

Meristic and morphometric data for reef fish specimens collected in the Indo-Pacific and Pacific Ocean

Website: <https://www.bco-dmo.org/dataset/823324>

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
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Abstract

This dataset contains meristic and morphometric data for specimens collected in the Indo-Pacific and Pacific Ocean and analyzed in Hoban & Williams 2020.

Table of Contents

- [Coverage](#)
 - [Dataset Description](#)
 - [Methods & Sampling](#)
 - [Data Processing Description](#)
 - [Related Publications](#)
 - [Related Datasets](#)
 - [Parameters](#)
 - [Project Information](#)
 - [Program Information](#)
 - [Funding](#)
-

Coverage

Spatial Extent: N:8.08895 E:80.7718 S:-12.17253 W:-134.85639

Methods & Sampling

Hoban & Williams (2020) is a phylogeographic survey and taxonomic species description. Specimens were collected throughout the Central Pacific using rotenone and hand nets and/or pole spears. Fin clips were taken for genetic analysis and whole specimens were retained for taxonomic analysis. Specimens were sequenced at the mitochondrial COI marker for phylogeographic and phylogenetic analyses. Taxonomic analysis was by morphometric and meristic characters per Williams (1986).

Instruments: Specimens were collected on SCUBA using pole spears and/or hand nets and rotenone. Counts and measurements were taken using a dissecting microscope and dial calipers to the nearest 0.1mm.

Data Processing Description

Meristic and morphometric data were aggregated and analyzed with a principal components analysis using R

3.6.1.

BCO-DMO Data Manager Processing Notes:

* Data file specimens-Hoban2020a.csv imported into our data system.

* Missing data identifiers 'nan' and 'NA' are displayed as 'nd' for 'no data' which is the default display of missing data in our data system.

* Latitude and longitude values rounded to 5 decimal places.

[[table of contents](#) | [back to top](#)]

Related Publications

Hoban, M. L., & Williams, J. T. (2020). Cirripectes matatakaro, a new species of combtooth blenny from the Central Pacific, illuminates the origins of the Hawaiian fish fauna. PeerJ, 8, e8852. doi:[10.7717/peerj.8852](https://doi.org/10.7717/peerj.8852)
Results

[[table of contents](#) | [back to top](#)]

Related Datasets

IsSupplementTo

Hoban, M.L. and Williams, J.T. (2019). Cirripectes cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial. PopSet: 1791081300. GenBank Accessions: MN649903-MN649936, MN649877-MN649902, MN649937-MN650012. The National Center for Biotechnology Information PopSet: 1791081300. Available from <https://www.ncbi.nlm.nih.gov/popset>?DbFrom=nucore&Cmd=Link&LinkName=nucore_popset&IdsFromResult=1791081418
<https://www.ncbi.nlm.nih.gov/popset/?term=MN649936>

[[table of contents](#) | [back to top](#)]

Parameters

Parameters for this dataset have not yet been identified

[[table of contents](#) | [back to top](#)]

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 Papahānaumokuākea 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.

[[table of contents](#) | [back to top](#)]

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.

[[table of contents](#) | [back to top](#)]

Funding

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

[[table of contents](#) | [back to top](#)]