Abundance by species for parrotfish assemblages across 82 sites on the northern Great Barrier Reef, Australia from surveys conducted in September of 2014

Website: https://www.bco-dmo.org/dataset/828489
Data Type: Other Field Results
Version: 1
Version Date: 2020-11-05

Project
» Origins of Hawaiian Reef Fishes (Hawaiian Fish Origins)

Program
» Indo-Pac Research Coordination Network (Indo-Pac RCN)

Contributors	Affiliation	Role
Bowen, Brian	University of Hawai'i at Mānoa (HIMB)	Principal Investigator
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Abstract
Abundance by species for parrotfish assemblages from surveys conducted on the Northern Great Barrier Reef, Australia in September of 2014. The survey included 82 sites across 31 reef structures spanning six degrees of latitude. These data were published in Johnson et al. (2019).

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Coverage

Spatial Extent: **N**:-11.05949 **E**:146.251861 **S**:-16.863446 **W**:143.03557
Temporal Extent: 2014-09

Dataset Description

Abundance by species for parrotfish assemblages across 82 sites on the northern Great Barrier Reef, Australia in September of 2014.

Methods & Sampling

Methodology:

Authors surveyed parrotfish assemblages, reef habitat, and predatory coral reef fishes at 82 sites across 31

reef structures on the Northern GBR spanning 6 degrees of latitude.

Sampling and analytical procedures:

Divers conducted a 40-minute timed swim at 6-10m depth while surveying fish and habitat using a diver-operated stereo video system. A second diver surveyed sharks, caragids, and other highly mobile reef predators on a 20m wide transect. A handheld GPS towed on a buoy enabled accurate reconstruction of survey paths and distances. Parrotfish were recorded to species and measured to nearest mm fork length (FL) using EventMeasure software. Parrotfish with FL < 10cm were excluded. Divers also quantified environmental variables including reef slope, substrate rugosity, and live coral cover. Additional explanatory variables included predator biomass, geographic position (lat/lon), total reef area (ha), and management zone (according to GBRMPA 2003 zoning scheme).

Authors investigated changes in patterns of parrotfish community structure across the Northern GBR in relation to geographic and biophysical factors, as well as across management regimes, using redundancy analysis (RDA). RDA was performed using the “vegan” package in R version 3.5.1.

Data Processing Description

Video was processed with EventMeasure software (SeaGIS Pty Ltd., Bacchus Marsh, Victoria, Australia).

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Related Publications

Johnson, G., Taylor, B., Robbins, W., Franklin, E., Toonen, R., Bowen, B., & Choat, J. (2019). Diversity and Structure of Parrotfish Assemblages across the Northern Great Barrier Reef. Diversity, 11(1), 14. doi:10.3390/d11010014
Results

SeaGIS (2020). EventMeasure - Event logging & 3D measurement. SeaGIS SeaGIS Pty Ltd. Retrieved November 10, 2020, from https://www.seagis.com.au/event.html
Software

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Related Datasets

IsReferencedBy

Bowen, B., Johnson, G. (2020) **Biomass by species for parrotfish assemblages across 82 sites on the northern Great Barrier Reef, Australia from surveys conducted in September of 2014.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-11-05 http://lod.bco-dmo.org/id/dataset/828480 [view at BCO-DMO]
Relationship Description: Data from the same survey at 82 sites across 31 reef structures on the Northern Great Barrier Reef, Australia in 2014.

Bowen, B., Johnson, G. (2020) **Parrotfish assemblages, reef habitat, and predatory coral reef fish data from a survey at 82 sites across 31 reef structures on the Northern Great Barrier Reef, Australia in September of 2014.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-11-10 http://lod.bco-dmo.org/id/dataset/828497 [view at BCO-DMO]
Relationship Description: Data from the same survey at 82 sites across 31 reef structures on the Northern Great Barrier Reef, Australia in 2014.

Bowen, B., Johnson, G. (2020) **Parrotfish diversity metrics from a survey across 82 sites on the northern Great Barrier Reef, Australia from surveys conducted in September of 2014.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-11-10 http://lod.bco-dmo.org/id/dataset/828688 [view at BCO-DMO]
Relationship Description: Data from the same survey at 82 sites across 31 reef structures on the Northern

Great Barrier Reef, Australia in 2014.

