Brine samples from both sea ice and cryopeg near Utqiaġvik, Alaska, USA from 2017-05-08 to 2018-05-10

Website: https://www.bco-dmo.org/dataset/817221
Data Type: Other Field Results
Version: 1
Version Date: 2020-06-30

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
Deming, Jody W.	University of Washington (UW)	Principal Investigator
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Abstract
Brine samples were collected from both sea ice and cryopeg near Utqiaġvik, Alaska, USA. Snow and ice thickness along with sackhole core depth information are available for sea ice samples. Bacterial and viral abundances along with temperature, pH, salinity, inorganic nutrients, organic nutrients, EPS, and water isotopes were measured for select samples.

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Coverage

Spatial Extent: **N**:71.473 **E**:-156.5049 **S**:71.2944 **W**:-156.7294
Temporal Extent: 2017-05-06 - 2018-05-11

Dataset Description

Brine samples were collected from both sea ice and cryopeg near Utqiaġvik, Alaska, USA. Snow and ice thickness along with sackhole core depth information are available for sea ice samples. Bacterial and viral abundances along with temperature, pH, salinity, inorganic nutrients, organic nutrients, EPS, and water isotopes were measured for select samples.

Methods & Sampling

Sea ice brines were collected by the sackhole brine collection method. Briefly, sea ice cores were drilled approximately three quarters of the way through the ice column and removed to allow brine from the surrounding sea ice to percolate for collection over several hours. Brines were collected and pooled into 20 L acid-washed and sample rinsed cubitainers for transport to the Barrow Arctic Research Center.

Cryopeg brines were collected from discrete boreholes drilled in the floor of the CRREL Ice Mine (also known as the Barrow Permafrost Tunnel). Briefly, permafrost boreholes were drilled with an ethanol-rinsed SIPRE corer, and brines were collected from the boreholes with a sterile vacuum pump apparatus. Detailed notes about cryopeg brine collection can be found in Cooper et al. 2019.

Biological abundance samples were fixed in the field immediately after each sample collection with formaldehyde at a final concentration of 2%. All samples were placed in insulated containers and transported to the Barrow Arctic Research Center within a few hours of collection and stored at 4˚C until aliquots were taken for each measurement. Nutrient and isotope aliquots were frozen and stored at -20˚C for transport back to the University of Washington and the University of Alaska Fairbanks. All analytical methods except for isotope measurements are detailed in Cooper et al. 2019

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- converted date to follow ISO 8601 convention

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Data Files

File
sample.csv (Comma Separated Values (.csv), 12.58 KB) MD5:57ce30f8f8a75d82daf269c19c3cb357 Primary data file for dataset ID 817221

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Related Publications

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

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Parameters

Parameter	Description	Units
sheet_name	name of the sheet in the source file	unitless
Station	Station identifier	unitless

lat	latitude with positive values indicating North	decimal degrees
lon	longitude with negative values indicating West	decimal degrees
Date	date of sampling following ISO-8601 format	unitless
Sample_type	type of sample collected	unitless
Snow_thickness	Thickness of the snow	centimeters (cm)
Ice_thickness	Thickness of the ice	centimeters (cm)
Sackhole_Ice_Borehole_depth	Sackhole/Ice/Borehole depth	centimeters (cm)
Temperature	UNKNOWN	degrees Celsius (C)
pH	pH observed by paper indicator strips	unitless
Salinity	Salinity observed by refractometer for brines or by conductivity for bulk (direct-melted) sea ice	parts per thousand (ppt)
Bacterial_abundance	Bacterial abundance	cells per milliliter (cells/mL)
VLP_abundance	Virus like particle abundance	virus like particle per milliliter (VPL/mL)
PON_ug_N_mL	Particulate organic nitrogen	micrograms of Nitrogen per milliliter (µg N/mL)
POC_ug_C_mL	Particulate organic Carbon	micrograms of Carbon per milliliter (µg C/mL)
dEPS	dissolved extracellular polyssacharide substances (through a 0.4 micron filter)	g glu-eq/mL
pEPS	particulate extracellular polyssacharide substances (over a 0.4 micron filter)	g glu-eq/mL
Chl_a	Chlorophyll A	milligrams per meter cubed (mg/m3)
Chl_a_Phaeo_ratio	ratio of chlorophyll a to phaeopigment	unitless

DOC_uM_C	Dissolved organic carbon	micromole Carbon (µM C)
PO4	PO4	micromole (µM)
SiO4	SiO4	micromole (µM)
NO3	NO3	micromole (µM)
NO2	NO2	micromole (µM)
NH4	NH4	micromole (µM)
d2H	delta 2 H	parts per thousand (o/oo)
d18O	delta 18 O	parts per thousand (o/oo)
pcnt_dividing_cells	percent dividing cells	unitless
PON_mg_N_mL	Particulate organic nitrogen	milligrams Nitrogen per milliliter (mg N/mL)
POC_mg_C_mL	Particulate organic Carbon	milligrams Carbon per milliliter (mgCN/mL)

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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.

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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.

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Funding

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

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