

Morphological measurements and meristics for *Etelis* samples collected in the Indo-Pacific Ocean between 1997 and 2012

Website: <https://www.bco-dmo.org/dataset/873174>

Data Type: Other Field Results

Version: 1

Version Date: 2022-04-14

Project

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

Program

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

Contributors	Affiliation	Role
Bowen, Brian	University of Hawaii	Principal Investigator
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Abstract

Morphological measurements and meristics 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 Dataset "Etelis genetics" <https://www.bco-dmo.org/dataset/873427> for genetic accession identifiers and methodology. The column "Field_ID" can be used to relate the *Etelis* genetics and *Etelis* morphology datasets.]

Methods for taking morphological measurements and meristics generally followed Hubbs & Lagler (1958), with some exceptions. The first anal spine was not measured because it was very short for this species. Upper and

lower gillrakers were counted separately, as were rudiments. Length of caudal fin is measured from base of the fin to tip of upper lobe. Length of caudal fin concavity is the length of upper lobe minus the length of middle of caudal fin base to middle of the concavity.

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. [See Related Dataset "Etelis genetics" <https://www.bco-dmo.org/dataset/873427> for genetic accession identifiers and methodology.]

Location: Indo-Pacific

Taxon Identifier (species, AphiaID,LSID)

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

Processing Description

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).

* Species column added to dataset with value "Etelis boweni" and verified by the data submitter.

* Taxa ID added to metadata *Etelis boweni*,1536489,urn:lsid:marinespecies.org:taxname:1536489

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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

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Related Datasets

IsRelatedTo

Bowen, B., Andrews, K. R. (2022) **Genetic sequence identifiers 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 2022-04-21 doi:10.26008/1912/bco-dmo.873427.1 [[view at BCO-DMO](#)]

*Relationship Description: Genetic sequence identifiers and sample information for the *Etelis* samples. The column Field_ID can be used to relate these two datasets.*

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.*

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Parameters

Parameter	Description	Units
Sample_ID	Sample Identifier	unitless
Field_ID	Field ID: sample identifier	unitless
Sample_Type	Species (Genus species)	unitless
Species	Sample type (holotype or paratype)	unitless
Standard_length	Tip of snout to the caudal peduncle	centimeters (cm)
Body_depth	Maximum distance between the dorsal and ventral portions of the fish [Proportion of standard length]	unitless
Body_width	Maximum distance across body [Proportion of standard length]	unitless
Head_length	Tip of snout to posterior portion of operculum [Proportion of standard length]	unitless
Snout_length	Tip of snout to most anterior part of the eye [Proportion of standard length]	unitless
Orbit_diameter	Maximum horizontal diameter of orbit [Proportion of standard length]	unitless
Interorbital_width_fleshy	Width of fleshy interorbital [Proportion of standard length]	unitless
Upper_jaw_length	Antermost point of the premaxillary to posterior point of the maxillary [Proportion of standard length]	unitless
Caudal_peduncular_depth	Depth at center of caudal peduncle [Proportion of standard length]	unitless
Caudal_peduncular_length	Posterior end of the anal fin base to the caudal base [Proportion of standard length]	unitless
Predorsal_length	Tip of the upper jaw to origin of first dorsal fin [Proportion of standard length]	unitless
Preanal_length	Tip of upper jaw to first anal fin ray [Proportion of standard length]	unitless
Prepelvic_length	Tip of upper jaw to first pelvic fin ray [Proportion of standard length]	unitless
D_base	Length of dorsal fin base [Proportion of standard length]	unitless
Spinous_D_base	Length of spinous dorsal fin base [Proportion of standard length]	unitless
D_spine_1st	Length of first dorsal spine [Proportion of standard length]	unitless
D_spine_2nd	Length of second dorsal spine [Proportion of standard length]	unitless
D_ray_1st	Length of first dorsal soft ray [Proportion of standard length]	unitless
Longest_D_ray_last	Length of the longest (last) fin ray [Proportion of standard length]	unitless
A_base	Length of anal fin base [Proportion of standard length]	unitless
A_spine_2nd	Length of second anal spine [Proportion of standard length]	unitless
A_spine_3rd	Length of third anal spine [Proportion of standard length]	unitless
A_ray_1st	Length of first anal fin ray [Proportion of standard length]	unitless
Longest_A_ray	Length of longest anal fin ray [Proportion of standard length]	unitless
C_length_upper_lobe	Length of upper lobe of caudal fin [Proportion of standard length]	unitless
C_concavity	Depth of caudal fin concavity [Proportion of standard length]	unitless
Pectoral_fin_length	Length of pectoral fin [Proportion of standard length]	unitless
Pelvic_fin_spine_length	Length of pelvic fin spine [Proportion of standard length]	unitless
Pelvic_fin_length	Length of pelvic fin [Proportion of standard length]	unitless

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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