Lake surface sediment and submarine canyon sediment bacterial V1-V3 iTag sequence libraries collected from CA and MN in 2012.

Website: https://www.bco-dmo.org/dataset/717352
Data Type: Cruise Results
Version: Final
Version Date: 2017-10-19

Project
» Buried alive: Microbial responses to sediment flux with implications for the deep biosphere (Buried Alive)

Program
» Center for Dark Energy Biosphere Investigations (C-DEBI)

Contributors	Affiliation	Role
Harrison, Benjamin Kimball	Central Michigan University	Principal Investigator, Contact
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Dataset Description

Lake surface sediment and submarine canyon sediment bacterial V1-V3 iTag sequence libraries. Submarine Canyon Sediment Bacteria data are presented in Harrison et al (2018). Lake Surface Sediment Bacteria data are published in Harrison et al (2016).

Methods & Sampling

Submarine Canyon Sediment Bacteria:

A ~35cm multicore was collected from La Jolla submarine canyon and sectioned using pre-sterilized tools shipboard at 1cm intervals for preservation at -80 deg C. DNA was extracted from ~2g subsamples using the MoBio PowerSoil DNA kit with an additional heating step applied during lysis. Sequence libraries were assembled for select bulk sediment samples for the v1–v3 region of the 16S rRNA gene using Eubacteria-specific primers (Muyzer et al. 1993) on the Illumina MiSeq platform (Bartram et al. 2011) at the University of Minnesota Genomics Center (UMGC).

Lake Surface Sediment Bacteria (excerpt from Harrison et al., 2016)**:**

A 1.5 m hollow steel wedge was filled with a mixture of dry ice pellets and isopropyl alcohol and then lowered

into the sediment. The coring device was held in place for 15 min and then raised back to the surface, where the dry ice slurry was poured off and unfrozen mud scraped off the sides. The device was then filled with lake surface water, and the frozen core slabs levered off the sides. The recovered frozen cores were wrapped in aluminum foil and placed on dry ice for transport. In the laboratory, the cores were placed on cardboard and kept frozen by regular contact with dry ice pellets. The sampling plane (facing away from the coring device) was smoothed down using a hand-held electric wood planer and utility knives until undisturbed laminae were clearly resolved. Core sections were selected by visual inspection on the basis of lamina thickness and continuity across the sampling plane.

Laminae were excised with pre-sterilized utility knife blades from the top 9 cm of the Twin Lake freeze core: five corresponding to white layers deposited during spring/summer blooms and four corresponding to winter deposition of organic matter and terrigenous particles. 0.2 g of material was collected from the sampling plane as described above, beginning at the lamina base and removing material no greater than 1 mm above that level.

From the Lake McCarrons freeze core, five spring/summer laminae were collected from sub-sampled portions of the 16–24 cm depth range by sequentially exposing the z-plane surface of the horizon with sterilized utility knife blades."

Additional 5 mm frozen sediment wedges cross-cutting sediment laminae were taken at 2 cm intervals between 0 cm and 30 cm depth and 5 cm intervals from 30 cm to 65 cm, using pre-sterilized instruments. Subsamples were stored at -80 deg C for later extraction. An additional ambient-temperature piston core was collected from Lake McCarrons sediment at a position roughly adjacent (within 5 m) to the freeze core site and subsampled on shore within 2 h after removal. The presence and vertical migration of gas bubbles was observed in core sediment. 2 cc sediment aliquots were collected at 10 cm depth intervals starting at 2 cm beneath the sediment-water interface through predrilled windows, excluding the exterior 1 cm of material in contact with the coring tube. Subsamples were stored at -80 deg C.

DNA extraction, amplification and sequencing

Depth intervals corresponding to ambient core subsamples and excised laminae were used to select among the high-frequency bulk sediment samples of the McCarrons core. DNA was extracted from all sediment subsamples with a MoBio Soil DNA kit with an additional heating step added to the lysing step of manufacturer protocols (Harrison and Orphan 2012).

Sequence libraries were assembled for select bulk sediment samples for the v1–v3 region of the 16S rRNA gene using Eubacteria-specific primers (Muyzer et al. 1993) on the Illumina MiSeq platform (Bartram et al. 2011).

Data Processing Description

BCO-DMO Data Processing Notes:

- information was compiled from the submitted metadata forms to form this table of data.
- columns that were created for table: accession, NCBI_link, depth, lat, lon, location, deployment, description

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Data Files

File	
sediment_bacteria.csv	(Comma Separated Values (.csv), 995 bytes) MD5:0067c1e7e2a2509b725f658d20839129
Primary data file for dataset ID 717352	

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Related Publications

Bartram, A. K., Lynch, M. D. J., Stearns, J. C., Moreno-Hagelsieb, G., & Neufeld, J. D. (2011). Generation of Multimillion-Sequence 16S rRNA Gene Libraries from Complex Microbial Communities by Assembling Paired-End Illumina Reads. Applied and Environmental Microbiology, 77(11), 3846–3852. doi:10.1128/aem.02772-10 https://doi.org/10.1128/AEM.02772-10
Methods

Harrison, B. K., Myrbo, A., Flood, B. E., & Bailey, J. V. (2016). Identification of subannual patterns in microbial community signatures from individual sedimentary laminae using a freeze-coring approach. Limnology and Oceanography, 61(2), 735–747. doi:10.1002/lno.10250
Results

