Under the ice bacterial cultures and genome sequences from the R/V Kronprins Haakon in the Arctic Ocean from May 18 to 21, 2023

Website: https://www.bco-dmo.org/dataset/965379
Data Type: experimental, Other Field Results
Version: 1
Version Date: 2025-06-18

Project
» Collaborative Research: Drivers and effects of latent phage activation in marine SAR11 (SAR11 Prophage)

Contributors	Affiliation	Role
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Abstract
Bacteria were cultured and sequenced from the Arctic Ocean under 2-meter-thick sea ice to identify patterns of gene, loss, and rearrangement. Cultures were obtained by high-throughput dilution to extinction cultivation using cryopreserved samples. Bacteria selected for genome sequencing were grown in 1 liter of Puget Sound seawater media and sequenced using the Oxford Nanopore Technologies (ONT) R10.4.1 Flongle flow cells with the SQK-RAD114 rapid library prep kit (Oxford Nanopore Technologies, Oxford, United Kingdom). Time-series data indicate that this collection represents up to 60% of the marine bacterial community in the Arctic. Their complete genomes provide insights into the evolutionary processes that underlie diversity and adaptation to the Arctic Ocean.

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Coverage

Spatial Extent: **Lat**:81.04 **Lon**:10.62
Temporal Extent: 2023-05-21

Methods & Sampling

Samples for cultivation were collected at 81.04° N, 10.62° E, from 25 meters (m) below the ice/water interface using a Hydro-Bios 2-liter (L) water sampler. Fifty milliliters (mL) were transferred to a polycarbonate bottle and then 1 mL of seawater was amended to 10% (v/v) glycerol, flash frozen in liquid nitrogen, and stored at -80 degrees Celsius (°C) until used for high-throughput dilution to extinction cultivation. Seawater for culture media (10 L) was collected at 80.96° N, 9.66° E from 1 m below the ice/water interface into acid washed and miliQ rinsed cubitainers. Seawater was then filter-sterilized using a tangential flow filtration (TFF) system equipped with a 30 kDa Pellicon XL Polyethersulfone Biomax filter (MilliporeSigma, Burlington, MA). The resulting media was collected in 1 L acid-washed and autoclaved polycarbonate bottles, incubated for 2 months at 4 °C, and

checked for bacterial growth to ensure sterility prior to use.

Data Processing Description

Cultures selected for whole genome sequencing were revived from freezer stocks in 1 L acid washed and autoclaved polycarbonate bottles containing TFF sterilized Puget Sound seawater media. Cells were collected on 47-millimeter (mm) 0.2-micrometer (µm) pore size Isopore membrane filters (MilliporeSigma, Burlington, MA) when cultures reached maximum cell densities (between 10^5 and 10^6 cells per mL). High molecular weight DNA was extracted using the Autogen Quickgene DNA Tissue Kit (Autogen, Holliston, MA) following the extraction protocol for animal tissue with minor modifications as noted below.

Filters were cut into small pieces using sterile forceps and scissors and placed in sterile 2 mL DNA LoBind tubes (Eppendorf, Hamburg, Germany) containing 200 microliters (µL) of TE buffer. Filters were then frozen at -80 °C for 20 minutes and heated until thawed at 95 °C. All recommended extraction volumes were doubled, and DNA was eluted in 200 µL of molecular grade water. DNA was cleaned using 1X volume:volume DNA magnetic beads (Sergi Lab Supplies, Seattle WA) with two 80% ethanol washes, then eluted in 20 µL of molecular grade water. DNA was quantified using a Qubit dsDNA Quantitation High Sensitivity kit (Invitrogen, Waltham, MA) and sequenced using the Oxford Nanopore Technologies (ONT) R10.4.1 Flongle flow cells with the SQK-RAD114 rapid library prep kit (Oxford Nanopore Technologies, Oxford, United Kingdom). Bases were called with Dorado (github.com/nanoporetech/dorado), using the dna_r10.4.1_e8.2_400bps_hac@v4.2.0 model.

BCO-DMO Processing Description

- Imported original file "Arctic_genomes_metadata.xlsx" into the BCO-DMO system.
- Converted Date column to YYYY-MM-DD format.
- Removed "° N" and "° E" from the Lat and Lon columns.
- Renamed fields to comply with BCO-DMO naming conventions.
- Saved the final file as "965379_v1_arctic_genomes.csv".

