Counts of Protobranch bivalves collected in a series of epibenthic sled samples taken on R/V Endeavor cruise EN447 in the Western North Atlantic (34-39N, 68-70W) in 2008 (ENAB project)

Website: https://www.bco-dmo.org/dataset/542513
Data Type: Cruise Results
Version: 1
Version Date: 2014-12-17

Project
» Evolution in the North Atlantic Basin (ENAB)

Contributors	Affiliation	Role
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Abstract
This dataset includes counts of Protobranch bivalves collected in a series of epibenthic sled samples taken on R/V Endeavor cruise EN447 in the Western North Atlantic (34-39N, 68-70W) in 2008.

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Coverage

Spatial Extent: **N**:39.87987 **E**:-68.0762 **S**:34.915 **W**:-71.228
Temporal Extent: 2008 - 2008

Dataset Description

Protobranch bivalves collected in a series of epibenthic sled samples taken in the western North Atlantic from 1000-5200 m depth. The project investigators are only using the mollusks, all other taxa are unsorted, stored in 95% ethanol and available for others to use.

Methods & Sampling

Using an epibenthic sled, sampling was conducted at 25 stations along a transect from south of Cape Cod to near Bermuda and ranging in depth from 1000 to 5200m. After samples were brought on board, the mud was sieved (1mm mesh) using cold (2-3 degrees C) seawater and the bivalves and gastropods were picked from the samples, identified to genus or species and the first 20-30 individuals frozen (-80) in individual 1.5 ml tubes with any additional individuals placed in ethanol in a common station tube and then stored at -80. All other taxa were placed unsorted in 95% ethanol and are now stored at 4 degrees C. Because the initial sorting was done

at sea under less than ideal conditions, the investigators resorted the samples under a microscope in the lab. So far, over 2600 protobranchs distributed among 27 species have been collected.

Sampling success was good, although somewhat sporadic, especially early in the cruise. The investigators used 2 different sleds - a heavy version with closing door and a lighter version where the doors remained open on ascent. The heavier sled was used for the first 12 samples. Because the collections from the heavier sled were less than expected (based on previous epibenthic sled samples of this area). the lighter sled was used for the remainder of the cruise. The lighter sled usually returned with much better samples, although this could also reflect the investigators' increased experience in sampling later in the cruise.

Samples are currently stored at UMass, but will be moved to the MCZ at Harvard for more permanent storage and curation.

Data Processing Description

BCO-DMO Processing Notes:
- transposed species columns to rows;
- converted lat and lon in degrees and decimal minutes to decimal degrees.

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Data Files

File
protobranchs.csv (Comma Separated Values (.csv), 35.00 KB) MD5:dd7e6c8e5c23e712575ea04135a6af7f Primary data file for dataset ID 542513

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Parameters

Parameter	Description	Units
station	Station number.	unitless
depth	Sample depth.	meters (m)
station_depth_total	Total count of all individuals at that station/depth.	unitless
species	Name of the species.	unitless
count	Total count of individuals of the species at the station/depth.	unitless
lat	Latitude of the sampling station.	decimal degrees
lon	Longitude of the sampling station.	decimal degrees

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Instruments

Dataset-specific Instrument Name	epibenthic sled
Generic Instrument Name	Epibenthic Sled
Dataset-specific Description	Sampling was conducted using an epibenthic sled. 25 stations were sampled along a transect from south of Cape Cod to near Bermuda and ranging in depth from 1000 to 5200m
Generic Instrument Description	An epibenthic sled is a semi-quantitative bottom-sampling device designed to trawl just above the bottom at the sediment water interface (the epibenthic zone). The sled consists of a rectangular steel frame with a mesh net (often more than one) attached to it. Towed along the ocean floor, its weight scrapes into the benthos, collecting any organisms on the surface or in the first few centimeters of sediment. It also collects the organisms in the water column just above the benthos. Descriptions from WHOI and Census of Marine Life.

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Deployments

EN447

Website	https://www.bco-dmo.org/deployment/542217
Platform	R/V Endeavor
Start Date	2008-06-04
End Date	2008-06-21

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Project Information

Evolution in the North Atlantic Basin (ENAB)

Website: http://www.etterlab.umb.edu/Evolution.html

Coverage: Western North Atlantic (34 – 39N, 68 - 70W)

In the early 1990s, we proposed the first explicit model of population differentiation and speciation in the deep-sea fauna, the depth-differentiation hypothesis (Etter and Rex 1991). According to this theory, the potential for population differentiation decreases with depth because the bathyal zone (200-4000 m) has stronger selective gradients and more opportunity for geographic isolation to impede gene flow than does the more environmentally uniform abyssal plain (>4000 m). To determine whether depth-related variation is genetic, and therefore a consequence of evolutionary change, we developed new methods to extract and sequence mitochondrial DNA from archived deep-sea molluscan species collected in earlier expeditions that had been fixed in formalin and preserved in alcohol. These genetic studies, summarized in Etter et al. (2005) and reviewed in this proposal, support the depth-differentiation hypothesis. More importantly, they have revealed

the limitations of using preserved material, and have resulted in a much more specific research agenda for the future.

Here we propose the first deep-sea sampling program specifically directed at answering fundamental evolutionary questions. We describe 3 hypotheses about evolution in the deep sea that emerged from our previous work. 1) The depth differentiation hypothesis suggesting population divergence decreases with depth. 2) The strong break in population structure at 3300 m may represent an unrecognized phylogeographic barrier. 3) Abyssal populations may be sinks that suffer chronic local extinction from being too rare to mate successfully, and are maintained by continued immigration from more abundant bathyal source populations. Our plan is to test each of these hypotheses using deep-sea protobranch bivalves, but for rigorous tests we need multiple independent loci. Nuclear loci are essential as independent measures of population structure, gene flow and historical influences, but are also critical to establish whether some of the remarkable divergences we have documented represent cryptic species. The formalin fixed tissues we have now are too degraded to obtain nuclear loci, so we are proposing to collect fresh samples to develop the nuclear loci (introns). The primary focus of this proposal (first three years of work) will be to collect the samples and develop nuclear markers from those samples that are sufficiently variable in deep-sea protobranchs to test each of the hypotheses and distinguish intra versus interspecific variation.

The deep-sea supports one of the most diverse and unique marine communities, the evolutionary and historical development of which are virtually unknown. The proposed research will contribute very significantly to answering the two most basic question about evolutionary diversification in this vast environment: Where does it occur, and how? It will also create a solid conceptual and methodological context for future evolutionary studies in the deep sea. The source-sink hypothesis of abyssal biodiversity is the most synthetic and comprehensive explanation of large-scale patterns of species diversity in the deep ocean. If proven correct by the proposed study of population genetic structure, it will greatly simplify our understanding of both evolutionary and ecological causes of species diversity patterns.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0726382

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