Reef fish NCBI genetic sequence accession numbers for sequences from reef fish specimens collected in the Indo-Pacific and Pacific Ocean

Website: https://www.bco-dmo.org/dataset/823315
Data Type: Other Field Results
Version: 1
Version Date: 2020-09-07

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 NCBI GenBank accession numbers for sequences from reef fish specimens collected in the Indo-Pacific, Pacific Ocean. These results were published in Hoban & Williams, 2020.

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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.

Instruments: Specimens were collected on SCUBA using pole spears and/or hand nets and rotenone. DNA barcodes were produced with an ABI 3130XL genetic analyzer (Applied Biosystems, Foster City, California).

Data Processing Description

DNA sequences were trimmed, edited, and aligned using Geneious R6. Phylogeographic and population analyses were conducted using a modified version of the R package pegas and the package poppr. We used PartitionFinder 2. Phylogenetic analyses were performed using MrBayes 3.2.7 and verified with Tracer v1.7.1. Trees were visualized in FigTree and figures were produced using the R package ggtree.

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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
Results

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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=nuccore&Cmd=Link&LinkName=nuccore_popset&IdsFromResult=1791081418
https://www.ncbi.nlm.nih.gov/popset/?term=MN649936

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	ABI 3130XL genetic analyzer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	DNA barcodes 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.

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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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