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
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	Canon Legria underwater video cameras
Generic Instrument Name	Underwater Camera
Dataset-specific Description	Handheld stereo video system consisting of two Canon Legria underwater video cameras.
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

Origins of Hawaiian Reef Fishes (Hawaiian Fish Origins)

Coverage: Central and West Pacific Ocean

Project summary:
This research is designed to resolve the origins of Hawaiian reef fishes. All living inhabitants of the Hawaiian archipelago necessarily originate elsewhere, due to the volcanic history of the island arc. Hawaii also has the highest endemism (native species) in the Pacific, with 25% of the 625 near-shore fish species found nowhere else. Where did these fishes come from? Two prominent hypotheses regarding the origins of Hawaiian marine species maintain that colonists arrive either from the south (via the Line Islands and Johnston Atoll) or from the west (via Japan). Previous research has shown that Hawaiian endemic limpets (genus *Cellana*) colonized from Japan (Bird et al. 2011 Mol. Ecol. 20:2128 – 2141). Andrews et al. (2014; PLoS One 9: e91665) report evidence for a colonization pathway from the south (Johnston Atoll) to the middle of the archipelago in the Papahanaumokuakea Marine National Monument (PMNM). In this project, we will sample locations to the south

of Hawaii (Johnston and Line Islands) and to the west of Hawaii (Ogasawara and Ryukyu Islands) for a suite of 20 reef fishes in order to resolve the origins of Hawaiian biodiversity. Advanced rebreather technology allows dives with longer bottom time and more efficient sample collection, and our program is pioneering the applications of this advance diving technology. To test alternate hypotheses in the lab, we will employ both population genetics (shifts in genotype frequencies) and phylogenetics (DNA sequence divergence) for more ancient separations. Restriction-digest associated DNA sequencing (RAD-seq) is the best method for studies of phylogeography, phylogenetics, and population biology because it provides high coverage of homologous portions of the genome from multiple individuals for comparatively low cost and effort. We use the ezRAD approach developed in the shared Bowen-Toonen Lab.

Description from NSF award abstract:
The Hawaiian Islands are the product of a volcanic hot spot in the middle of the North Pacific. Hence every living thing on this isolated archipelago has origins elsewhere. This project will investigate the origins of Hawaiian reef fishes, which are important both as a food source and a cultural touchstone in native Hawaiian communities. Two prominent hypotheses maintain that marine fish originally arrived from the south (Line Islands and Johnston Atoll) or from the west (Japan). To test these hypotheses, this research will augment existing specimens from Hawaii with expeditions to Johnston Atoll (closest shallow habitat to the south), the northern Line Islands (Palmyra), southern Line Islands (Christmas Island), and Ryukyu Islands and Ogasawara Islands in Japan. Advanced genetic techniques will be used to resolve the closest relatives to the Hawaiian fish species and the pathways by which reef species colonize Hawaii and help establish patterns of biodiversity. In cases where Hawaiian species are closely related to widespread sister species, this project will detect hotspots of genetic divergence. Because this research will reveal the sources of Hawaiian marine biodiversity, results can be used to help define priorities for reef protection. The project will support two graduate students and train at least two more in all aspects of the project from rebreather diving, specimen collection and curation, information management, and advanced genetic techniques. There will be outreach efforts to schools through existing programs, and expedition teams will include a videographer to provide footage for the award-winning Voice of the Sea program, broadcast locally. Expeditions will also include an outreach specialist to handle media reports and promote awareness and concern for reefs in the communities surrounding study sites.

The investigators will sample a suite of 20 reef fishes at locations to the south (Johnston and Line Islands) and west (Ogasawara and Ryukyu Islands) of Hawaii to resolve the origins of Hawaiian biodiversity. The investigators will employ both population genetics (shifts in genotype frequencies) and phylogenetics (DNA sequence divergence) for more ancient separations to test their hypotheses. Restriction-digest associated DNA sequencing (RAD-seq) will be employed for the phylogeography, phylogenetics, and population biology studies because it provides high coverage of homologous portions of the genome from multiple individuals for comparatively low cost and effort.

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Program Information

Indo-Pac Research Coordination Network (Indo-Pac RCN)

Website: https://indopacificnetwork.wikispaces.com/

Description from NSF award abstract:
The objective of this Research Coordination Network project is to develop an international network of researchers who use genetic methodologies to study the ecology and evolution of marine organisms in the Indo-Pacific to share data, ideas and methods. The tropical Indian and Pacific Oceans encompass the largest biogeographic region on the planet, the Indo-Pacific. It spans over half of the Earth's circumference and includes the exclusive economic zones of over 50 nations and territories. The Indo-Pacific is also home to our world's most diverse marine environments. The enormity and diversity of the Indo-Pacific poses tremendous logistical, political and financial obstacles to individual researchers and laboratories attempting to study the marine biology of the region. Genetic methods can provide invaluable information for our understanding of processes ranging from individual dispersal to the composition and assembly of entire marine communities.

The project will:
(1) assemble a unique, open access database of population genetic data and associated metadata that is compatible with the developing genomic and biological diversity standards for data archiving,

(2) facilitate open communication and collaboration among researchers from across the region through international workshops, virtual communication and a collaborative website,
(3) promote training in the use of genetic methodologies in ecology and evolution for researchers from developing countries through these same venues, and
(4) use the assembled database to address fundamental questions about the evolution of species and the reservoirs of genetic diversity in the Indo-Pacific.

The network will provide a model for international collaborative networks and genetic databasing in biodiversity research that extends beyond the results of this Research Coordination Network effort.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1558852

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