SRA accession and experiment metadata for Chesapeake Bay sediment incubation in 2019

Website: https://www.bco-dmo.org/dataset/963432
Data Type: Other Field Results, experimental
Version: 1
Version Date: 2025-06-02

Project
» Collaborative Research: Probing the Metabolic and Electrical Interactions of Cable Bacteria in Anoxic Sediments (Anoxic Sediment Bacteria Interactions)

Contributors	Affiliation	Role
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Abstract
Surficial sediment obtained from mesohaline zone of Chesapeake Bay were homogenized and incubated in sediment core liners for 64 days in aerated aquaria. Cable bacteria were allowed to grow unimpeded in a subset of cores. Downward growth of cable bacteria was inhibited by a barrier filter embedded at 0.5 cm in a subset of cores. Sediment cores were destructively sampled and sectioned at 0.5 cm depth increments at 6 times points over the approximately 2 months. This dataset includes Sequence Read Archive (SRA) and BioSample accessions under BioProject PRJNA833464, accessions SAMN27993143 to SAMN27993196 and sampling metadata. These data were published in Liau et al. (2022).

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Coverage

Location: Lab Incubation of sediments from Chesapeake Bay, Station CB4.3C, 38.555050 N 76.427940 W, 26 m
Spatial Extent: **Lat**:38.55505 **Lon**:-76.42794
Temporal Extent: 2019-12-01 - 2020-08-31

Methods & Sampling

A time series incubation experiment was performed to investigate potential interactions between marine cable bacteria and their associated microbial community. Sediment was collected from the main channel of Chesapeake Bay from a mesohaline region that experiences severe and prolonged seasonal oxygen depletion. The upper 10 cm of sediments were homogenized under a gentle N2 gas stream to minimize oxidation, and re-packed into polycarbonate core liners (Ø = 2.5 cm, height = 8 cm), sealed with a silicone stopper at the bottom, and left open to aquarium water at the top. The sediment cores were constructed so that the sediment surface was flush with the core liner. Sediment cores were incubated in continuously aerated aquaria

maintained at bottom water temperature (16oC), in artificial seawater (Red Sea Salts TM), in the dark, at bottom water salinity (S=15.5), and this enabled a rapid proliferation of cable bacteria. Water level and salinity in the aquaria was monitored daily and topped with deionized water as necessary to maintain water level and salinity (approximately twice weekly). At six time points (Days 3, 6, 10, 14, 20, 46), triplicate cores were selected at random for microsensor profiling, followed by destructive sampling. One sediment core was sampled for microscopy and nucleic acid preservation, and a separate sediment core was sampled under anaerobic conditions for porewater geochemistry. Sediment cores were each sectioned at 0.5 cm increments to 3 cm. In a subset of sediment cores, downward growth of cable bacteria was blocked by embedding a 25 mm filter (0.2 µm polycarbonate; Millipore) at 0.5 cm depth. The filter was held in place with a specially constructed filter-holder equipped with a rubber Oring to ensure a water-tight seal. Sediment cores with barrier filters were similarly sampled on Days 3, 20, 46 for microsensor profiling, microscopy, nucleic acid analyses, and porewater geochemistry.

For nucleic acid sequencing analysis, sediments were collected in cryogenic tubes, flash frozen in liquid nitrogen, and stored at -80oC. DNA and RNA were extracted separately. Extracted RNA was purified with Norgen CleanAll DNA/RNA Clean-Up and Concentration Kit (Norgen Biotek). Residual DNA in the RNA extracts was digested with two rounds of TURBO DNAse treatment (Invitrogen) and cDNA synthesis was accomplished by reverse transcription-polymerase chain reaction using SuperScript III First-Strand Synthesis System for RT-PCR (Invitrogen), according to manufacturer's protocol. DNA and cDNA concentrations were quantitated with Qubit dsDNA Broad Range assay kits using Qubit 2.0 fluorometer (Invitrogen). The V4-V5 region of the microbial 16S rRNA gene (DNA and cDNA) was amplified using the modified primer pair of the Earth Microbiome Project (515F-Y/926R; Parada *et al.,* 2016). For DNA samples, amplicons were amplified, barcoded, and sequenced at Bioanalytical Services Laboratory (Baslab) at the Institute of Marine and Environmental Technology (IMET; Baltimore, MD, USA) using an Illumina Miseq platform (2 x 300 bp). For RNA samples, cDNA amplicons were sequenced using an Illumina Miseq platform (2 x 250 bp) by Genewiz (NJ, USA).

