Sequence data accession numbers originating from seawater homarine addition experiments conducted on R/V Rachel Carson RC0078 cruise in the Salish Sea in June 2022

Website: https://www.bco-dmo.org/dataset/997408
Data Type: Cruise Results
Version: 1
Version Date: 2026-04-22

Project
» Collaborative Research: Resolving the production and fate of nitrogenous metabolites in the surface ocean (Nitrogenous Metabolites)

Contributors	Affiliation	Role
Ingalls, Anitra E.	University of Washington (UW)	Principal Investigator
Sosa, Oscar A.	University of Puget Sound	Principal Investigator
Heal, Katherine	Pacific Northwest National Laboratory (PNNL)	Co-Principal Investigator
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset contains BioSample/SRA accession identifiers and links for metatranscriptomic samples from seawater homarine-addition incubation experiments conducted during R/V Rachel Carson cruise RC0078 in June 2022 in the Salish Sea near the Strait of Juan de Fuca. Treatments included homarine-amended and unamended control seawater used to identify microorganisms and genes responsive to homarine.

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Coverage

Location: Seawater was sampled with the R/V Rachel Carson CTD from 4 m depth during RC0078 (Station 2) in the Salish Sea near the Strait of Juan de Fuca on June 5, 2022.
Spatial Extent: **Lat**:48.249167 **Lon**:-122.991667
Temporal Extent: 2022-06-05

Methods & Sampling

CTD data were collected in the Salish Sea on the R/V Rachel Carson, cruise RC0078 in June 2022.

Seawater was transferred to acid-clean, blue-tinted, 5-L polycarbonate carboys for acclimation in a deck incubator with flow-through surface seawater. A set of three carboys were supplied with 0.1 mM carbon as homarine and three other unamended carboys served as control group. We incubated samples for 3.5 hours and proceeded to concentrate the microbial fraction by filtering each through a 47 mm-diameter, 0.22 µm pore-size polycarbonate membrane with a peristaltic pump. The filters were flash-frozen in liquid nitrogen at sea and were transferred to -80°C storage in the lab.

BCO-DMO Processing Description

- Loaded CSV file "bcodmo_RC0078_hom_exp_sra_metadata.csv" using filename as resource name, with "nd" and empty strings treated as missing values
- Renamed field "year_month_day" to "Date"
- Renamed fields: Depth_meters to Depth, Latitude_N to Latitude, Longitude_E to Longitude, accession_number_url to accession_sra_url, accession_number_text to accession_number
- Output to "997408_v1_rc0078_hom_exp_sra_metadata.csv"

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Related Publications

Ferrer-Gonzalez, F., Heal, K., Sacks, J., Romero-Maysonet, Y., Finch, A., Carlson, L., Coe, L., Bartolek, Z., Luthy, C., Gaffney, M., Angier, S., Flynn, S., Gómez, C. B., Dunn, J., Bay, K., Yamamoto, L., Tien, M., Armbrust, E. V., Durham, B., ... Ingalls, A. (2025). Conserved pathway for homarine catabolism in environmental bacteria. https://doi.org/10.21203/rs.3.rs-7359689/v1
Results

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Related Datasets

References

University of Puget Sound. Homarine-degrading marine bacteria. 2022/07. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA862506. NCBI:BioProject: PRJNA862506.

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Parameters

Parameter	Description	Units
Cruise	Cruise ID	unitless
Station	Station number	unitless
Cast	Cast number of CTD collection	unitless
Depth	Depth of sample collection	meters
Date	Date of sample collection (UTC)	unitless
Latitude	Latitude, positive is North	decimal degrees
Longitude	Longitude, negative is West	decimal degrees
treatment_type	Experiment identifier that indicates carboy number and whether carboy was supplied with 0.1 mM carbon as homarine or whether it served as a control; identifiers are control 1, control 2, control 3, homarine 1, homarine 2, and homarine 3.	unitless
accession_sra_url	External link to the SRA linked to Biosample	unitless
accession_number	Biosample accession identifier	unitless

