Metatranscriptome data for pools of 10 nematodes picked from halocline and nearby control sediments from R/V Atlantis cruise AT18-14 in the Eastern Mediterranean in 2011 (DHAB Metazoans project)

Website: https://www.bco-dmo.org/dataset/559351
Version: 27 May 2015
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Project
» Investigations into the Physiological State of DHAB Metazoans (DHAB Metazoans)

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Dataset Description

Metatranscriptome data for pools of 10 nematodes picked from halocline and nearby control sediments; samples collected from the Eastern Mediterranean Deep-sea Hypersaline Anoxic Basins (DHAB) Urania, L'Atalante, Discovery (roughly 35 13N, 21 29 E; depth ~3500 m).

Methods & Sampling

Pushcore and scoop samples were collected by ROV *Jason.* Scoop samples were preserved immediately on the seafloor in RNAlater. Upon retrieval to the ocean surface cores were quickly profiled for oxygen and then subsamples were preserved in RNAlater. Nematodes were picked from whole preserved sediments in the laboratory using a dissection microscope, rinsed 3x in RNAlater, and collected in pools of 10 nematodes for RNA extraction. Metatranscriptome libraries for Illumina sequencing were prepared using 5 micro liters of total RNA and the Ovation 3'DGE System (NuGen) and a Zymo Research Concentrator Kit.

Data Processing Description

All resulting reads were aligned to the protein database NCBI-Nr for initial screening of prokaryotic contaminants. Raw reads are deposited in the Genbank SRA with Run IDs SRR2038214 (Atalante Control) SRR2038319 (Discovery Control), SRR2038321 (Atlalante Lower Interface, or halo cline), SRR2038320 (Atalante White Zone, or upper halo cline), SRR2038323 (Discovery Upper Interface).

Despite polyA enrichment during cDNA creation, which should enrich for eukaryotic mRNA, the resulting

transcriptomic sequences were dominated by bacterial and archaeal sequence reads in most samples (average 60%). Once filtered of contaminant prokaryotic reads, approximately half (average 45%) of the remaining DHAB and Control reads were affiliated to nematode sequences when they were compared to sequences in the nematode-specific transcript database NEMBASE4 (Elsworth, Wasmuth & Blaxter 2011).

BCO-DMO Processing:
- Added latitude and longitude using values previously provided in the "DHAB halocline sediment pyrotags - eukaryotes" dataset.

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Data Files

File
DHAB_nematodes.csv (Comma Separated Values (.csv), 928 bytes) MD5:c30edc000dd5ffd4e9a79edfee92eb02 Primary data file for dataset ID 559351

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Parameters

Parameter	Description	Units
sample	Description of sample.	text
lat	Approximate latitude of sampling site.	decimal degrees
lon	Approximate longitude of sampling site.	decimal degrees
cruise_id	Cruise identification number. (AT18-14 = R/V Atlantis cruise number 18-14)	text
BioSample_id	GenBank BioSample identification number.	text
SRA_exp_id	GenBank Sequence Read Archive experiment identification.	text
SRA_run_id	GenBank Sequence Read Archive run identification.	text
BioProject_id	GenBank BioProject identification and hyperlink.	text

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Instruments

Dataset-specific Instrument Name	ROV Jason
Generic Instrument Name	ROV Jason
Generic Instrument Description	The Remotely Operated Vehicle (ROV) Jason is operated by the Deep Submergence Laboratory (DSL) at Woods Hole Oceanographic Institution (WHOI). WHOI engineers and scientists designed and built the ROV Jason to give scientists access to the seafloor that didn't require them leaving the deck of the ship. Jason is a two-body ROV system. A 10-kilometer (6-mile) fiber-optic cable delivers electrical power and commands from the ship through Medea and down to Jason, which then returns data and live video imagery. Medea serves as a shock absorber, buffering Jason from the movements of the ship, while providing lighting and a bird's eye view of the ROV during seafloor operations. During each dive (deployment of the ROV), Jason pilots and scientists work from a control room on the ship to monitor Jason's instruments and video while maneuvering the vehicle and optionally performing a variety of sampling activities. Jason is equipped with sonar imagers, water samplers, video and still cameras, and lighting gear. Jason's manipulator arms collect samples of rock, sediment, or marine life and place them in the vehicle's basket or on "elevator" platforms that float heavier loads to the surface. More information is available from the operator site at URL. https://ndsf.whoi.edu/jason/

