

# Codes for invertebrate larval types found in water column near methane seep sites (SEEPC Project)

**Website:** <https://www.bco-dmo.org/dataset/659951>

**Data Type:** Cruise Results

**Version:**

**Version Date:** 2016-09-28

## Project

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

Contributors	Affiliation	Role
<a href="#">Young, Craig M.</a>	University of Oregon (OIMB)	Principal Investigator
<a href="#">Maslakova, Svetlana A.</a>	University of Oregon (OIMB)	Co-Principal Investigator
<a href="#">Copley, Nancy</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Table of Contents

- [Dataset Description](#)
  - [Data Processing Description](#)
- [Data Files](#)
- [Parameters](#)
- [Project Information](#)
- [Funding](#)

## Dataset Description

This dataset is a list of general larval forms and their codes, used in the larval collection datasets:

### Related datasets:

[SEEPC larval collections: MOCNESS](#)

[SEEPC larval collections: SyPRID](#)

[SEEPC Bivalve DNA Barcoding Results](#)

## Data Processing Description

### BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed some parameters to BCO-DMO standard

[ [table of contents](#) | [back to top](#) ]

## Data Files

File
<b>larval_type_codes.csv</b> (Comma Separated Values (.csv), 623 bytes) MD5:0f1f8df44b2e736108e239898cb46179 Primary data file for dataset ID 659951

[ [table of contents](#) | [back to top](#) ]

## Parameters

Parameter	Description	Units
larval_type	general larval form	unitless
abbreviation	abbreviation for the general larval form	unitless

[ [table of contents](#) | [back to top](#) ]

---

## 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)

[ [table of contents](#) | [back to top](#) ]

---

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1030453</a>

[ [table of contents](#) | [back to top](#) ]