

Genetic sequence identifiers for Etelis samples collected in the Indo-Pacific Ocean between 1997 and 2012

Website: <https://www.bco-dmo.org/dataset/873427>

Data Type: Other Field Results

Version: 1

Version Date: 2022-04-21

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

Genetic sequence identifiers for Etelis samples collected in the Indo-Pacific Ocean between 1997 and 2012. These data were published in Andrews et al. (2021).

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Coverage

Spatial Extent: N:32 E:-120.1551564 S:-35 W:29.8892

Temporal Extent: 1997 - 2012

Acquisition Description

The holotype was purchased at Yanbu fish market after being collected by hook and line in a nearby area and was deposited at the National Museum of Marine Biology & Aquarium (NMMB-P). Fifteen paratypes were obtained from Western Australia and deposited at the fish collection of California Academy of Sciences, San Francisco (CAS). These paratypes were part of a previous study using morphological and genetic data which revealed that two morphologically similar species were being identified as *E. carbunculus*, leading the authors to propose an undescribed species of *Etelis* (Andrews et al. 2016). That study generated DNA sequence data from cytochrome *b* (*cytb*) for the paratypes, and the sequences have been deposited in GenBank (Accession numbers MW151867- MW151881). See "Related Datasets" for links to the NCBI Popsets that contain these sequences.

[See Related Dataset "Etelis morphoglogy" <https://www.bco-dmo.org/dataset/873174> for morphological measurements, meristics for the Etelis samples. The column "Field_ID" can be used to relate the Etelis genetics and Etelis morphology datasets.]

DNA sequences from *cytb* and cytochrome oxidase I (COI) were obtained from the *E. boweni* holotype and four *E. radiosus* specimens from the Yanbu fish market using previously described protocols (Andrews *et al.* 2016). The sequences were aligned with sequences used in phylogenetic analyses in Andrews *et al.* 2016, including *cytb* and COI sequences from six *E. boweni* and six *E. carbunculus* specimens collected across the Indo-Pacific, along with sequences from all other recognized *Etelis* species (six *E. coruscans* specimens, seven *E. radiosus* specimens, five *E. oculatus* specimens), and one specimen from each of two outgroups (*Pristipomoides filamentosus* and *Aphareus rutilans*). All sequences were then trimmed to a common length for each locus, for a total of 375 bp for *cytb* and 599 bp for COI.

Location: Indo-Pacific

Species List:

ScientificName,AphiaID,LSID

Aphareus rutilans,218468,urn:lsid:marinespecies.org:taxname:218468

Etelis boweni,1536489,urn:lsid:marinespecies.org:taxname:1536489

Etelis carbunculus,212545,urn:lsid:marinespecies.org:taxname:212545

Etelis coruscans,212544,urn:lsid:marinespecies.org:taxname:212544

Etelis oculatus,159789,urn:lsid:marinespecies.org:taxname:159789

Etelis radiosus,276518,urn:lsid:marinespecies.org:taxname:276518

Pristipomoides filamentosus,218511,urn:lsid:marinespecies.org:taxname:218511

Processing Description

Maximum likelihood phylogenetic analysis was conducted with concatenated *cytb* and COI sequences using the GTR-GAMMA model in RAXML (Stamatakis 2014) with sequence data partitioned by locus, and parameters and rates allowed to vary between partitions. We first conducted 50 maximum likelihood searches with distinct starting trees, and then performed 1,000 bootstrap replicates on the best-scoring tree. Sequence data generated for this study were deposited in GenBank (accession numbers MW138043- MW138047, MW151862- MW151866).

BCO-DMO Data Manager Processing Notes:

* Exact locations for these samples are not available due to fish market acquisition. The region is known ("Indo-Pacific"). Bounding box coordinates were calculated in python using the multipolygon from marineregions.org (MRID: 14289).

* A unique list of scientific names in this dataset were matched using the World Register of Marine Species taxa match tool. All names exactly matched the accepted synonym of a species name on 2022-04-22.

* location names delimited with a column in the data changed to semicolon-delimited (for csv support).

