

NCBI accession metadata for microbial community responses to bacterial extracellular vesicles in the Sargasso Sea, collected on R/V Atlantic Explorer cruises AE2412 and AE2427 in Apr and Nov 2024

Website: <https://www.bco-dmo.org/dataset/997617>

Data Type: Cruise Results, 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
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Abstract

This experiment details changes in marine microbial community composition in response to different carbon sources. To determine whether marine microbes can utilize bacterial extracellular vesicles as a carbon source, we conducted bottle incubations in the Sargasso Sea onboard the R/V Atlantic Explorer kept in a flow-through system. Surface seawater samples were supplemented with either buffer (control), glucose, or extracellular vesicles purified from the cyanobacterium *Prochlorococcus* or the heterotroph *Alteromonas*. Community samples were collected over a period of four days aboard the R/V Atlantic Explorer, during cruises AE2412 and AE2427 in April and November 2024. 6S rRNA amplicon sequencing (targeting the V4-V5 region) was carried out to enable analysis of changes in the community. This dataset provides the accession metadata for this sequencing. These data will be useful in understanding how bacterial extracellular vesicles - numerically abundant nanoscale structures released by all cells - function as a component of marine dissolved organic carbon pools. Samples were collected by Samantha Silvestri, Dr. Ashley Stein, Christian Nielsen, and Caroline Jongbloed of Wellesley College; and Dr. Krista Longnecker of Woods Hole Oceanographic Institution.

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Coverage

Location: BATS station, Sargasso Sea

Temporal Extent: 2024-04-25 - 2024-11-20

Methods & Sampling

Community samples were collected over a period of four days board the R/V Atlantic Explorer, during cruises AE2412 and AE2427 in April and November 2024.

Replicate 250 mL polycarbonate bottles were filled with 200 mL of surface seawater collected in the Sargasso Sea. Each bottle received either 100 ul of 1x PBS buffer (control), 0.01% glucose (final w/v), or purified extracellular vesicles (approximately 1e9 EVs/mL final concentration). Replicates were placed in a deckboard flow-through incubator and sampled after 0, 24, 48, and 72 hours. The microbial community was sampled by filtering water through a 47mm 0.2 µm Supor filter and frozen at -80 C. DNA was extracted using a phenol-chloroform method utilizing AMPureXP beads (Biller et al 2018). 16S amplicon generation (V4-V5 primers) and sequencing on an Illumina MiSeq was conducted at the Integrated Microbiome Resource, Dalhousie University.

BCO-DMO Processing Description

- Loaded TSV file "SRA_metadata_012628.tsv" using filename as resource name; treated empty strings and "nd" as missing values; headers from row 1
- Removed quotation marks from the title field using find/replace
- Reordered fields to: study, bioproject_accession, biosample_accession, accession, sample_name, library_ID, library_strategy, library_source, library_selection, library_layout, title, platform, instrument_model
- Output written to "997617_v1_sra_microbial_community_composition.csv"

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Related Publications

Biller, S. J., Berube, P. M., Dooley, K., Williams, M., Satinsky, B. M., Hackl, T., ... Chisholm, S. W. (2018). Marine microbial metagenomes sampled across space and time. *Scientific Data*, 5, 180176.

doi:[10.1038/sdata.2018.176](https://doi.org/10.1038/sdata.2018.176)

Methods

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Parameters

Parameter	Description	Units
study	The overall research project identifier	unitless
bioproject_accession	Links to the BioProject database, which provides a central location for related projects	unitless
biosample_accession	Accession number for the sample, in the format of SAMN#, identifies the biological sample being studied	unitless
accession	The unique identifier for data files and associated metadata in the Sequence Read Archive (SRA)	unitless
sample_name	Unique name for each sample	unitless
library_ID	Short unique ID for each sample library	unitless
library_strategy	Describes the sequencing protocol; amplicon (primer targeted) or genomic/metagenomic	unitless
library_source	Source for library material (genomic DNA, PCR product, etc)	unitless
library_selection	Library selection method (PCR based or not)	unitless
library_layout	Layout of library (single or paired end reads)	unitless
title	Short project title	unitless
platform	Sequencing platform used	unitless
instrument_model	Model of sequencing instrument used	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq100
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	16S amplicon generation (V4-V5 primers) and sequencing on an Illumina MiSeq was conducted at the Integrated Microbiome Resource, Dalhousie University.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Deckboard flow-through incubator
Generic Instrument Name	Incubator
Dataset-specific Description	Replicates were placed in a deckboard flow-through incubator and sampled after 0, 24, 48, and 72 hours.
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).

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Deployments

AE2412

Website	https://www.bco-dmo.org/deployment/988823
Platform	R/V Atlantic Explorer
Start Date	2024-04-25
End Date	2024-04-28

AE2427

Website	https://www.bco-dmo.org/deployment/988830
Platform	R/V Atlantic Explorer
Start Date	2024-11-20
End Date	2024-11-26

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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.

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Funding

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

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