a depth of 4-5 meters at three pH conditions

and recovered after approximately 2 years of deployment and all motile organisms greater than 2 millimeters were removed from the structures, photographed, subsampled for genetic analysis, and preserved in 95% ethanol.

Genetic Barcoding
DNA was extracted from tissue subsamples using a standard proteinase-k digestion followed by phenol-chloroform extraction on an AutoGenprep 965. The standard Cytochrome Oxidase Subunit I (COI) barcoding fragment (658 bp) was amplified using the jgLCO1490/jgHCO2198 primer pair. Automated sequencing was performed in both directions directly on purified PCR products using Applied Biosystems BigDye terminator V3.1 Sequence reactions were purified using Millipore 96-well plates loaded with Sephadex G-50 and run on an ABI 3130xl genetic analyzer.

Data Processing Description

BCO-DMO processing description:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Added a conventional header with dataset name, PI names, version date
- Converted dates to YYYY-MM

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Data Files

File	
inverts_accession.csv	(Comma Separated Values (.csv), 131.17 KB) MD5:33c4f46c4f149d9f0d80ec30699f0b5d
Primary data file for dataset ID 874478	

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Related Publications

Plaisance, L., Matterson, K., Fabricius, K., Drovetski, S., Meyer, C., & Knowlton, N. (2021). Effects of low pH on the coral reef cryptic invertebrate communities near CO2 vents in Papua New Guinea. PLOS ONE, 16(12), e0258725. https://doi.org/10.1371/journal.pone.0258725
Results

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Parameters

Parameter	Description	Units
Organism	Taxonomic identification to the lowest rank available	unitless
Sampling_locality	Specific locality where the organism was sampled	unitless
Collection_date	Sampling date in format YYYY-MM	date
Specimen_voucher	Voucher number in the collections of the National Museum of Natural History	unitless
Accession	COI NCBI GenBank accession number	unitless

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Instruments

Dataset-specific Instrument Name	ABI 3130xl
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	ABI 3130xl: 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.
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	AutoGenprep 965
Generic Instrument Name	DNA Extractor
Dataset-specific Description	The AutoGenprep 965 is a high-throughput, automated platform that performs DNA extraction.
Generic Instrument Description	A device that is used to isolate and collect DNA for subsequent molecular analysis.

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Project Information

Investigating Structural Changes In Reef-Associated Biodiversity Along A Natural Gradient In Ocean Acidification (OA_Gradient_Biodiversity)

Coverage: Papua New Guinea, Esa' Ala province

NSF award abstract:

Recent research has revealed that ocean acidification, caused by carbon dioxide dissolving into the ocean, has a broad range of negative consequences for marine organisms, especially organisms that build calcium shells or skeletons such as corals. However, most studies have focused on a limited number of species in laboratory settings and have therefore ignored the many indirect effects originating from more complex species interactions that occur in nature. Coral reefs harbor more species than any other marine ecosystem. Moreover, they are economically very important, providing food and other services such as touristic attractions and pharmaceuticals. Because of the sensitivities of coral species to ocean acidification, reef ecosystems are potentially severely threatened, but we still have no idea how entire reef communities will respond. The project will take advantage of a recently discovered, naturally acidified coral reef system in Papua New Guinea that is bathed by waters of variable levels of acidity, including levels comparable to those expected globally by the end of the 21st century. This project investigates the consequences of ocean acidification for the biodiversity of animals that live cryptically within the interstices of coral reefs. These animals represent the bulk of coral reef diversity; they play very important roles in the reef food chain but are poorly understood. Using DNA markers and photo analysis, cryptic species living at three different acidity levels (present day, expected in 50 years, expected in 100 years) will be quantified and identified in order to elucidate the changes occurring in coral reef communities as oceans acidify. Results will broaden understanding of the consequences of ocean acidification and allow for more accurate monitoring and effective management strategies for coral reefs. Scientific results will be shared at international conferences and published in peer-reviewed journals, and data collected will be made publicly available. The project will also foster active collaborations among scientists,

professional educators, and science communicators from the Smithsonian Institution and Washington DC high school students underrepresented in Science, Technology, Engineering and Math (STEM) fields. The students will be trained in ocean acidification science and will be involved in developing outreach products for Smithsonian onsite and online audiences, expanding the ability of the Smithsonian to share these results with the general public.

Ocean acidification (OA) is now affecting the fragile coral reef ecosystems already impacted by decades of local pressures (e.g., pollution, overfishing). Numerous laboratory experiments have shown deleterious effects of low pH on calcification, growth, and reproduction of reef organisms. Studies have also highlighted differences in species' responses depending on whether they are tested alone or in multi-species assemblages, suggesting the importance of indirect effects in sensitivity to OA that cannot be assessed from laboratory experiments. For this reason, shallow tropical submarine carbon dioxide seeps provide invaluable opportunities to assess the ecological consequences of long-term exposure to low pH for coral reefs in situ by providing a natural gradient in pH across reef seascapes. Among these are the reefs at Milne Bay Province, Papua New Guinea, which exhibit a strong gradient from normal to low pH waters but otherwise resemble normal reef conditions in terms of other chemical properties and temperature. Most work to date on acidified reefs, including at Milne Bay, has focused on corals and other conspicuous organisms. However, the vast majority of reef diversity is comprised of the understudied cryptic communities living within the reef structure. These trophically crucial groups are likely to be at risk from OA due to reduction in three-dimensional complexity typical of acidified reefs, but there are scant data. This research will measure structural changes in these communities across the well-characterized pH gradients of the Milne Bay reefs. The investigators will study diversity patterns in volumetrically standardized sampling structures deployed at three pH regimes (regular ~8.0, medium ~7.8-7.9 and low ~7.6-7.8) spanning the pH range predicted over the next one hundred years. Using photo analysis, and DNA barcoding of the bigger motile and sessile taxa and metabarcoding of the bulk sessile and small motile fractions , the investigators will evaluate spatial coverage, diversity and abundance of the species present across the pH gradient. The study will test the hypothesis that invertebrate diversity will decrease with decreasing pH and that taxonomic composition will shift to a community more resistant to acidified waters (e.g. non-calcifiers). Thus, the project's overall goal is to assess the likely impacts of future ocean acidification on the highly diverse cryptic fauna associated with coral reef ecosystems. This research has implications for both our understanding of the ecology of coral reefs and management strategies in the light of global changes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1558868

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