Temperature, salinity, water isotope, and inorganic nutrient profiles of sea ice core sections collected offshore near Utqiaġvik, Alaska, USA in May 2017 and 2018.

Website: https://www.bco-dmo.org/dataset/816755
Data Type: Other Field Results
Version: 1
Version Date: 2020-06-25

Project
» Understanding How Virus Infection Affects Gene Flow and Microbial Evolution in Extreme Polar Environments (Arctic Subzero Brines)

Program
» Marine Microbiology Initiative (MMI)

Contributors	Affiliation	Role
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Abstract
Sea ice cores were collected at 71.2944˚N, 156.7153˚W and 71.3729˚N, 156.5073˚W in May 2017 and at 71.4730˚N, 156.7294˚W in May 2018. Sea ice cores were drilled with a MARK II ice auger (Kovacs Enterprise). The cores were sectioned immediately after collection with a clean rust-proof, custom alloy bow saw in the field in 5 cm sections and each was collected in sterile Whirlpak® bags. Core sections were melted at room temperature before volumes were allocated for nutrient, water isotope, and bulk salinity measurements. Analytical measurements were made upon sample return to the University of Washington and to the University of Alaska Fairbanks. Associated temperature profile data were acquired from the nearby UAF Sea Ice Mass Balance site.

Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
- Data Files
- Related Publications
- Parameters
- Project Information
- Program Information
- Funding

Coverage

Spatial Extent: **N**:71.473 **E**:-156.5049 **S**:71.3729 **W**:-156.7294
Temporal Extent: 2017-05-06 - 2018-05-09

Dataset Description

Temperature, salinity, water isotope, and inorganic nutrient profiles of sea ice core sections collected offshore near Utqiaġvik, Alaska, USA in May 2017 and 2018.

Methods & Sampling

Sea ice cores were collected at 71.2944˚N, 156.7153˚W and 71.3729˚N, 156.5073˚W in May 2017 and at 71.4730˚N, 156.7294˚W in May 2018. Sea ice cores were drilled with a MARK II ice auger (Kovacs Enterprise). The cores were sectioned immediately after collection with a clean rust-proof, custom alloy bow saw in the field in 5 cm sections and each was collected in sterile Whirlpak® bags. Core sections were melted at room temperature before volumes were allocated for nutrient, water isotope, and bulk salinity measurements. Analytical measurements were made upon sample return to the University of Washington and to the University of Alaska Fairbanks. Associated temperature profile data were acquired from the nearby UAF Sea Ice Mass Balance site.

[table of contents | back to top]

Data Files

File
profile.csv (Comma Separated Values (.csv), 10.52 KB) MD5:d7bace532f951e5bafa473a1fcb736eb Primary data file for dataset ID 816755

[table of contents | back to top]

Related Publications

Colangelo-Lillis, J., Eicken, H., Carpenter, S. D., & Deming, J. W. (2016). Evidence for marine origin and microbial-viral habitability of sub-zero hypersaline aqueous inclusions within permafrost near Barrow, Alaska. FEMS Microbiology Ecology, 92(5), fiw053. doi:10.1093/femsec/fiw053
Methods

Cooper, Z. S., Rapp, J. Z., Carpenter, S. D., Iwahana, G., Eicken, H., & Deming, J. W. (2019). Distinctive microbial communities in subzero hypersaline brines from Arctic coastal sea ice and rarely sampled cryopegs. FEMS Microbiology Ecology, 95(12). doi:10.1093/femsec/fiz166
Results

[table of contents | back to top]

Parameters

Parameter	Description	Units
sheet_name	name of the sheet in the source file	unitless
location	text description of the location	unitless
date	date presented following ISO-8601 format	unitless
Sea_ice_depth	depth in sea ice	centimeters (cm)
Bulk_salinity	Bulk salinity by conductivity meters	unitless
UAF_Mass_Balance_Temperature	UAF Mass Balance Temperature	degrees Celsius (C)
PO4	PO4	microMole (uM)
SiO4	SiO4	microMole (uM)
NO3	NO3	microMole (uM)
NO2	NO2	microMole (uM)
NH4	NH4	microMole (uM)
d2H	delta 2 H	parts per thousand (o/oo)
d18O	delta 18 O	parts per thousand (o/oo)
notes	comments	unitless
lat	latitude with positive values indicating North	decimal degrees
lon	longitude with negative values indicating West	decimal degrees

[table of contents | back to top]

Project Information

Understanding How Virus Infection Affects Gene Flow and Microbial Evolution in Extreme Polar Environments (Arctic Subzero Brines)

GBMF Summary:

In support of developing a virus–bacterium–alga culture system and advancing methods to investigate how virus infection and stress impact gene flow and microbial evolution in cold, highly saline environments.

[table of contents | back to top]

Program Information

Marine Microbiology Initiative (MMI)

Website: https://www.moore.org/initiative-strategy-detail?initiativeId=marine-microbiology-initiative

A Gordon and Betty Moore Foundation Program.

Forging a new paradigm in marine microbial ecology:

Microbes in the ocean produce half of the oxygen on the planet and remove vast amounts of carbon dioxide, a greenhouse gas, from the atmosphere. Yet, we have known surprisingly little about these microscopic organisms. As we discover answers to some long-standing puzzles about the roles that marine microorganisms play in supporting the ocean's food webs and driving global elemental cycles, we realized that we still need to learn much more about what these organisms do and how they do it—including how they evolved and contribute to our ocean's health and productivity.

The Marine Microbiology Initiative seeks to gain a comprehensive understanding of marine microbial communities, including their diversity, functions and behaviors; their ecological roles; and their origins and evolution. Our focus has been to enable researchers to uncover the principles that govern the interactions among microbes and that govern microbially mediated nutrient flow in the sea. To address these opportunities, we support leaders in the field through investigator awards, multidisciplinary team research projects, and efforts to create resources of broad use to the research community. We also support development of new instrumentation, tools, technologies and genetic approaches.

Through the efforts of many scientists from around the world, the initiative has been catalyzing new science through advances in methods and technology, and to reduce interdisciplinary barriers slowing progress. With our support, researchers are quantifying nutrient pools in the ocean, deciphering the genetic and biochemical bases of microbial metabolism, and understanding how microbes interact with one another. The initiative has five grant portfolios:

Individual investigator awards for current and emerging leaders in the field.
Multidisciplinary projects that support collaboration across disciplines.
New instrumentation, tools and technology that enable scientists to ask new questions in ways previously not possible.
Community resource efforts that fund the creation and sharing of data and the development of tools, methods and infrastructure of widespread utility.
Projects that advance genetic tools to enable development of experimental model systems in marine microbial ecology.
We also bring together scientists to discuss timely subjects and to facilitate scientific exchange.

Our path to marine microbial ecology was a confluence of new technology that could accelerate science and an opportunity to support a field that was not well funded relative to potential impact. Around the time we began this work in 2004, the life sciences were entering a new era of DNA sequencing and genomics, expanding possibilities for scientific research – including the nascent field of marine microbial ecology. Through conversations with pioneers inside and outside the field, an opportunity was identified: to apply these new sequencing tools to advance knowledge of marine microbial communities and reveal how they support and influence ocean systems.

After many years of success, we will wind down this effort and close the initiative in 2021. We will have invested more than $250 million over 17 years to deepen understanding of the diversity, ecological activities and evolution of marine microbial communities. Thanks to the work of hundreds of scientists and others

involved with the initiative, the goals have been achieved and the field has been profoundly enriched; it is now positioned to address new scientific questions using innovative technologies and methods.

[table of contents | back to top]

Funding

Funding Source	Award
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF5488

[table of contents | back to top]