MOCNESS collections of invertebrate larvae throughout water column near methane seep sites: Barbados Accretionary Prism, 2012; Gulf of Mexico, 2014; Western Atlantic Margin, 2015

Website: https://www.bco-dmo.org/dataset/659926
Data Type: Cruise Results
Version:
Version Date: 2017-02-13

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

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Dataset Description

This dataset is a collection log showing the preliminary identification of larval types and the final disposition of individual larval specimens from MOCNESS plankton samples.

Related datasets:
SEEPC larval collections: SyPRID
larval type codes
SEEPC Bivalve DNA Barcoding Results

Methods & Sampling

One-meter MOCNESSS nets fitted with 300 um mesh nets were towed obliquely over methane seep sites, closing and opening nets at intervals that varied with the depth. Upon recovery, all samples were sorted completely over the next 12 hours or less, picking all individual invertebrate larvae from the samples, assigning morphotypes, photographing with a microscope, and preserving either for Scanning Electron Microscopy (glutaraldehyde, 2012 only) or for molecular genetics (95% ETOH).

Data Processing Description

2012: All larvae prepared for SEM were imaged. Larvae of some of the major groups (notably molluscs, bryozoans) were sequenced.

2014 and 2015: Larvae of some of the major groups (notably molluscs and bryozoans) were sequenced.

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
larval_collections_MOC.csv (Comma Separated Values (.csv), 421.84 KB) MD5:5911a29e28a7df38edc9ce1ed3c38efd Primary data file for dataset ID 659926

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Parameters

Parameter	Description	Units
cruise_id	cruise identification	unitless
year	year of sampling	year
date	date of sampling formatted as yyyy-mm-dd	year-month-day
site	sampling site	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
depth_range	collection depth range	meters
larva_id	unique number assigned to each individual larva	unitless

larval_type	Abbreviation for the general larval form: Actinotroch - AC Amphioxus - AX Anthozoan larva AN Asteroid Juvenile - AJ Auricularia - AU Bipinnaria - BI Bivalve veliger - BV Brachiolaria - BR Brachiopods - BC Chaetopterid CH Cyprid - CP Chaetognath - CT Cyphonautes - CY Doliolaria - DO Echinopluteus - EC Entoprocts - EN Egg - EG Gastropod veliger - GV Glottidia - GL Gymnosome larva - GY Megalopa MG Mitraria - MI Mullers - MU Nectochaete - NE Pelagosphaera - PE Pentacula - PN Pilidium - PI Planulae - PL Planuliform - PA Planuliform palaeonemertean - PP Pteropod shell - PT Ophiopluteus - OP Ophiuroid juvenile - OJ Sponge larva - SL Tadpole - TA Trochophore - TR Tornaria - TO Unknown - UK Zoanthid - ZO Zoea - Z	unitless
morphotype	initial morphological classification; numbered sequentially within larval forms	unitless
fixation	method of preservation	unitless
comments	comments and notes	unitless

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Instruments

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).

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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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