BCO-DMO Curation Notes

- Imported "SRA_samples_ChesapeakeBaySediments_IncubationExpt(Liau).xlsx" into BCO-DMO system
- Replace spaces in parameter names with underscores to comploy with BCO-DMO requirements and style
- Export file as "963432_v1_sra_cb_incubation.csv"

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Data Files

File	
963432_v1_sra_cb_incubation.csv	(Comma Separated Values (.csv), 2.19 KB) MD5:27eeebbf846a4ccef5a44608f591c5ff
Primary data file for dataset ID 963432, version 1	

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Related Publications

Liau, P., Kim, C., Saxton, M. A., & Malkin, S. Y. (2022). Microbial succession in a marine sediment: Inferring interspecific microbial interactions with marine cable bacteria. Environmental Microbiology. Portico. https://doi.org/10.1111/1462-2920.16230
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Related Datasets

IsRelatedTo

Malkin, S. (2021) **H2S from microsensor profiles of ex situ sediment cores collected in the Chesapeake Bay and measured during 2017-2018.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-04-07 doi:10.26008/1912/bco-dmo.847949.1 [view at BCO-DMO]
Relationship Description: This dataset includes measurements collected from the same set of field sampling campaigns using the same sediment cores.

Malkin, S. (2021) **pH from microsensor profiles of ex situ sediment cores collected in the Chesapeake Bay and measured during 2017-2018.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-04-07 doi:10.26008/1912/bco-dmo.847923.1 [view at BCO-DMO]
Relationship Description: This dataset includes measurements collected from the same set of field sampling campaigns using the same sediment cores.

Malkin, S. (2022) **Geochemistry and microscopy from incubation experiments of Chesapeake Bay sediments conducted at Horn Point Laboratory.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-11-02 doi:10.26008/1912/bco-dmo.883171.1 [view at BCO-DMO]
Relationship Description: This dataset includes measurements collected from the same set of field sampling campaigns.

Malkin, S. (2022) **O2 microsensor profiling conducted alongside the destructive sampling of Chesapeake Bay sediments during incubation experiments at Horn Point Lab.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-11-08 doi:10.26008/1912/bco-dmo.883412.1 [view at BCO-DMO]
Relationship Description: This dataset includes measurements collected from the same set of field sampling campaigns using the same sediment cores.

References

University of Maryland Center for Environmental Sciences. Chesapeake Bay Surface Sediment Seasonal Study. 2020/05. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA613483.

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Parameters

Parameter	Description	Units
sample_name	Unique Sample Name	unitless
bioproject_accession	Accession number in NCBI	unitless
Treatment	Whether filter was used: Filter, NoFilter	unitless
DayfromStart	Time from start of incubation, (3, 6, 10, 14, 20, 46)	days
Depth_Top	Top depth of the sediment section examined	cm
Depth_Bottom	Bottom depth of the sediment section examined	cm

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Instruments

Dataset-specific Instrument Name	continuously aerated aquaria
Generic Instrument Name	Aquarium
Dataset-specific Description	Sediment cores were incubated in continuously aerated aquaria maintained at bottom water temperature (16oC), in artificial seawater (Red Sea Salts TM), in the dark, at bottom water salinity (S=15.5), and this enabled a rapid proliferation of cable bacteria.
Generic Instrument Description	Aquarium - a vivarium consisting of at least one transparent side in which water-dwelling plants or animals are kept

