NCBI accession metadata for transcriptomic expression sequences run from cultures of Alteromonas macleodii MIT1002 grown with bacterial extracellular vesicles as a carbon source

Website: https://www.bco-dmo.org/dataset/997637
Data Type: experimental
Version: 1
Version Date: 2026-04-28

Project
» Collaborative Research: Quantifying the role of microbial extracellular vesicles in marine dissolved organic matter production and consumption (VesicleDOM)

Contributors	Affiliation	Role
Biller, Steven	Wellesley College	Principal Investigator
Longnecker, Krista	Woods Hole Oceanographic Institution (WHOI)	Co-Principal Investigator
Stein, Ashley	Wellesley College	Scientist
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
To examine how marine bacteria utilize extracellular vesicles as a nutrient source, we compared the transcriptomic response of Alteromonas macleodii MIT1002 cells grown on purified extracellular vesicles (purified from Alteromonas MIT1002 or Prochlorococcus MIT9312) as compared to glucose or a no-carbon control. Our study provides insights into the cellular mechanisms through which these cells may take up extracellular vesicle material and the specific types of molecules within vesicles that can be utilized for carbon and/or energy. This dataset contain accession metadata for sequences run from cultures of Alteromonas macleodii MIT1002. Data were collected by Dr. Ashley Stein and Dr. Steven Biller, Wellesley College. The raw RNAseq reads have been deposited in the National Center for Biotechnology Information (NCBI) GEO database under accession GSE314643.

Table of Contents

Coverage

Location: Wellesley College, Wellesley MA
Temporal Extent: 2024-08 - 2024-08

Methods & Sampling

This lab experiment was conducted at Wellesley College, Welleslsey MA in August 2024. *Alteromonas macleodii* MIT1002 were grown at 24 °C in a natural seawater-based media containing 0.2 µM filtered, autoclaved seawater supplemented with 3 mM NH_4Cl, 50 µM NaH_2PO_4, Pro99 trace metals, and 0.01% (w/v) glucose. Overnight cultures of *Alteromonas* were washed twice in media lacking added glucose (-C). Cultures were diluted to 5e6 cells/mL and supplemented with with either 1x PBS (negative control), *Prochlorococcus* extracellular vesicles, *Alteromonas* extracellular vesicles, or glucose as a carbon source, each in triplicate. Cultures were incubated at 24°C with shaking at 120 rpm. Samples were collected at two timepoints

(representing early and late exponential growth phase) by pelleting at 10,000 xg for 15 minutes, flash freezing on dry ice, and storing at -80 °C. Cells were resuspended and lysed in 600 µL Zymo TriReagent and RNA was extracted using the Zymo Trizol RNA Extraction RNA spin column kit following the manufacturer's protocol. The columns were washed and treated with DNAse per manufacturers recommendation. RNA was eluted in 50 µL of RNase-free water and quantified using the Qubit RNA High Sensitivity kit (Invitrogen). Ribosomal RNA was depleted using the Qiagen QIAseq FastSelect kit, then the Kapa RNA Hyperprep kit. Paired-end 150nt sequencing data was generated on an Illumina NovaSeq X. RNA library preparation and sequencing was carried out by the Bauer Core Facility (Harvard University).

BCO-DMO Processing Description

- Loaded "Alteromonas_GEO_accessions.tsv" (TSV format) using filename as resource name, with "nd" and empty strings treated as missing values
- Deleted field "GEO_link"
- Reordered fields to: Biosample_ID, SRA_Experiment_ID, GEO_Sample_ID, Bacterium, Carbon_Substrate, Timepoint, Replicate
- Renamed resource to "997637_v1_alteromonas_geo_accessions"
- Output saved as 997637_v1_alteromonas_geo_accessions.csv

[table of contents | back to top]

Parameters

Parameter	Description	Units
Biosample_ID	NCBI BioSample accession number, contains descriptive information about the physical biological materials	unitless
SRA_Experiment_ID	NCBI Sequence Read Archive accession number for this experimental sample	unitless
GEO_Sample_ID	NCBI Gene Expression Omnibus accession number	unitless
Bacterium	Bacterial strain sequenced	unitless
Carbon_Substrate	Carbon source added to culture	unitless
Timepoint	Culture growth phase when sampled	unitless
Replicate	Biological replicate	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina NovaSeq X
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Ribosomal RNA was depleted using the Qiagen QIAseq FastSelect kit, then the Kapa RNA Hyperprep kit. Paired-end 150nt sequencing data was generated on an Illumina NovaSeq X.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Incubator
Generic Instrument Name	Incubator
Dataset-specific Description	Cultures were incubated at 24°C with shaking at 120 rpm.
Generic Instrument Description	A device in which environmental conditions (light, photoperiod, temperature, humidity, etc.) can be controlled. Note: we have more specific terms for shipboard incubators (https://www.bco-dmo.org/instrument/629001) and in-situ incubators (https://www.bco-dmo.org/instrument/494).

[table of contents | back to top]

Project Information

Collaborative Research: Quantifying the role of microbial extracellular vesicles in marine dissolved organic matter production and consumption (VesicleDOM)

Coverage: Laboratory; Vineyard Sound, MA, USA; Bermuda Atlantic Time Series Station

NSF Award Abstract:
Microbial production and consumption of organic carbon play critical roles in the marine food web and global carbon cycling. Bacteria release organic matter in a variety of chemical forms and in diverse contexts, ranging from individual molecules to small aggregates and larger biological particles. In recent years we have come to understand that most, if not all, marine microbes release nanoscale structures called extracellular vesicles from their surfaces. These discrete particles, which are abundant in the oceans, are capable of transporting multiple classes of organic molecules between organisms and can serve as a potential nutrient source for other microbes. Extracellular vesicles thus represent a potentially important component of marine microbial food webs, but the magnitude and dynamics of this contribution are unknown. Further, the packaging of material within vesicles may influence the accessibility of this organic material as compared with truly ‘dissolved’ substances to different groups of marine organisms, potentially biasing nutrient exchanges. Broader impacts of this work is providing hands-on research experiences for female undergraduate students - including those from groups historically underrepresented in STEM fields - and training in data analysis tools.

The goal of this project is to advance the understanding of the role that extracellular vesicles play in marine dissolved organic carbon pools and microbial food webs. To determine the contribution of vesicles to organic matter release by marine microbes, the investigators are quantifying the fraction of excreted carbon and nitrogen associated with vesicles released by multiple marine cyanobacteria and heterotrophs. The project is examining how vesicles are ‘consumed’ by heterotrophs to calculate a mass balance of vesicle utilization and

produce detailed gene expression data to explore how cells respond to the presence of vesicles. Finally, experiments with coastal and oligotrophic marine communities are providing insights into which organisms utilize vesicles in the field, and whether they are broadly accessible to all microbes or are instead preferentially consumed by a subset of microbes. Collectively, these experiments are opening up a new area of research into the mechanisms underlying the microbial loop and provide foundational insights into the roles of extracellular vesicles in ocean ecosystems.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2049004
NSF Division of Ocean Sciences (NSF OCE)	OCE-2044346

[table of contents | back to top]