DNA barcode sequencing results for bivalve larvae collected on N. Atlantic cruises at cold seeps sites off of Barbados, the East coast of the U.S. and the Gulf of Mexico (SEEPC project)

Website: https://www.bco-dmo.org/dataset/688111
Data Type: Cruise Results
Version: 1
Version Date: 2017-04-21

Project
» Connectivity in western Atlantic seep populations: Oceanographic and life-history processes underlying genetic structure (SEEPC)

Contributors	Affiliation	Role
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Abstract
DNA barcode sequencing results for bivalve larvae collected on N. Atlantic cruises at cold seeps sites off of Barbados, the East coast of the U.S. and the Gulf of Mexico (SEEPC project). This dataset provides the closest GenBank match for larval bivalve specimens resulting from DNA barcode sequencing, the percent match of the identification, and some information on the specimen collections.

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Coverage

Spatial Extent: **N**:37 **E**:-58 **S**:11 **W**:-95
Temporal Extent: 2011-06 - 2015-07

Dataset Description

This dataset provides the closest GenBank match for larval bivalve specimens resulting from DNA barcode sequencing, the percent match of the identification, and some information on the specimen collections.

NCBI GenBank accessions are not yet available [2017-04-21]. Please contact the PI for further information.

Related datasets:
SEEPC larval collections: MOCNESS
SEEPC larval collections: SyPRID
larval type codes

Methods & Sampling

Bivalve larvae were collected either by MOCNESS or Sentry's SyPRID Sampler. The Multiple Opening and Closing Net Environmental Sensing System has 8 separate plankton nets which can be controlled from the ship, allowing for samples along discrete depth ranges. Sentry's Precision Robotic Impeller Driven Sampler allows for the collection of larvae from just a few meters off the sea floor. DNA was extracted, purified, amplified, and sequenced using standard lab protocols and universal primers (except where indicated).

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- renamed some parameters to BCO-DMO standard
- replaced blanks, '?', '-' with 'nd' (no data)
- reformatted date from m/d/yyyy to yyyy-mm-dd
- removed 'm' from depth values
- converted lat and lon to decimal degrees
- removed or replaced special characters
- added cruise_id and year columns

Version: 2017-02-13 [added EN531 collection data]
Replaces version: 2016-09-30

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Data Files

File
bivalve_barcode_log.csv (Comma Separated Values (.csv), 31.20 KB) MD5:adb9f64ba137d7fbb87eb6c1fc9282fb Primary data file for dataset ID 688111

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Parameters

Parameter	Description	Units
larva_id	larval specimen identifier	unitless
larval_type	morphotype based on gross larval morphology; BV = Bivalve	unitless
species	closest species match to the tested sequence in GenBank	unitless
gene_id_pcent	gene(s) tested and how closely it matched the GenBank sequence	percent
cruise_id	cruise identifier	unitless
date_collected	date collected and preserved (formatted as yyyy-mm-dd)	unitless
site	collection site: BAP=Barbados Acretionary Prism; WAM=Western Atlantic Margin; GOM=Gulf of Mexico	unitless
depth_range	range of depths in which the larva was collected (formatted as yyyy-mm-dd)	meters
date_extraction	date the DNA was extracted; purified; and amplified for each larva	unitless
comment	overall results for each larva	unitless

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Instruments

Dataset-specific Instrument Name	Applied Biosystems 3730xl DNA Analyzer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	The sequencing was done by Sequetech in California
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	
Generic Instrument Name	AUV Sentry
Dataset-specific Description	Fitted out with the SyPRID (Sentry’s Precision Robotic Impeller Driven) Sampler
Generic Instrument Description	The autonomous underwater vehicle (AUV) Sentry is a fully autonomous underwater vehicle capable of exploring the ocean down to 6,000 meters (19,685 feet) depth. Sentry builds on the success of its predecessor the ABE, with improved speed, range, and maneuverability. Sentry's hydrodynamic shape also allows faster ascents and descents. Sentry carries a superior science sensor suite and an increased science payload enabling it to be used for both mid-water and near-seabed oceanographic investigations. Sentry produces bathymetric, sidescan, subbottom, and magnetic maps of the seafloor and is capable of taking digital bottom photographs in a variety of deep-sea terrains such as mid-ocean ridges, deep-sea vents, and cold seeps at ocean margins. Sentry is uniquely able to operate in extreme terrain, including volcano caldera and scarps. Sentry's navigation system uses a doppler velocity log and inertial navigation system, aided by acoustic navigation systems (USBL or LBL). The USBL system also provides acoustic communications, which can be used to obtain the vehicle state and sensor status as well as to retask the vehicle while on the bottom. In addition its standard sensors, Sentry has carried a variety of science-supplied sensors, including the Nakamura redox potential probe, ACFR 3-D imaging system, and the Tethys in-situ mass spectrometer. Sentry can be used to locate and quantify hydrothermal fluxes. Sentry is also capable of a much wider range of oceanographic applications due to its superior sensing suite, increased speed and endurance, improved navigation, and acoustic communications. Sentry can be used as a stand alone vehicle or in tandem with Alvin or an ROV to increase the efficiency of deep-submergence investigations. More information is available from the operator site at URL: http://www.whoi.edu/main/sentry