Dataset-specific Instrument Name	IIllumina Miseq platforms
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	IIllumina Miseq platforms were used for sequencing.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Qubit 2.0 fluorometer
Generic Instrument Name	Fluorometer
Dataset-specific Description	A Qubit 2.0 fluorometer was used to quantify amplified DNA or cDNA.
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

Dataset-specific Instrument Name	Uwitec gravity corer
Generic Instrument Name	Gravity Corer
Dataset-specific Description	A Uwitec gravity corer was used to collect sediments.
Generic Instrument Description	The gravity corer allows researchers to sample sediment layers at the bottom of lakes or oceans. The coring device is deployed from the ship and gravity carries it to the seafloor. From: http://www.whoi.edu/instruments/viewInstrument.do?id=1079

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Project Information

Collaborative Research: Probing the Metabolic and Electrical Interactions of Cable Bacteria in Anoxic Sediments (Anoxic Sediment Bacteria Interactions)

Coverage: Chesapeake Bay sediments; Mid-Atlantic Coastal sediments

NSF Award Abstract:
Marine sediments represent the world's largest repository of stored organic carbon, and understanding how microorganisms break down this carbon is an imperative for understanding global carbon cycling. Yet long-standing questions remain regarding how networks of microorganisms work together to accomplish the complete breakdown of organic carbon in marine sediments. Sediment microbes interact in a myriad of ways that couple their metabolism to the break down of organic carbon, including by sharing products of metabolism. Accumulating evidence further suggests that some microorganisms can interact by transferring electrons directly to other unrelated microorganisms. This ability occurs across diverse microorganisms and appears to be widespread in the biosphere, particularly in anaerobic environments such as marine sediments. This project addresses emerging questions about the identity and metabolic linkages between microorganisms that work together in natural anaerobic marine and estuarine sediments to break down organic carbon. The investigators approach these questions by focusing on the influence of a keystone bacterium on its surrounding microbial community. "Cable bacteria" are a recently discovered group of long filamentous bacteria that act as electrical conductors in aquatic sediments providing a conduit for electrons to commute from deeper sulfidic sediments up to the surface oxygen layer by the process of centimeter-scale electron transport. Since their discovery about 6 years ago, these bacteria have been observed in a wide range of depositional sedimentary environments, often at extremely high cell densities. Where these bacteria are abundant, such as in coastal marine muds, they drive intense localized changes in pH and strongly influence the mineral cycling. This research explores the direct and indirect influence of cable bacteria on the metabolic activity of associated microorganisms. This project also advance the education and training of two early-career investigators, two PhD students, and undergraduate students. The skills and expertise gained from these PhD research projects will enable the students to be competitive in academic pursuits and in bioinformatics and technology applications relevant to private industry. The scientific discoveries emerging from this work is being incorporated into undergraduate and graduate level courses in marine microbial ecology. The research team will reach out to the broader community by hosting public lectures promoting a better understanding of environmental microbial ecology.

The proposed work is to investigate the role of cable bacteria in structuring sediment microbial communities. Due to their growth strategy and morphology, cable bacteria are particularly amenable to experimental manipulation, providing an outstanding opportunity to better understand community interactions among microorganisms in a natural and complex anaerobic environment. The investigators will explore the interactions and relationships between cable bacteria and their associated microbial community by manipulating the growth and activity of cable bacteria and quantifying the resultant microbial community response. Specifically, this project aims to (1) identify microorganisms whose growth is enhanced by cable bacteria, (2) identify metabolic

processes linked with cable bacteria activity using metatranscriptomics, (3) test specific metabolic links between sediment microorganisms and cable bacteria activity using a DNA-stable isotope probing (SIP) approach, and (4) visually confirm the identity and quantify key microorganisms associated with cable bacteria using microscopy. As more is learned about the identity and the mechanisms by which microorganisms are metabolically linked in anoxic sediments, we will be better able to understand and make predictions about how microorganisms function in their environment and how they can be utilized in bioengineered systems.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756877

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