

# Jason sample event log from the R/V Atlantis (Alvin AT29-04) cruise in the Blake Ridge Diapir, Cape Fear Diapir, and the United States Western Atlantic Margin during July 2015 (SEEPC project)

**Website:** <https://www.bco-dmo.org/dataset/615127>

**Version:** 2015-10-06

## Project

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

Contributors	Affiliation	Role
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## Dataset Description

**Related Dataset:** [AT29-04: sample log - WAM](#): <http://www.bco-dmo.org/dataset/615510>

## Methods & Sampling

Sampling was performed by HOV Alvin in the Gulf of Mexico using the following methods:

- Grab - using the claw of either port or starboard manipulator to pick up the sample
- Push core - used to collect sediment core samples, or invertebrates residing in the sediment
- Slurp - use of a vacuum system to collect sample from the seafloor or water column

## Data Processing Description

### BCO-DMO Processing:

- replaced blanks with underscores, except for comments column
- removed hyphens from site names

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## Data Files

File
<b>AT2904_dive_log.csv</b> (Comma Separated Values (.csv), 1.05 KB) MD5:c96266e8bf80adca0f781a3b239535d4 Primary data file for dataset ID 615127

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## Parameters

Parameter	Description	Units
dive_id	unique ID for each Alvin dive	unitless
date	sampling date	YYYYMMDD
site	ID associated with particular geographic location/region	unitless
lat	latitude (North is positive; South is negative)	decimal degrees
lon	longitude (East is positive; West is negative)	decimal degrees
depth	depth below surface	meters
comments	free text comments	unitless

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## Deployments

**AT29-04**

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/568866">https://www.bco-dmo.org/deployment/568866</a>
<b>Platform</b>	R/V Atlantis
<b>Report</b>	<a href="http://dmoserv3.whoi.edu/data_docs/SEEPC/AT29-04_SeepC_cruise_report.pdf">http://dmoserv3.whoi.edu/data_docs/SEEPC/AT29-04_SeepC_cruise_report.pdf</a>
<b>Start Date</b>	2015-07-08
<b>End Date</b>	2015-07-28
<b>Description</b>	<p>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 rvddata.us.</p>

#### AT29-04\_Alvin\_Dives

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/615161">https://www.bco-dmo.org/deployment/615161</a>
<b>Platform</b>	HOV Alvin
<b>Start Date</b>	2015-07-09
<b>End Date</b>	2015-07-27
<b>Description</b>	Alvin dives for SEEPC project

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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 download)

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1031050</a>

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