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)

Contributors	Affiliation	Role
Deming, Jody W.	University of Washington (UW)	Principal Investigator
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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.

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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.

Acquisition Description

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.

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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

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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

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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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Funding

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

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