Dataset-specific Instrument Name	
Generic Instrument Name	MOCNESS1
Dataset-specific Description	MOCNESS plankton system with 300 um mesh nets.
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System or MOCNESS is a family of net systems based on the Tucker Trawl principle. The MOCNESS-1 carries nine 1-m2 nets usually of 335 micrometer mesh and is intended for use with the macrozooplankton. All nets are black to reduce contrast with the background. A motor/toggle release assembly is mounted on the top portion of the frame and stainless steel cables with swaged fittings are used to attach the net bar to the toggle release. A stepping motor in a pressure compensated case filled with oil turns the escapement crankshaft of the toggle release which sequentially releases the nets to an open then closed position on command from the surface. -- from the MOCNESS Operations Manual (1999 + 2003).

Dataset-specific Instrument Name	Bio-Rad C1000 Touch Thermal Cycler
Generic Instrument Name	Thermal Cycler
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

AT21-02

Website	https://www.bco-dmo.org/deployment/535929
Platform	R/V Atlantis
Report	http://dmoserv3.whoi.edu/data_docs/SEEPC/AT21-02_CruiseREPORT.pdf
Start Date	2012-06-01
End Date	2012-06-17
Description	Cruise information and original data are available from the NSF R2R data catalog. http://www.whoi.edu/cruiseplanning/synopsis.do?id=1942 The primary objective of the SeepC Project is to advance our general knowledge of connectivity in the deep sea using taxa found at seeps as model systems. The focus is on species and processes occurring in the Intra-American Sea (including the Caribbean, Gulf of Mexico, and eastern seaboard of the US), with attention to oceanographic circulation, life histories, and genetics. Science objectives (from the WHOI Cruise Planning Synopsis): Mooring recoveries and sampling at 3 Barbados seep sites (El Pilar, Orenoque A, Orenoque B) plus MOCNESS tows and some mapping (multibeam, CHIRP). We may add sample sites if we are able to undertake an advance SENTRY survey in the region (pending request). Our aim would be to add new sites separated by as much as 150-200 km max along a depth gradient and along an isobath. Use of SENTRY would allow us to undertake precision sampling of known sites, 1 to 1.5 days per station at each of 6 to 8 seep stations. This is part of the Seep Connectivity Project funded by NSF to investigate historical and contemporary linkages among Barbados, Gulf of Mexico, and Blake Ridge seep species. Activities at each site: 1) Sub-bottom profiling to locate seep areas 2) MOCNESS tows for larval sampling 3) Mooring recoveries (current meter, 2 sediment/larval traps per mooring) 4) Intensive sampling of seep fauna for genetic and reproduction studies

AT26-15

Website	https://www.bco-dmo.org/deployment/517377
Platform	R/V Atlantis
Start Date	2014-05-21
End Date	2014-06-14
Description	Start: Depart Gulfport, MS 05/21/2014 End: Arrive St. Petersburg, FL 06/14/2014 The AT26-15 cruise was conducted as part of the project "Connectivity in western Atlantic seep populations: Oceanographic and life-history processes underlying genetic structure" (SeepC) funded by NSF OCE-1031050. The cruise included coordinated deployments of DSV Alvin and AUV Sentry. Science objectives (from the WHOI Cruise Planning Synopsis): The primary objective of the SeepC Project is to advance our general knowledge of connectivity in the deep sea using taxa found at seeps as model systems. The focus is on species and processes occurring in the Intra-American Sea (including the Caribbean, Gulf of Mexico, and eastern seaboard of the US), with attention to oceanographic circulation, life histories, and genetics. Our efforts include improving the oceanographic model for the IAS near the seabed using current data from moorings at several depths and locations and coupling this model to a Lagrangian larval transport model. We stress the importance of iterative interactions among the science teams to advance our understanding of connectivity in the deep sea through descriptive and hypothesis-driven research. We will develop effective and best methods for hypothesis testing under the constraints of working in a relatively inaccessible environment and will build capacity in understanding connectivity in deep-sea systems.