,
Methods

Harrison, B. K., Myrbo, A., Flood, B. E., & Bailey, J. V. (2018). Abrupt burial imparts persistent changes to the bacterial diversity of turbidite-associated sediment profiles. Geobiology, 16(2), 190–202. doi:10.1111/gbi.12271
Results

,
Methods

Muyzer, G., De Waal, E. C., & Uitterlinden, A. G. (1993). Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. Applied and Environmental Microbiology, 59(3), 695-700.
Methods

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Parameters

Parameter	Description	Units
accession	NCBI accession number	unitless
NCBI_link	NCBI accession link	unitless
depth	Water sample depth	meters
lat	Latitude	decimal degrees
lon	Longitude	decimal degrees
location	Location where sampling occurred	unitless
deployment	Deployment name and number	unitless
description	Description of NCBI accession	unitless

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Deployments

NH1212

Website	https://www.bco-dmo.org/deployment/717360
Platform	R/V New Horizon
Report	http://gdc.ucsd.edu/index.php?page=22&cruiseid=NH1212&table=cruise_info
Start Date	2012-11-10
End Date	2012-11-16

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Project Information

Buried alive: Microbial responses to sediment flux with implications for the deep biosphere (Buried Alive)

Website: http://www.nsf.gov/awardsearch/showAward?AWD_ID=0939564

Coverage: California, Japan, and Minnesota

Previous investigation of the microbial diversity of unconsolidated marine sediments has not yet constrained the importance of cell transport associated with physical processes of sedimentation and fluid advection. Organisms must migrate in order to maintain position with respect to geochemical gradients, and many marine bacteria exhibit chemotactic behavior to optimize their position. However, certain microorganisms in subsurface environments form persistent attachments to solid particles or are non-motile, leading to the differential burial of a subset of active cells (i.e. what is preserved may differ from what is—or was—active at a given horizon). Deep sedimentary horizons may inherit a microbial community that fails to maintain its optimum position with respect to geochemical profiles, and the deep biosphere ultimately is composed of cells that survive this transition.

We seek to describe the permanence and overprinting of molecular signatures of microbial communities across discrete horizons associated with rapid sedimentation (e.g. turbidite emplacement), changes in bottom-water geochemistry, and depositional unconformities. This work involved the collection and study of sediment cores from 3 lakes in the Minneapolis-St. Paul Metropolitan, an intact turbidite profile from La Jolla Canyon on the California Borderland, and select core samples from a marine transgressive sequence drilled by IODP leg 337 off the Shimokita Peninsula, Japan. These core samples provided a key opportunity to study microbial relationships to sedimentology at high resolution. Preliminary work suggests microbial community signatures retain evidence of cell displacement resulting from sediment disturbance, and distinct patterns in diversity are not overprinted on decadal timescales.

This work was supported through a C-DEBI postdoctoral fellowship.

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Program Information

Center for Dark Energy Biosphere Investigations (C-DEBI)

Website: http://www.darkenergybiosphere.org

Coverage: Global

The mission of the Center for Dark Energy Biosphere Investigations (C-DEBI) is to explore life beneath the seafloor and make transformative discoveries that advance science, benefit society, and inspire people of all ages and origins.

C-DEBI provides a framework for a large, multi-disciplinary group of scientists to pursue fundamental questions about life deep in the sub-surface environment of Earth. The fundamental science questions of C-DEBI involve exploration and discovery, uncovering the processes that constrain the sub-surface biosphere below the oceans, and implications to the Earth system. What type of life exists in this deep biosphere, how much, and how is it distributed and dispersed? What are the physical-chemical conditions that promote or limit life? What are the important oxidation-reduction processes and are they unique or important to humankind? How does this biosphere influence global energy and material cycles, particularly the carbon cycle? Finally, can we discern how such life evolved in geological settings beneath the ocean floor, and how this might relate to ideas about the origin of life on our planet?

C-DEBI's scientific goals are pursued with a combination of approaches:
(1) coordinate, integrate, support, and extend the research associated with four major programs—Juan de Fuca Ridge flank (JdF), South Pacific Gyre (SPG), North Pond (NP), and Dorado Outcrop (DO)—and other field sites;

(2) make substantial investments of resources to support field, laboratory, analytical, and modeling studies of the deep subseafloor ecosystems;
(3) facilitate and encourage synthesis and thematic understanding of submarine microbiological processes, through funding of scientific and technical activities, coordination and hosting of meetings and workshops, and support of (mostly junior) researchers and graduate students; and
(4) entrain, educate, inspire, and mentor an interdisciplinary community of researchers and educators, with an emphasis on undergraduate and graduate students and early-career scientists.

Note: Katrina Edwards was a former PI of C-DEBI; James Cowen is a former co-PI.

Data Management:
C-DEBI is committed to ensuring all the data generated are publically available and deposited in a data repository for long-term storage as stated in their Data Management Plan (PDF) and in compliance with the NSF Ocean Sciences Sample and Data Policy. The data types and products resulting from C-DEBI-supported research include a wide variety of geophysical, geological, geochemical, and biological information, in addition to education and outreach materials, technical documents, and samples. All data and information generated by C-DEBI-supported research projects are required to be made publically available either following publication of research results or within two (2) years of data generation.

To ensure preservation and dissemination of the diverse data-types generated, C-DEBI researchers are working with BCO-DMO Data Managers make data publicly available online. The partnership with BCO-DMO helps ensure that the C-DEBI data are discoverable and available for reuse. Some C-DEBI data is better served by specialized repositories (NCBI's GenBank for sequence data, for example) and, in those cases, BCO-DMO provides dataset documentation (metadata) that includes links to those external repositories.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0939564

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