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Data Files

File	
965379_v1_arctic_genomes.csv	(Comma Separated Values (.csv), 4.20 KB) MD5:53765128df4dd8829a9c83711714144b
Primary data file for dataset ID 965379, version 1	

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Related Datasets

IsRelatedTo

University of Washington. Cultivation based population genomics of under sea ice bacteria. 2024/06. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA1129510. NCBI:BioProject: PRJNA1129510.

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Parameters

Parameter	Description	Units
isolate	cultivation number	unitless
Date	date of sample collection	unitless
Lat	latitude of sample collection	decimal degrees North
Lon	longitude of sample collection	decimal degrees East
id	taxonomic name	unitless
genome_length	total length in nucleotides	number of nucleotides
sequencing_coveargе	depth of sequence coverage	unitless
pcnt_gc	percent of guanine and cytosine residues	unitless
coding_ratio	ratio of protein coding genes	unitless
rRNA	number of 5S, 16S, and 23S ribosomal RNAs	unitless
genome_accession	NCBI accession number	unitless
bioproject	NCBI BioProject number	unitless
biosample	NCBI BioSample number	unitless
sequence_read_archive	NCBI SRA number	unitless

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Instruments

Dataset-specific Instrument Name	Hydro-Bios 2 L water sampler
Generic Instrument Name	Discrete water sampler
Generic Instrument Description	A device that collects an in-situ discrete water sample from any depth and returns it to the surface without contamination by the waters through which it passes, such as a water bottle.

Dataset-specific Instrument Name	Oxford Nanopore Technologies (ONT) R10.4.1 Flongle flow cells with the SQK-RAD114 rapid library prep kit
Generic Instrument Name	Nanopore Sequencer
Generic Instrument Description	A proprietary high-throughput DNA sequencing technology from Oxford Nanopore Technologies that can directly identify and sequence DNA molecules as they pass through nanopores, driven by electrophoresis.

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Deployments

2023007008

Website	https://www.bco-dmo.org/deployment/965511
Platform	R/V Kronprins Haakon
Start Date	2023-05-18
End Date	2023-05-21
Description	The cruise combines scientific objectives of this research council of Norway BREATHE project with a field school outreach program that trains early career researchers on the multidisciplinary research of Arctic sea ice. BREATHE sea ice field school Research Council of Norway (325405) Norwegian Institute of Marine Research (Cruise 2023007008) May 18–21, 2023 Chief Scientist Karley Campbell and Polona Itkin

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Project Information

Collaborative Research: Drivers and effects of latent phage activation in marine SAR11 (SAR11 Prophage)

Coverage: Puget Sound cruises & Laboratory experiments at UW

NSF Award Abstract:

Viruses are the most abundant biological entities in the ocean. When they infect plankton, they can alter food webs, induce shifts in nutrient cycles, and enhance genetic exchange. However, the mechanisms that control these important processes are largely unknown, which has limited our ability to predict infection outcomes in nature. The primary goal of this study is to identify key chemical, physical, and biological factors that influence host-virus interactions in cultured bacterioplankton and to use this information to build mathematical models

that predict infection dynamics in diverse marine ecosystems. Most of the marine viruses available for detailed study kill bacteria following infection. This novel study focuses on SAR11, the most abundant marine bacteria, which harbor dormant viruses called prophages, to determine what causes prophage activation and host death. Specifically, the research team uses field surveys and laboratory experiments with SAR11-prophage pairs to generate data and mathematical models to predict the outcomes of viral infections in SAR11 and other marine microbes.

The conditions that trigger prophage activation and their corresponding contributions to ecosystem processes are largely hypothetical, due primarily to difficulties identifying and culturing host cells with prophages. It is becoming increasingly clear that the impact and importance of these infections are under-characterized and under-estimated. The proposed research revises estimates of prophage activation in globally-important SAR11 by quantifying infection occurrence, identifying prophage activation inducers, and testing the effects of maintaining virus DNA in the host genomes. The frequency of prophage infections is determined by analyzing bacterial metagenomes generated with long-read sequencing technology. Controlled growth experiments under a range of conditions that cause stress (physical, chemical, and biological) and evaluation of shifts in gene expression are employed to identify drivers of prophage activation. The outcomes of prophage infections in culture serve to parameterize key interactions in numerical models that can then predict outcomes in nature. This study fills critical gaps in knowledge about the mechanisms that maintain the large and genetically diverse populations of bacteria and viruses in the ocean and has the potential to change our understanding and capacity to predict host-virus interactions under changing environmental conditions.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2201645

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