

Cytochrome b and radloci genotype identification data from fish sampled in the Belizean Barrier Reef in 2014.

Website: <https://www.bco-dmo.org/dataset/738714>

Data Type: Other Field Results

Version: 1

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Project

» [An Integrative Investigation of Population Connectivity Using a Coral Reef Fish](#) (Elacatinus Dispersal I)

Contributors	Affiliation	Role
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Abstract

Cytochrome b and radloci genotype identification data from fish sampled in the Belizean Barrier Reef in 2014.

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Coverage

Spatial Extent: N:18.3955 E:-87.1362 S:16.0028 W:-88.6743

Temporal Extent: 2014 - 2014

Dataset Description

Mitochondrial DNA cytochrome b and radloci genotype identification data from fish sampled in the Belizean Barrier Reef in 2014. Each of the 59 loci appear in two separate columns for each allele except for the mitochondrial DNA, which only appears in one column because there is only one allele at the locus.

Methods & Sampling

We collected tissue samples from 1126 *Elacatinus lori* individuals at 39 locations across the Belize barrier reef for population genetic analyses. We marked the location of each collection site with a Garmin GPSMAP 76Cx unit. Individuals were caught with slurp guns and we took a small clip from the caudal fin using scissors. All tissue samples were store in 95% EtOH. Genetic data were collected based on standard DNA extractions and a targeted amplicon sequencing approach. Details on all methods can be found in D'Aloia et al. (2017), *Conservation Genetics*.

Data Processing Description

To generate the two genotype files, we used a custom Perl script that was specifically developed to run on Cornell University's servers. All script details and filtering steps are described in detail in D'Aloia et al. 2017, *Conservation Genetics*. Missing data from genotype columns is denoted by 0.

BCO-DMO Data Processing Notes:

- Added decimal degree lat and lon to data
- Added date to data
- Merged cytb and radloci data into one spreadsheet

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Data Files

File
goby_genotypes.csv (Comma Separated Values (.csv), 323.76 KB) MD5:7a82fa721761f156c1cdd29c11fa8239
Primary data file for dataset ID 738714

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Related Publications

D'Aloia, C. C., Bogdanowicz, S. M., Harrison, R. G., & Buston, P. M. (2016). Cryptic genetic diversity and spatial patterns of admixture within Belizean marine reserves. *Conservation Genetics*, 18(1), 211–223.

doi:[10.1007/s10592-016-0895-5](https://doi.org/10.1007/s10592-016-0895-5)

Results

,
Methods

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Parameters

Parameter	Description	Units
year	Year of sampling	unitless
date	Date of sampling; yyyy/mm/dd	unitless
individual_id	Unique ID assigned to the fish	unitless
site_id	Location collected	unitless
lat	Latitude	decimal degrees
lon	Longitude	decimal degrees
Goby32_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby32_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby43_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless

Goby287_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby287_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby291_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby291_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby300_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby300_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby308_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby308_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby314_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby314_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby340_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby340_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby336_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby336_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby143_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby143_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby169_a	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Goby169_b	Genotype data for an individual fish two alleles per locus. Each of the 59 loci have two columns: a and b. This column contains unique genotype IDs.	unitless
Gobycytb	Genotype date gobycytb for an individual fish for a fragment of the mitochondrial DNA locus cytochrome b. This column contains unique genotype IDs.	unitless

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Instruments

Dataset-specific Instrument Name	GPSMAP 76Cx (Garmin)
Generic Instrument Name	GPS receiver
Dataset-specific Description	Used to collect GPS data
Generic Instrument Description	Acquires satellite signals and tracks your location. This term has been deprecated. Use instead: https://www.bco-dmo.org/instrument/560

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Deployments

Belize_2010

Website	https://www.bco-dmo.org/deployment/704795
Platform	lab Buston
Description	Buston lab expeditions to Belize beginning in 2010.

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Project Information

An Integrative Investigation of Population Connectivity Using a Coral Reef Fish (*Elacatinus Dispersal I*)

Website: <http://people.bu.edu/buston/lab/Welcome.html>

Coverage: Belizean Barrier Reef System (16.803 degrees North 88.096 degrees West)

Understanding the patterns, causes and consequences of larval dispersal is a major goal of 21st century marine ecology. Patterns of dispersal determine the rates of larval exchange, or connectivity, between populations. Both physical factors (e.g., water movement) and biological factors (e.g., larval behavior) cause variation in population connectivity. Population connectivity, in turn, has major consequences for all aspects of an organism's biology, from individual behavior to metapopulation dynamics, and from evolution within metapopulations to the origin and extinction of species. Further, understanding population connectivity is critical for the design of effective networks of marine reserves, creation of vital tools in conservation, and the development of sustainable fisheries.

Over the last decade, three methods, each of which tells something slightly different, have emerged as leading contenders to provide the greatest insights into population connectivity. First, coupled biophysical models make assumptions regarding water flow, larval behavior and ecology, to predict population connectivity. Second, indirect genetic methods use spatial distributions of allele frequencies to infer population connectivity. Third, direct genetic methods use parentage analyses, tracing recruits to specific adults, to measure population connectivity. Despite advances, lack of integration means that we do not know the predictive skill of biophysical models, or the extent to which patterns of dispersal predict spatial genetic structure. The overall objective of this proposal is to conduct an integrated investigation of population connectivity, using all three methods in one tractable system: the neon goby, *Elacatinus lori*, on the Belizean Barrier Reef. There are three motives for this choice of study system: i) fourteen highly polymorphic microsatellite loci have been developed, facilitating the assignment of recruits to parents using parentage analyses and the measurement of dispersal; ii) the physical oceanography of the Belizean Barrier Reef is well-studied, facilitating the development and testing of coupled biophysical models; and, iii) *E. lori* has a relatively small biogeographic range, facilitating analysis of the spatial distribution of allele frequencies throughout its range.

Broader Impacts. The grant will support one postdoc and two graduate students who will be trained in

scientific diving, marine fieldwork, population genetics, biophysical modeling, and mathematical modeling, and will gain collaborative research experience. PIs will incorporate research findings in their courses, which cover all these topics. The grant will also broaden participation of under-represented groups by supporting six undergraduates from groups traditionally underrepresented in STEM fields. In each year of the project there will be an All Participants meeting to reinforce the network of participants. A project website will be developed, in English and Spanish, on the theme of larval dispersal and population connectivity. This will include a resource for K-12 marine science educators developed in collaboration with a marine science educator. All PIs will ensure that results are broadly disseminated to the scientific community and general public via appropriate forms of media.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260424

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