# AUV Sentry collections of invertebrate larvae close to the bottom near methane seep sites from R/V Atlantis AT29-04 at the Western Atlantic Margin, 2015 (SEEPC project)

**Website**: https://www.bco-dmo.org/dataset/659965
**Data Type**: Cruise Results
**Version**:
**Version Date**: 2016-09-30

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

| Contributors | Affiliation | Role |
|---|---|---|
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## Table of Contents

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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 collected with the AUV Sentry.

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

### Methods & Sampling

AUV Sentry was deployed to perform a programmed survey pattern over the chosen site. Once Sentry was a given distance from the bottom, the SyPRID sampler was turned on to collect larvae until the start of Sentry's ascent. During descent and ascent, a valve was closed to prevent contamination of the deep water sample. 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) or for molecular genetics (95% ETOH).

### Data Processing Description

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 and '-' with 'nd' (no data)
- reformatted date from m/d/yyyy to yyyy-mm-dd
- removed 'm' from altitude values
- added cruise_id, lat and lon columns
- removed or replaced special characters

[ table of contents | back to top ]

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## Data Files

| File |
|---|
| **larval_collections_SyPRID.csv**(Comma Separated Values (.csv), 68.87 KB)<br>MD5:3e094d361663ea2d363e9515816f4ac6<br>Primary data file for dataset ID 659965 |

[ table of contents | back to top ]

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| cruise_id | cruise identification | unitless |
| 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 |
| dive | AUV Sentry dive number | unitless |
| filtration_time | SyPRID Sampler filtration time formatted as HH:MM | hours:minutes |
| altitude | distance sampled above the sea bottom | meters |
| larva_id | unique number assigned to each individual larva | unitless |
| larval_type | abbreviation for the general larval form | unitless |
| morphotype | initial morphological classification; numbered sequentially within larval forms | unitless |
| fixation | method of preservation | unitless |

[ table of contents | back to top ]

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | AUV Sentry |
| **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** | SyPRID |
| **Generic Instrument Name** | Sentry Precision Robotic Impeller Driven Sampler |
| **Generic Instrument Description** | The SyPRID (Sentry Precision Robotic Impeller Driven) sampler is an innovative deep-rated (6000 m) plankton sampler that partners with the Sentry Autonomous Underwater Vehicle (AUV) to obtain paired, large-volume plankton samples at specified depths and survey lines to within 1.5 m of the seabed and with simultaneous collection of sensor data. SyPRID uses a perforated Ultra-High-Molecular-Weight (UHMW) plastic tube to support a fine mesh net within an outer carbon composite tube (tube-within-a-tube design), with an axial flow pump located aft of the capture filter. The pump facilitates flow through the system and minimizes the bow wave at the mouth opening. The cod end, a hollow truncated cone, is also made of UHMW plastic and is designed to 'soften' the landing of zooplankton on the capture surface. SyPRID attaches as a saddle-pack to the Sentry vehicle. Sentry itself is configured with a flight control system that enables autonomous survey paths to altitudes as low as 1.5 m. In its inaugural deployment at the Blake Ridge Seep (2160 m) on the US Atlantic Margin, SyPRID was operated for 6 h at an altitude of 5 m. It recovered plankton samples from that stratum in excellent condition and with greater larval numbers than recovered in a typical 'near-bottom' MOCNESS sample from comparable habitats and depths. The prototype SyPRID and its next generations will enable studies of plankton or other particulate distributions associated with patchy habitats, localized physico-chemical strata (e.g., above and below the thermocline), or discrete water masses at an unprecedented spatial resolution for a large volume system [1]. More information is available by contacting: Carl Kaiser Program Manager Applied Ocean Physics & Engineering NDSF AUV Operations Manager Office Phone: +1 508 289 3269 ckaiser@whoi.edu [1] Billings, A., Kaiser, C., Young, C. M., Hiebert, L. S., Cole, E., Wagner, J. K. S., & Van Dover, C. L. (2017). SyPRID sampler: A large-volume, high-resolution, autonomous, deep-ocean precision plankton sampling system. In Deep Sea Research Part II: Topical Studies in Oceanography (Vol. 137, pp. 297–306). Elsevier BV. https://doi.org/10.1016/j.dsr2.2016.05.007 |

[ table of contents | back to top ]

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## Deployments

### 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. |

[ table of contents | back to top ]

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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)

[ table of contents | back to top ]

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## Funding

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

[ table of contents | back to top ]