AT29-04

Website	https://www.bco-dmo.org/deployment/568866
Platform	R/V Atlantis
Report	http://dmoserv3.whoi.edu/data_docs/SEEPC/AT29-04_SeepC_cruise_report.pdf
Start Date	2015-07-08
End Date	2015-07-28
Description	Science objectives (from the WHOI Cruise Planning Synopsis): The primary objective of the SeepC Project is to advance our general knowledge of connectivity in the deep sea using taxa found at seeps as model systems. The focus is on species and processes occurring in the Intra-American Sea (including the Caribbean, Gulf of Mexico, and eastern seaboard of the US), with attention to oceanographic circulation, life histories, and genetics. Questions that apply in shallow-water systems motivate this study: What phylogeographic breaks occur in the system? It is important to distinguish between phylogeography and connectivity. A phylogeographic break implies a long history of isolation or possibly cryptic speciation, while genetic population structure indicates gene flow is reduced, but still ongoing or recent. Do collections from different sites indicate a panmictic population of a given species? This is the fundamental question about connectivity and the scale of population genetic variation in marine species with planktonic larvae and it comprises extent of gene flow, directionality, and relative contributions. What bio-physical processes underlie observed connectivities? Biological processes (e.g., larval distributions in the water column, timing of reproduction, and planktonic larval duration) and physical processes of transport and dispersion interact to determine connectivity. Our efforts include improving the oceanographic model for the IAS near the seabed using current data from moorings at several depths and locations and coupling this model to a Lagrangian larval transport model. We stress the importance of iterative interactions among the science teams to advance our understanding of connectivity in the deep sea through descriptive and hypothesis-driven research. We will develop effective and best methods for hypothesis testing under the constraints of working in a relatively inaccessible environment and will build capacity in understanding connectivity in deep-sea systems. Science Activities: 1) Two mooring recoveries; 2) Alvin seep sampling: mussels, clams, tubeworms, and associated animals; targeting at least 30 individuals per species (manips, net, slurp); carbonates; 3) Sentry plankton sampling; 4) MOCNESS tows; 5) Sentry high-resolution mapping; 6) CTD casts; 7) XBTs; 8) Shipboard acoustics (methane plumes). BCO-DMO Note: Using Alvin dive positions for mapserver until full cruise track becomes available on rvdata.us.

EN531

Website	https://www.bco-dmo.org/deployment/521426
Platform	R/V Endeavor
Report	http://dmoserv3.whoi.edu/data_docs/SEEPC/Cruise.Report.EN531-08-14.2013.pdf
Start Date	2013-08-15
End Date	2013-08-18
Description	SEEPC project cruise. Cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Connectivity in western Atlantic seep populations: Oceanographic and life-history processes underlying genetic structure (SEEPC)

Coverage: Western Atlantic, Gulf of Mexico, Intra-American Sea

This project will evaluate connectivity on spatial scales that match those at which vent systems are being studied (3500 km), with a set of nested seeps (within the Barbados system) within which connectivity can be explored at more local spatial scales (30 to 130 km), and with species that span depth (600 m to 3600 m) and geographic ranges (30 km to 3500 km) and that have diverse life-history characteristics. Five deep-sea seep systems in the Intra- American Sea (IAS) are targeted: Blake Ridge, Florida Escarpment, Alaminos Canyon, Brine Pool, Barbados (El Pilar, Orenoque A, Orenoque B). The primary objective is to advance our general knowledge of connectivity in the deep sea. The focus is on species and processes occurring in the IAS, with attention to oceanographic circulation, life histories, and genetics. Questions that apply in shallow-water systems motivate this study:

1. What phylogeographic breaks occur in the system? It is important to distinguish between phylogeographic history and connectivity. A phylogeographic break with no shared alleles between populations implies a long history of isolation or possibly cryptic speciation.

2. Are populations connected by ongoing migration? This is the fundamental question about connectivity and the scale of genetic variation in marine species with planktonic larvae.

3. What biophysical processes underlie observed connectivities? Biological processes (e.g., larval distributions in the water column, timing of reproduction, and planktonic larval duration) and physical processes of transport and dispersion interact to determine connectivity.

The oceanographic model for the IAS will be improved and coupled to a Lagrangian larval transport model. The field program includes time-series sampling of larvae at seeps with records of current velocities, water column sampling to determine larval distribution potential, shipboard studies of larval biology and behavior, and sampling of benthic target species. Phylogenetic and population genetic tools will be used to explore historical and contemporary gene flow. Iterative interactions among the science teams will advance our understanding of connectivity in the deep sea and to develop effective and best methods for hypothesis testing under the constraints of working in a relatively inaccessible environment. Since their discovery, deep-sea chemosynthetic ecosystems have been novel systems within which to test the generality of paradigms developed for shallow-water species. This study will explore scale-dependent biodiversity and recruitment dynamics in deep-sea seep communities, and will identify key factors underlying population persistence and maintenance of biodiversity in these patchy systems.

Google Earth map showing positions of stations, CTD, XBT, multibeam locations (KMZ file dlownload)

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1030453

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