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Instruments

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	NCBI Description: Samples were DNase treated (RNase free). Library was prepared with Illumina's Stranded Total RNA Prep Ligation with Ribo-Zero Plus kit and 10 bp IDT for Illumina indices.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Sea-Bird SBE9 CTD profiler
Generic Instrument Name	CTD Sea-Bird SBE 911plus
Dataset-specific Description	Sea-Bird SBE9 CTD profiler
Generic Instrument Description	The Sea-Bird SBE 911 plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911 plus includes the SBE 9plus Underwater Unit and the SBE 11plus Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9 plus and SBE 11 plus is called a SBE 911 plus. The SBE 9 plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 plus and SBE 4). The SBE 9 plus CTD can be configured with up to eight auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorescence, light (PAR), light transmission, etc.). more information from Sea-Bird Electronics

Dataset-specific Instrument Name	deck incubator
Generic Instrument Name	Shipboard Incubator
Dataset-specific Description	Seawater was transferred to acid-clean, blue-tinted, 5-L polycarbonate carboys for acclimation in a deck incubator with flow-through surface seawater.
Generic Instrument Description	A device mounted on a ship that holds water samples under conditions of controlled temperature or controlled temperature and illumination.

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Deployments

RC0078

Website	https://www.bco-dmo.org/deployment/997314
Platform	R/V Rachel Carson (UW)
Start Date	2022-06-03
End Date	2022-06-09
Description	Project: DON-2022

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Project Information

Collaborative Research: Resolving the production and fate of nitrogenous metabolites in the surface ocean (Nitrogenous Metabolites)

NSF Award Abstract:
Photosynthetic microbes provide food for nearly all other life in the ocean. Their metabolism produces organic molecules called metabolites that can leak out of cells, be intentionally excreted into seawater, or be released during cell death. Once outside the cell, these metabolites are the basis for specific interactions among

microbes and determine community structure and activity. Yet, current understanding of metabolites in the ocean is limited by a historical lack of ability to measure them. The work proposed here will expand current knowledge of metabolite structures, concentrations, and production rates using recently developed analytical methods. These methods have already led to the discovery that homarine, a substituted pyridine first found in lobster in 1933, is the most abundant detectable metabolite in microbial communities of the North Pacific Ocean. While homarine is known as a predator deterrent, osmoprotectant, methyl donor, and antibiofouling agent, studies of its role in microbial community dynamics are lacking. The work proposed will clarify the role of homarine in the ocean’s microbial communities. This work will create an open-source metabolite database that will serve the broader field of metabolomics, a growing area in environmental, engineering, and medical sciences. This collaboration will also promote the careers of a graduate student and a postdoctoral researcher as well as an early career professor from an underrepresented group at a primarily undergraduate institution (PUI). Undergraduates from both institutions will contribute to project development and implementation, local cruises on the R.V. Carson, lab work, and dissemination of results. This research will be integrated into a curriculum-based research experience for undergraduates in a 200-level genetics course at the PUI, University of Puget Sound.

The proposed work will carry out field studies and laboratory experiments to test the hypothesis that metabolites are quantitatively significant forms of carbon and nitrogen flowing through microbial communities. The identity, quantity, and production rates of metabolites will also be determined. For homarine, the enzymes and organisms responsible for its transformations will be determined. Specific proposed activities will 1) Quantify nitrogenous metabolite pools and their net production rates (particulate and dissolved) in phytoplankton cultures and in marine surface water communities; 2) Isolate homarine consuming heterotrophic bacteria and use mutagenesis techniques, transcriptomics, and stable isotope assisted metabolomics to annotate genes and characterize the biochemical reactions involved in the degradation of homarine; 3) Carry out incubations of stable isotope labeled homarine in phytoplankton cultures, heterotrophic bacterial cultures sensitive to homarine, and natural communities to quantitatively evaluate the effect of homarine on growth, track homarine through metabolic pathways, and determine the kinetics of homarine uptake; 4) Identify homarine consumers and biochemical pathways for homarine use in the environment by mining existing environmental metatranscriptomes for homarine catabolism genes. The combination of these approaches will provide better understanding of the flow of nitrogen containing metabolites through marine microbial ecosystems. Results from this work will be disseminated through peer reviewed open-source publications as well as presentations to the scientific community and the general public.

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-2125886
NSF Division of Ocean Sciences (NSF OCE)	OCE-2124712

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