

# Reef Fish genetic accessions at NCBI Genbank from samples collected in the Indian Ocean, Pacific Ocean, and Red Sea from 2005 to 2015; related to 2016 publications

**Website:** <https://www.bco-dmo.org/dataset/716806>

**Data Type:** experimental

**Version:**

**Version Date:** 2017-12-18

## Project

» [Origins of Hawaiian Reef Fishes](#) (Hawaiian Fish Origins)

## Program

» [Indo-Pac Research Coordination Network](#) (Indo-Pac RCN)

Contributors	Affiliation	Role
<a href="#">Bowen, Brian</a>	University of Hawai'i at Mānoa (HIMB)	Principal Investigator, Contact
<a href="#">York, Amber D.</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Table of Contents

- [Coverage](#)
- [Dataset Description](#)
  - [Methods & Sampling](#)
  - [Data Processing Description](#)
- [Data Files](#)
- [Parameters](#)
- [Instruments](#)
- [Project Information](#)
- [Program Information](#)
- [Funding](#)

## Coverage

**Spatial Extent:** N:30 E:35 S:-20 W:-180

## Dataset Description

This dataset contains GenBank accession numbers for various genomic and mtDNA loci sequences from reef fish. The fish were sampled in multiple locations in the Indian Ocean, Pacific Ocean, and the Red Sea between 2005 to 2015.

### These data were published in the data sections of the following publications:

Coleman, R.R., J.A. Eble, J.D. DiBattista, L.A. Rocha, J.E. Randall, M.L. Berumen, B.W. Bowen. 2016. Regal phylogeography: range-wide survey of the marine angelfish *Pygoplites diacanthus* reveals evolutionary partitions between the Red Sea, Indian Ocean, and Pacific Ocean. *Molecular Phylogenetics and Evolution* 100:243 – 253. doi: [10.1016/j.ympev.2016.04.005](https://doi.org/10.1016/j.ympev.2016.04.005).

DiBattista J.D., J. Whitney, M.T. Craig, J.-P. A. Hobbs, L.A. Rocha, K.A. Feldheim, M.L. Berumen, B.W. Bowen. 2016. Surgeons and suture zones: hybridization among four surgeonfish species in the Indo-Pacific with variable evolutionary outcomes. *Molecular Phylogenetics and Evolution* 101:203 – 215. doi: [10.1016/j.ympev.2016.04.036](https://doi.org/10.1016/j.ympev.2016.04.036).

DiBattista, J.D., M.R. Gaither, J.-P. A. Hobbs, L.A. Rocha, B.W. Bowen. 2016. Angelfishes, paper tigers, and the devilish taxonomy of the *Centropyge flavissima* complex. *Journal of Heredity* 107:647 – 653. doi: [10.1093/jhered/esw062](https://doi.org/10.1093/jhered/esw062).

Tenggardjaja, K. A., Bowen, B. W., & Bernardi, G. (2014). Vertical and horizontal genetic connectivity in *Chromis verater*, an endemic damselfish found on shallow and mesophotic reefs in the Hawaiian Archipelago and adjacent Johnston Atoll. *PLoS One*, 9 (12), e115493. doi: [10.1371/journal.pone.0115493](https://doi.org/10.1371/journal.pone.0115493)

Tenggardjaja, K.A., B.W. Bowen, G. Bernardi. 2016. Reef fish dispersal in the Hawaiian Archipelago: comparative phylogeography of three endemic damselfishes. *Journal of Marine Biology*: Article ID 3251814. doi: [10.1155/2016/3251814](https://doi.org/10.1155/2016/3251814).

## Methods & Sampling

**Methodology:** Various genomic and mtDNA loci were sequenced from reef fishes.

**Sampling and analytical procedures:** Samples were taken as fine clips, then sequenced and analyzed to detect population structure and evolutionary genetic divergences. Species were collected with scuba gear, nets, and spears.

Raw sequence data was aligned with GENEIOUS R6 (Biomatters, LTD, Auckland, NZ) or GENEIOUS v.8.0.3 (Gene Codes, Ann Arbor, MI, USA). Sequence analyses were performed with BEAST v.2.2.0 and ARLEQUIN v. 3.5.

For details of these analyses, see the references listed in the "Description" section of this page.

## Data Processing Description

BCO-DMO Data Manager Processing Notes:

- \* added a conventional header with dataset name, PI name, version date
- \* modified parameter names to conform with BCO-DMO naming conventions
- \* added columns for max/min latitude and longitudes for species collections
- \* added column with DOIs for the journal references
- \* modified dataset so each row contains one range of accessions.
- \* replaced commas in the data with semicolons to support .csv format of data

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

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## Data Files

File
<b>accessions.csv</b> (Comma Separated Values (.csv), 2.79 KB) MD5:070ce4578de1ad420a8f0e3c3e1da4f0
Primary data file for dataset ID 716806

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

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## Parameters

Parameter	Description	Units
Species_Names	Name of species sampled	unitless
Sequence_Description	Description of type of sequence	unitless
Collection_Location	Location species were collected	unitless
Sequence_Analysis_Method	Sequence method and instrument	unitless
Genbank_Accession_Range	Range of accession numbers at National Center for Biotechnology Information (NCBI) Genbank	unitless
Genbank_First_Accession_Link	Link to the first accession in the accession range at National Center for Biotechnology Information (NCBI) Genbank	unitless
Collection_Max_Lat	Maximum species collection latitude	decimal degrees
Collection_Min_Lat	Minimum species collection latitude	decimal degrees
Collection_Max_Lon	Maximum species collection longitude	decimal degrees
Collection_Min_Lon	Minimum species collection longitude	decimal degrees
Journal_Publications	Journal publications these accessions were published in	unitless
Journal_Publication_DOI	Digital object identifier (DOI) for the journal publications these accessions were published in	unitless

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

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## Instruments

<b>Dataset-specific Instrument Name</b>	ABI 3730XL Genetic Analyzer
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	ABI 3730XL Genetic Analyzer (Applied Biosystems, Foster City, CA, USA)
<b>Generic Instrument Description</b>	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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

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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 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](#) ]

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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.

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

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1558852</a>

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