

Genotype data for *E. lori* individuals sequenced at 71 microsatellites from a 41 km-long transect of the Belize Barrier reef during 2018

Website: <https://www.bco-dmo.org/dataset/749774>

Data Type: Other Field Results

Version: 1

Version Date: 2018-10-22

Project

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

Contributors	Affiliation	Role
Buston, Peter	Boston University (BU)	Principal Investigator
D'Aloia, Cassidy C.	Boston University (BU)	Co-Principal Investigator
Biddle, Mathew	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

Genotype data for *E. lori* individuals sequenced at 71 microsatellites from a 41 km-long transect of the Belize Barrier reef during 2018.

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Coverage

Spatial Extent: N:16.981 E:-88.019983 S:16.625067 W:-88.077183

Temporal Extent: 2018 - 2018

Dataset Description

Genotype data for *E. lori* individuals sequenced at 71 microsatellites.

Methods & Sampling

We surveyed a 41 km-long transect of the Belize Barrier reef, centered at Carrie Bow Cay, by SCUBA to conduct a genetic parentage study of the reef fish *Elacatinus lori*. To collect settlers, we sampled ~ 100 individuals every kilometer. Individuals were collected from the outsides of sponges using slurp guns and placed them in plastic bags. At the surface, settlers were anesthetized with MS-222. For genetic analyses, DNA was extracted using a HotSHOT protocol; individuals were sequenced at 71 microsatellite loci using a multiplex PCR protocol for targeted amplicon sequencing. For full details see D'Aloia et al. (2018), Marine Ecology Progress Series.

Data Processing Description

Genotype data were analyzed using custom Perl scripts as described in D'Aloia et al. (2016), Conservation Genetics.

BCO-DMO Processing Notes:

- Every other column of data was for another allele, therefore we appended "_a" to the first and "_b" to the second column.
- renamed the individual_ID column to sample_ID
- created two additional columns, sample_id and individual_ID, from the sample_ID column by splitting on the underscore.
- mapped sample_id value to latitude and longitude coordinates for the sample_ID.
- sorted data on sample_ID and individual_ID.
- added BCO-DMO conventional header.

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Data Files

File
goby_sibship.csv (Comma Separated Values (.csv), 1.33 MB) MD5:50536b3dafed50dbd4d1048c75bbd7be
Primary data file for dataset ID 749774

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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)

General

D'Aloia, C., Xuereb, A., Fortin, M., Bogdanowicz, S., & Buston, P. (2018). Limited dispersal explains the spatial distribution of siblings in a reef fish population. Marine Ecology Progress Series. doi:[10.3354/meps12792](https://doi.org/10.3354/meps12792)

Results

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Parameters

Parameter	Description	Units
sample_ID	identifier for the sample	unitless
site_id	identifier for the site	unitless
individual_ID	identifier for the individual	unitless
lat	approximate latitude in degrees north	decimal degrees

lon	approximate longitude in degrees east	decimal degrees
Elor_564_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_564_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_2975_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_2975_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_3015_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_3015_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_605_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_605_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_639_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Elor_639_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
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Goby21378_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Goby21378_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
Goby25362_a	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless

Goby25362_b	field name is the microsatellite locus name. Data is Haplotype id for each microsatellite allele	unitless
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Instruments

Dataset-specific Instrument Name	multiplex PCR protocol
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	individuals were sequenced at 71 microsatellite loci using a multiplex PCR protocol for targeted amplicon sequencing.
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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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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