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Deployments

AT18-14

Website	https://www.bco-dmo.org/deployment/58732
Platform	R/V Atlantis
Start Date	2011-11-25
End Date	2011-12-08
Description	According to the pre-cruise plan, the two main science objectives are: (1) water column sampling at two basins: Discovery and Urania Basins, at 3 depths: brine (approx 3500-4000m depth), halocline (~3500m), and reference (~2000m) using a new sampler, the SID-ISMS (under construction), with the vessel CTD/Niskin rosette as backup and (2) sediment coring at both basins, using ROV Jason. Cores will be collected in 3 locations for each basin, the "bathtub ring" where the halocline impinges on the seafloor, the brine, and a reference core sample from above the halocline. Station "Discovery" (35° 19.213' N 21° 41.351' E) will be occupied for 6 days as will "Station 2" (35° 13.674' N 21° 28.58' E). The proposed science activities include: (1) water column sampling using the SID-ISMS to collect in situ filtered water (ship must hold position during deployment while instrument is working) and preserved in situ for molecular work; (2) water column sampling using the SID-ISMS to collect in situ filtered and preserved samples for FISH/microscopy experiments; (3) grazing experiment using SID-ISMS to collect water from halocline of each basin and measure the grazing rates of protozoa over a 6 hour period. The instrument must remain at depth during the 6 hour SID-ISMS grazing experiments. The sampler can be lifted to ~3000 m depth to get it away from the bottom, but the ship must maintain position to avoid dragging the sampler; (4) coring of "bathtub ring" at each basin using the ROV Jason that will be used to locate the bathtub ring and then collect cores at that location; (5) coring of brine at each basin (ROV Jason will reach into the brine from the bathtub ring area and will collect cores). Corers will be a combination of large Jason pushcores (property of co-PI Bernhard) and also some RNAlater samplers (similar to those used by Tim Shank (WHOI). The RNAlater samplers must be fabricated (and perhaps some borrowed from the Shank lab group); and (6) coring of a reference sample from outside the halocline (above) at each basin (normal seawater sediments). The research team aboard the R/V Atlantis, headed south on 25 November 2011 from Piraeus (port of Athens, Greece), to the study areas about 100 miles west of the island of Crete. No cruise report will be submitted for this cruise, but the science party did maintain a blog at the Dive and Discover site for Dive and Discover Expedition 14 - The Mediterranean Deep Brines (URL: http://www.divediscover.whoi.edu/expedition14/index.html). During the cruise, 5 ROV Jason dives, 10 SID-ISMS deployments, 1 multicorer (no samples recovered), and 3 Niskin rosette casts were completed. Image data from the ROV Jason dives for the AT18-14 cruise are available from the WHOI ROV Jason Virtual Van by clicking the year 2011 on the page's left side panel, and then clicking on the link for AT18-14. The cruise was supported by NSF-BIOLOGY awards: http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=0849578 (Edgcomb) http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=1061391 (Bernhard) Original cruise data are available from the NSF R2R data catalog

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Project Information

Investigations into the Physiological State of DHAB Metazoans (DHAB Metazoans)

Coverage: Eastern Mediterranean; 35.3 N, 21.7 E

Invasion of the Body Snatchers!

Description text from the NSF award abstract:
Although it has been known for many decades that metazoans inhabit anoxic habitats either on a periodic, transient, or semi permanent basis, none have been shown to complete an entire life cycle without access to oxygen. The remarkable recent observation that loriciferan metazoans complete a full life cycle without access to dissolved oxygen raises questions in the fields of physiology and evolution. The habitat from which the anaerobic animals were collected is sediment from a Deep Hypersaline Anoxic Brine (DHAB) in the eastern

Mediterranean Sea at a water depth greater than 3 kilometers. DHABs are one of the most extreme marine environments known to science, with a water chemistry considered anathema to eukaryotic life. While the possibility of anaerobic metazoa is exciting, there are other potential explanations that warrant investigation before biology textbooks are rewritten. One alternative scenario is that remnant metazoa bodies were inhabited by anaerobic bacteria and/or archaea.

The overall goal of this project is to determine if the dominant loriciferan and nematode taxon in each of three DHABs represent living populations. Because remnant DNA can be preserved in anoxic settings for long periods of time, the project will include in situ preservation for RNA analysis. Further, because there is also some chance of RNA preservation in these anoxic sedimentary environments, the study will include analyses of the more ephemeral mRNA and also Transmission Electron Microscopy (TEM). On three ship days added to a funded cruise to sample DHABs for other purposes, an ROV will be used to preserve samples in situ. The specific aims are to: (1) Use RNA and DNA analysis to establish if metazoan ribosomal RNA and functional genes were active at the time of in situ preservation in the dominant two metazoan taxa from each DHAB. (2) Identify the prokaryotes associated with DHAB metazoans using RNA analysis and FISH/CARD FISH. (3) Assess the state of cellular ultrastructure in metazoans using TEM to determine the state of organelles (e.g., nuclei, Golgi, hydrogenosomes) and if DHAB metazoans have specialized cellular structures.

Regardless of results, significant information will be obtained. If the metazoans are not living in the DHABs, then a paradigm shift is unnecessary and physiology text books do not need to be rewritten. If the metazoans are living in the DHAB, then a paradigm shift is required.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1061391

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