# 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 |
|---|---|---|
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| Eicken, Hajo | University of Alaska Fairbanks (UAF) | Co-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)<br>MD5:57ce30f8f8a75d82daf269c19c3cb357<br>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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