Data from fish genotyped at 14 and 20 loci at different life stages in the Belizean Barrier Reef in 2013.

Website: https://www.bco-dmo.org/dataset/738724
Data Type: Other Field Results
Version: 1
Version Date: 2018-06-18

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, Contact
D'Aloia, Cassidy C.	Woods Hole Oceanographic Institution (WHOI)	Co-Principal Investigator
Ake, Hannah	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Data from fish genotyped at 14 and 20 loci at different life stages in the Belizean Barrier Reef in 2013.

Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Related Publications
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Coverage

Spatial Extent: **Lat**:16.789722 **Lon**:-88.075833
Temporal Extent: 2013 - 2013

Dataset Description

Data from fish genotyped at 14 and 20 loci at different life stages. Sampling completed on the Belizean Barrier Reef in 2013.

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 *Elactinus lori*. All underwater sampling was conducted using SCUBA at an average (±SD) depth of 16.03 ± 2.19 m. A waypoint was recorded from the boat at the beginning and end of every collection dive, with the midpoint of each dive taken as the location for all individuals sampled on that dive. 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 adults, we collected non-lethal tissue samples at three regions along the transect (n ≈ 1,000 per region). Each adult was collected with a slurp gun and restrained in a net; we took a small tissue sample from the caudal fin using scissors. All tissue was stored in 95% EtOH. At each adult collection sponge, we also measured: sponge depth (m, using dive computers), number of tubes per sponge,

and length of largest sponge tube (nearest cm, using a tape measure).

For genetic analyses, DNA was extracted using a HotSHOT protocol; fragments were amplified using the Type-It Microsatellite PCR Kit (Qiagen) and screened on an ABI 3730 automated sequencer.

Otoliths were extracted from the 120 settlers that were assigned to parents. Otoliths were dissected, cleared of tissue, immersed in oil for 2-7 days, and rings were counted under a 50× oil immersion lens

Further details on all methods can be found in D'Aloia et al. (2015), *PNAS.*

Data Processing Description

Alleles were scored using GENEMAPPER v.4.0.

BCO-DMO Data Processing Notes:

-Combined 14 and 20 loci data into one spreadsheet
-Replaced ? with nd
-Added year column, and loci column to identify the number of loci sampled

[table of contents | back to top]

Data Files

File
genotypes.csv (Comma Separated Values (.csv), 1.23 MB) MD5:2ce38ad23e2476301a67ac46e621ddb9 Primary data file for dataset ID 738724

[table of contents | back to top]

Related Publications

D'Aloia, C. C., Bogdanowicz, S. M., Francis, R. K., Majoris, J. E., Harrison, R. G., & Buston, P. M. (2015). Patterns, causes, and consequences of marine larval dispersal. Proceedings of the National Academy of Sciences, 112(45), 13940–13945. doi:10.1073/pnas.1513754112
Results
,
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
individual_id	Unique ID assigned to each fish	unitless
year	Year of sampling	unitless

loci	The number of loci individuals were genotyped at; 14 loci or 20 loci. Individuals genotyped at 20 loci were used in the final parentage analysis. Each loci have two columns because each individual has two alleles per locus.	unitless
life_stage	Whether an individual is a potential offspring (O) or parent (P).	unitless
tetB_25745	The number of reptitive units in the microsatellite allele.	count
tetB_25745_2	The number of reptitive units in the microsatellite allele.	count
tetB_29109	The number of reptitive units in the microsatellite allele.	count
tetB_29109_2	The number of reptitive units in the microsatellite allele.	count
triB_1419	The number of reptitive units in the microsatellite allele.	count
triB_1419_2	The number of reptitive units in the microsatellite allele.	count
triG_18144	The number of reptitive units in the microsatellite allele.	count
triG_18144_2	The number of reptitive units in the microsatellite allele.	count
tetG_985	The number of reptitive units in the microsatellite allele.	count
tetG_985_2	The number of reptitive units in the microsatellite allele.	count
tetY_6326	The number of reptitive units in the microsatellite allele.	count
tetY_6326_2	The number of reptitive units in the microsatellite allele.	count
tetR_25632	The number of reptitive units in the microsatellite allele.	count
tetR_25632_2	The number of reptitive units in the microsatellite allele.	count
tetB_6231	The number of reptitive units in the microsatellite allele.	count
tetB_6231_2	The number of reptitive units in the microsatellite allele.	count

triB_23889	The number of reptitive units in the microsatellite allele.	count
triB_23889_2	The number of reptitive units in the microsatellite allele.	count
triG_25362	The number of reptitive units in the microsatellite allele.	count
triG_25362_2	The number of reptitive units in the microsatellite allele.	count
triG_21378	The number of reptitive units in the microsatellite allele.	count
triG_21378_2	The number of reptitive units in the microsatellite allele.	count
tetY_14528	The number of reptitive units in the microsatellite allele.	count
tetY_14528_2	The number of reptitive units in the microsatellite allele.	count
triY_6266	The number of reptitive units in the microsatellite allele.	count
triY_6266_2	The number of reptitive units in the microsatellite allele.	count
tetR_23415	The number of reptitive units in the microsatellite allele.	count
tetR_23415_2	The number of reptitive units in the microsatellite allele.	count
tetB_24561	The number of reptitive units in the microsatellite allele.	count
tetB_24561_2	The number of reptitive units in the microsatellite allele.	count
tetB_5796	The number of reptitive units in the microsatellite allele.	count
tetB_5796_2	The number of reptitive units in the microsatellite allele.	count
tetB_1184	The number of reptitive units in the microsatellite allele.	count
tetB_1184_2	The number of reptitive units in the microsatellite allele.	count
tetG_24777	The number of reptitive units in the microsatellite allele.	count

tetG_24777_2	The number of reptitive units in the microsatellite allele.	count
tetG_26721	The number of reptitive units in the microsatellite allele.	count
tetG_26721_2	The number of reptitive units in the microsatellite allele.	count
tetY_25176	The number of reptitive units in the microsatellite allele.	count
tetY_25176_2	The number of reptitive units in the microsatellite allele.	count

[table of contents | back to top]

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

[table of contents | back to top]

Deployments

Belize_2010

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

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]