

Reef Fish genetic accession numbers at NCBI Genbank

Website: <https://www.bco-dmo.org/dataset/788903>

Data Type: experimental

Version: 1

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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

Reef Fish genetic accession numbers at NCBI Genbank.

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Methods & Sampling

Arango et al. (2018) and Pyle et al. (2018) collectively describe 4 new species, three damselfish and a basslet. Specimens were collected with hand nets during deep dives using mixed-gas, closed-circuit rebreathers, and brought to the surface alive with the aid of a hypodermic needle to vent gas from the swim bladders. Methods for morphometric counts and measurements follow standard procedures as detailed in Pyle et al. (2016; Zookeys 641:165). DNA barcodes (COI) were produced with an ABI 3130XL genetic analyzer (Applied Biosystems, Foster City, California) at the Hawai'i Institute of Marine Biology EPSCoR Sequencing Facility.

Wilcox et al. (2018) and Tenggardjaja et al. (2018) are phylogeographic surveys. Fish fin clips were collected on shallow reefs with conventional SCUBA, using hand nets and pole spears. Tissue samples were preserved in salt-saturated DMSO buffer. Various mitochondrial and nuclear loci were sequenced for phylogeographic analyses. Collection data for Wilcox et al., including lat-long information, is provided in Table S2 (see Supplemental Files below). Locations for samples in Tenggardjaja et al. are limited to island sites (no lat-long available). See paper cited below for details.

In all cases the DNA sequences were aligned, edited and trimmed to a common length using Geneious Pro DNA analysis software (v.5.6.6 and v.6.2; Kearse et al. 2012; Bioinformatics 28: 1647–1649). Maximum Likelihood, Neighbor-Joining, and Maximum Parsimony tree-building methods were implemented using Mega v.5.2.2, and all sequences are available in GenBank. Where appropriate, population genetic parameters were calculated with ARLEQUIN 3.5 (Excoffier and Lischer 2010; Mol Ecol Resour 10:564–567).

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Data Files

File
accessions_2019.csv (Comma Separated Values (.csv), 2.34 KB) MD5:b57d8f7ba09272e6712c9574c1018189
Primary data file for dataset ID 788903

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Supplemental Files

File
Table S2 (Wilcox et al. 2018) Lionfish sample information filename: Table_S2_Lionfish_sample_information.xlsx (Microsoft Excel, 41.17 KB) MD5:b2c9a19796940e515271d6332a12d7e4
Lionfish sample information from Wilcox et al. (2018)

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Related Publications

Arango, B. G., Pinheiro, H. T., Rocha, C., Greene, B. D., Pyle, R. L., Copus, J. M., ... Rocha, L. A. (2019). Three new species of Chromis (Teleostei, Pomacentridae) from mesophotic coral ecosystems of the Philippines. *ZooKeys*, 835, 1–15. doi:[10.3897/zookeys.835.27528](https://doi.org/10.3897/zookeys.835.27528)
Methods

Pyle, R. L., Greene, B. D., Copus, J. M., & Randall, J. E. (2018). *Tosanoides annepatrice*, a new basslet from deep coral reefs in Micronesia (Perciformes, Percoidae, Serranidae). *ZooKeys*, 786, 139–153. doi:[10.3897/zookeys.786.28421](https://doi.org/10.3897/zookeys.786.28421)
Methods

Tenggardjaja, K. A., Bowen, B. W., & Bernardi, G. (2018). Comparative phylogeography of widespread and endemic damselfishes in the Hawaiian Archipelago. *Marine Biology*, 165(8). doi:[10.1007/s00227-018-3395-y](https://doi.org/10.1007/s00227-018-3395-y)
Methods

Wilcox, C. L., Motomura, H., Matsunuma, M., & Bowen, B. W. (2017). Phylogeography of Lionfishes (Pterois) Indicate Taxonomic Over Splitting and Hybrid Origin of the Invasive Pterois volitans. *Journal of Heredity*, 109(2), 162–175. doi:[10.1093/jhered/esx056](https://doi.org/10.1093/jhered/esx056)
Methods

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Parameters

Parameter	Description	Units
Species_Name	Species name	unitless
Sequence_Description	Description of the type of sequence	unitless
Collection_Location	Locations where species were collected	unitless
Sequence_Analysis_Method	Sequencing and analysis methods	unitless
Journal_Publications	Relevant publications	unitless
Journal_Publication_DOI	DOI of the relevant publication	unitless
Genbank_Accession_Range	Genbank Accession numbers	unitless

Instruments

Dataset-specific Instrument Name	ABI 3130XL
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	DNA barcodes (COI) were produced with an ABI 3130XL genetic analyzer (Applied Biosystems, Foster City, California).
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	
Generic Instrument Name	Hand Net
Dataset-specific Description	Arango et al. (2018) and Pyle et al. (2018) used closed-circuit rebreather technology to access reefs and used hand nets to collect specimens. Wilcox et al. (2018) and Tenggardjaja et al. (2018) used conventional SCUBA to capture specimens with hand nets and pole spears.
Generic Instrument Description	A hand net (also called a scoop net or dip net) is a net or mesh basket held open by a hoop. They are used for scooping fish near the surface of the water.

Dataset-specific Instrument Name	SCUBA
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	Wilcox et al. (2018) and Tenggardjaja et al. (2018) used conventional SCUBA to capture specimens with hand nets and pole spears.
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

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.

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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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