Microsatellite genotype data from Curlew Caye on the Belizean Barrier reef collected in 2011.

Website: https://www.bco-dmo.org/dataset/728239
Data Type: Other Field Results
Version: 2
Version Date: 2018-08-16

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

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:18.3955 **E**:-87.1362 **S**:16.0028 **W**:-88.6743
Temporal Extent: 2011-05-28 - 2011-08-22

Dataset Description

Geolocation and microsatellite genotype data from fish identified in Curlew Caye. See the related dataset for information on fish identified in these data: https://www.bco-dmo.org/dataset/728230

Methods & Sampling

We surveyed a 500 m long by 125 m wide study area on the reef at Curlew Caye, Belize by SCUBA to map and collect tissue samples from all *Elactinus lori* individuals, at depths from 10 m to 25 m. We began by fully censusing the focal study area: we marked the location of all host sponges (*Aplysina fistularis*) and fish (*E. lori*). GPS data were collected with a Garmin GPSMAP 76Cx unit in an underwater housing. Waypoints are accurate within 5 m. At each sponge we recorded: depth (m, using dive computers), number of tubes per sponge, length of largest sponge tube (nearest cm, using a tape measure). We also counted the number of fish per sponge, and noted which life history stage they fell into: resident ≥ 18 mm standard length (SL) or settler (<18 mm SL).

Next, we collected tissue samples from all residents (n = 425) and settlers (n = 194). Individuals were caught with slurp guns. We took a small clip from the caudal fin from residents; whole-settler specimens were collected and euthanized in MS-222. Additional settler tissue samples were collected from three sites North, and three sites south of the focal study area. (n ≈ 30 per site). All tissue samples were store in 95% EtOH. Microsatellite genotype data were collected based on standard DNA extractions (DNAdvance kit, Beckman

Coulter, Inc., USA), multiplex PCR using the Type-It Microsatellite PCR kit (Qiagen, USA), and screening on an ABI 3730 automated sequencer. Further details on all methods can be found in D'Aloia et al. (2013), *Molecular Ecology*.

Data Processing Description

No data have been processed. All files include original field data.

BCO-DMO Data Processing Notes:

-Reformatted column names to comply with naming standards
-Replaced blank cells with nd
-Columns year, lat and lon were added based on metadata provided by the PI

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Data Files

File
microsatellite_genotypes.csv (Comma Separated Values (.csv), 105.85 KB) MD5:856faa307e4b3e985fe2933d45ca396a Primary data file for dataset ID 728239

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Related Publications

D'Aloia, C. C., Bogdanowicz, S. M., Majoris, J. E., Harrison, R. G., & Buston, P. M. (2013). Self-recruitment in a Caribbean reef fish: a method for approximating dispersal kernels accounting for seascape. Molecular Ecology, 22(9), 2563–2572. doi:10.1111/mec.12274
Methods

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Parameters

Parameter	Description	Units
individual_ID	Unique ID assigned to fish	unitless
location	Region on reef fish was from	unitless
sl	Standard length of fish	millimeters
Locus1_1419triBA	Number of repeats in the microsatellite allele.	count
Locus1_1419triBB	Number of repeats in the microsatellite allele.	count

Locus2_14528tetYA	Number of repeats in the microsatellite allele.	count
Locus2_14528tetYB	Number of repeats in the microsatellite allele.	count
Locus3_18144triGA	Number of repeats in the microsatellite allele.	count
Locus3_18144triGB	Number of repeats in the microsatellite allele.	count
Locus4_21378triGA	Number of repeats in the microsatellite allele.	count
Locus4_21378triGB	Number of repeats in the microsatellite allele.	count
Locus5_23415tetRA	Number of repeats in the microsatellite allele.	count
Locus5_23415tetRB	Number of repeats in the microsatellite allele.	count
Locus6_23889triBA	Number of repeats in the microsatellite allele.	count
Locus6_23889triBB	Number of repeats in the microsatellite allele.	count
Locus7_25362triGA	Number of repeats in the microsatellite allele.	count
Locus7_25362triGB	Number of repeats in the microsatellite allele.	count
Locus8_25632tetRA	Number of repeats in the microsatellite allele.	count
Locus8_25632tetRB	Number of repeats in the microsatellite allele.	count
Locus9_25745tetBA	Number of repeats in the microsatellite allele.	count
Locus9_25745tetBB	Number of repeats in the microsatellite allele.	count
Locus10_29109tetBA	Number of repeats in the microsatellite allele.	count
Locus10_29109tetBB	Number of repeats in the microsatellite allele.	count
Locus11_6231tetBA	Number of repeats in the microsatellite allele.	count

Locus11_6231tetBB	Number of repeats in the microsatellite allele.	count
Locus12_6266triYA	Number of repeats in the microsatellite allele.	count
Locus12_6266triYB	Number of repeats in the microsatellite allele.	count
Locus13_6326tetYA	Number of repeats in the microsatellite allele.	count
Locus13_6326tetYB	Number of repeats in the microsatellite allele.	count
Locus14_985tetGA	Number of repeats in the microsatellite allele.	count
Locus14_985tetGB	Number of repeats in the microsatellite allele.	count
year	Year of sampling	unitless
offspring_parent	Whether the fish was a potential offspring (O) or parent (P)	unitless

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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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