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Related Publications

Andrews, K. R., Fernandez-Silva, I., Randall, J. E., & Ho, H. (2021). *Etelis boweni* sp. nov., a new cryptic deepwater eteline snapper from the Indo-Pacific (Perciformes: Lutjanidae). *Journal of Fish Biology*, 99(2), 335–344. Portico. <https://doi.org/10.1111/jfb.14720>

Results

Andrews, K. R., Williams, A. J., Fernandez-Silva, I., Newman, S. J., Copus, J. M., Wakefield, C. B., Randall, J. E., & Bowen, B. W. (2016). Phylogeny of deepwater snappers (Genus *Etelis*) reveals a cryptic species pair in the Indo-Pacific and Pleistocene invasion of the Atlantic. *Molecular Phylogenetics and Evolution*, 100, 361–371. <https://doi.org/10.1016/j.ympev.2016.04.004>

Methods

Hubbs CL, Lagler KF (1958). *Fishes of the Great Lakes region*. Ann Arbor: The University of Michigan Press. <https://isbnsearch.org/isbn/0472464353>

Methods

Stamatakis, A. (2014). RAXML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics*, 30(9), 1312–1313. doi:[10.1093/bioinformatics/btu033](https://doi.org/10.1093/bioinformatics/btu033)

Methods

Related Datasets

IsRelatedTo

Bowen, B., Andrews, K. R. (2022) **Microsatellite genotypes, and cytb sequences for Etelis coruscans, Etelis carbunculus, and Etelis sp. and sample collection information in the Indo-Pacific Ocean from 1997 and 2012.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-04-26 doi:10.26008/1912/bco-dmo.873568.1 [[view at BCO-DMO](#)]

Relationship Description: The Etelis range-wide data set was designed to resolve population structure and management units for Etelis carbunculus. In the course of this population genetic study, it became apparent that the putative Etelis carbunculus actually contained two species, the foundation for the "Etelis genetics" and "Etelis morphology" data sets.

Bowen, B., Andrews, K. R. (2022) **Morphological measurements and meristics for Etelis samples collected in the Indo-Pacific Ocean between 1997 and 2012.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-04-14 <http://lod.bco-dmo.org/id/dataset/873174> [[view at BCO-DMO](#)]

Relationship Description: Morphological measurements, meristics for the Etelis samples. The column Field_ID can be used to relate these two datasets.

References

Andrews, K.R., Fernandez-Silva, I., Randall, J.E. and Ho, H.C. (2021). Etelis boweni cytochrome b (cytb) gene, partial cds; mitochondrial. The National Center for Biotechnology Information PopSet: 2017807418. Available from <https://www.ncbi.nlm.nih.gov/popset/2017807418>

Andrews, K.R., Fernandez-Silva, I., Randall, J.E. and Ho, H.C. (2021). Etelis boweni voucher YB16 cytochrome c oxidase subunit I (COX1) gene, partial cds; mitochondrial. GenBank accession: MW138047.1. Available from <https://www.ncbi.nlm.nih.gov/nuccore/MW138047.1/>

Andrews, K.R., Fernandez-Silva, I., Randall, J.E. and Ho, H.C. (2021). Etelis cytochrome b (cytb) gene, partial cds; mitochondrial. The National Center for Biotechnology Information PopSet: 2017807408. Available from <https://www.ncbi.nlm.nih.gov/popset/2017807408>

Andrews, K.R., Williams, A.J., Fernandez-Silva, I., Newman, S.J., Copus, J.M., Wakefield, C.B., Randall, J.E. and Bowen, B.W. (2016). Etelinae cytochrome b (cytb) gene, partial cds; mitochondrial. PopSet: 1020878023. Available from <https://www.ncbi.nlm.nih.gov/popset/1020878023>

Andrews, K.R., Williams, A.J., Fernandez-Silva, I., Newman, S.J., Copus, J.M., Wakefield, C.B., Randall, J.E. and Bowen, B.W. (2016). Etelinae cytochrome oxidase subunit I (COI) gene, partial. cds; mitochondrial. PopSet: 1020877959. Available from <https://www.ncbi.nlm.nih.gov/popset/1020877959>

Andrews, K.R., Williams, A.J., Fernandez-Silva, I., Newman, S.J., Copus, J.M., Wakefield, C.B., Randall, J.E. and Bowen, B.W. (2016). Etelis cytochrome b (cytb) gene, partial cds; mitochondrial. PopSet: 1020878057. Available from <https://www.ncbi.nlm.nih.gov/popset/1020878057>

Parameters

Parameter	Description	Units
Field_ID	Field ID: sample identifier	unitless
Species	Species (Genus species)	unitless
Status	Status: specimen status	unitless
Sample_Location	Sample location	unitless
cytb	cytb: NCBI GenBank accession number for cytochrome b sequence	unitless
COI	COI: NCBI GenBank accession number for cytochrome oxidase I sequence	unitless
Reference	Reference: specimen citation	unitless

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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.

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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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