The global proteome of replete laboratory cultures of Alteromonas macleodii MIT1002

Website: https://www.bco-dmo.org/dataset/875612
Data Type: experimental
Version: 1
Version Date: 2022-06-14

Project
» C-CoMP Model Bacteria Physiological Studies (C-CoMP Model Bacteria)

Program
» Center for Chemical Currencies of a Microbial Planet (C-CoMP)

Contributors	Affiliation	Role
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Abstract
This dataset represents the global proteome of replete laboratory cultures of Alteromonas macleodii MIT1002 (collected in triplicate). This dataset is an initial examination of the proteome allocation of this heterotrophic bacteria and will contribute to C-CoMP's efforts that are focused on understanding the physiology of model marine bacteria. A total of 2075 proteins were identified in MIT1002. The Moran laboratory at University of Georgia grew and prepared the cultures and the Saito laboratory at Woods Hole Oceanographic Institution conducted the proteomics analyses.

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Coverage

Temporal Extent: 2021-03-01 - 2021-05-01

Methods & Sampling

Cultures (50 ml each) of *Ruergeria pomeroyi* DSS-3 and *Alteromonas macleodii* MIT1002 were harvested in triplicate, centrifuged at 8000 x g for 10 minutes, flash frozen, stored at -80 degrees C, and shipped to Woods Hole Oceanographic Institution for proteomics analysis. Cultures were filtered and filters were extracted using SDS detergent and a SP3 magnetic bead purification followed by trypsin digestion alkylation and reduction. The methods are described in Saito et al. 2020 and were modified from the methods originally published by Hughes et al. 2014. Analysis was conducted by 2D active modulation Orbitrap mass spectrometry as described in McIlvin and Saito 2021.

This dataset reports results for the *Alteromonas macleodii* MIT1002 samples. See related datasets for the *Ruergeria pomeroyi* DSS-3 samples.

Note: the sample ids ending in a1, b1, and c1 differentiate biological triplicates from one another.

Data Processing Description

Data Processing:
The raw mass spectra files were searched against the SEQUEST high thread database within Proteome Discoverer software (v2.4). Processed files were then loaded into Proteome Software (Scaffold v5) and filtered to False Discovery Rates less than 1% using Percolator (0.7% peptide FDR and 0.03% Protein FDR using decoy database). Percolator was used for PSM validation based on PEP scoring. The output was reported as exclusive unique spectral counts. No normalization was applied to this dataset.

Raw data files are currently being submitted to the ProteomeXchange repository through PRIDE under accession number PXD034365. Raw file names are: *220427_CCoMP_AHANA_MIT1002_CS_a1, 220427_CCoMP_AHANA_MIT1002_CS_b1, 220427_CCoMP_AHANA_MIT1002_CS_c1*.

BCO-DMO Processing:
- modified parameter names;
- replaced commas with semi-colons in the protein_name column.

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Data Files

File
MIT1002.csv (Comma Separated Values (.csv), 167.86 KB) MD5:2df36830f3ab3820c3304cda5461737e Primary data file for dataset ID 875612

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Related Publications

Hughes, C. S., Foehr, S., Garfield, D. A., Furlong, E. E., Steinmetz, L. M., & Krijgsveld, J. (2014). Ultrasensitive proteome analysis using paramagnetic bead technology. Molecular Systems Biology, 10(10), 757. doi:10.15252/msb.20145625
Methods

McIlvin, M. R., & Saito, M. A. (2021). Online Nanoflow Two-Dimension Comprehensive Active Modulation Reversed Phase–Reversed Phase Liquid Chromatography High-Resolution Mass Spectrometry for Metaproteomics of Environmental and Microbiome Samples. Journal of Proteome Research, 20(9), 4589–4597. doi:10.1021/acs.jproteome.1c00588
Methods

Saito, M. A., McIlvin, M. R., Moran, D. M., Santoro, A. E., Dupont, C. L., Rafter, P. A., … Waterbury, J. B. (2020). Abundant nitrite-oxidizing metalloenzymes in the mesopelagic zone of the tropical Pacific Ocean. Nature Geoscience, 13(5), 355–362. doi:10.1038/s41561-020-0565-6
Methods

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Related Datasets

IsRelatedTo

McIlvin, M., Saito, S. (2022) Model Bacteria Physiological Studies Dataset 1: Triplicate replete proteomes for Ruergeria pomeroyi DSS-3 Dataset 2: Triplicate replete proteomes for Alteromonas macleodii MIT1002. Publication date: 2022-06-10. https://www.ebi.ac.uk/pride/archive/projects/PXD034365

Saito, M. A., Moran, M. A. (2022) **The global proteome of replete laboratory cultures of Ruergeria pomeroyi DSS-3.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-06-14 doi:10.26008/1912/bco-dmo.875600.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
protein_id	A numerical identifier that uniquely identifies this protein within this dataset	unitless
protein_name	A name identifying this protein	unitless
ncbi_id	unique ID (typically the NCBI protein accession number) assigned to each protein name	unitless
molecular_weight_kDa	The molecular weight in kilo-Daltons of the protein	kilo-Daltons
MIT1002_CS_a1_SC	Exclusive unique spectral counts for proteins in sample MIT1002_CS_a1	unnormalized spectral counts
MIT1002_CS_b1_SC	Exclusive unique spectral counts for proteins in sample MIT1002_CS_b1	unnormalized spectral counts
MIT1002_CS_c1_SC	Exclusive unique spectral counts for proteins in sample MIT1002_CS_c1	unnormalized spectral counts

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Instruments

Dataset-specific Instrument Name	Dionex nano-HPLC
Generic Instrument Name	High-Performance Liquid Chromatograph
Dataset-specific Description	Data were collected with a Thermo Fusion Orbitrap mass spectrometer interfaced with a Dionex nano-HPLC configured with 2D active modulation chromatography using the methods of McIlvin and Saito 2021.
Generic Instrument Description	A High-performance liquid chromatograph (HPLC) is a type of liquid chromatography used to separate compounds that are dissolved in solution. HPLC instruments consist of a reservoir of the mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by high pressure pumping of the sample mixture onto a column packed with microspheres coated with the stationary phase. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase.

Dataset-specific Instrument Name	Thermo Fusion Orbitrap
Generic Instrument Name	Mass Spectrometer
Dataset-specific Description	Data were collected with a Thermo Fusion Orbitrap mass spectrometer interfaced with a Dionex nano-HPLC configured with 2D active modulation chromatography using the methods of McIlvin and Saito 2021.
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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Project Information

C-CoMP Model Bacteria Physiological Studies (C-CoMP Model Bacteria)

The Center for Chemical Currencies of a Microbial Planet (C-CoMP) is focused on understanding how marine microorganisms determine the fate of labile carbon in the surface ocean. To study these chemical-biological dynamics across a variety of scales and in response to changing environmental conditions, the physiology of marine bacteria that drive chemical exchange must be explored in depth using a variety of microbiological, molecular biological, and integrative 'omics (e.g. proteomics, metabolomics, and genomics) methodologies. This project has been created to host data generated via these methods to investigate the physiological mechanisms underpinning the biogeochemical functions of model marine bacteria.

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Program Information

Center for Chemical Currencies of a Microbial Planet (C-CoMP)

Website: https://ccomp-stc.org/

Coverage: North Atlantic, BATS, global/other

Functions carried out by microscopic inhabitants of the surface ocean affect every aspect of life on our planet, regardless of distance from the coast. Ocean phytoplankton are responsible for half of the photosynthesis on Earth, the first step in a complex system that annually withdraws 50 billion metric tons of carbon from the atmosphere to sustain their growth. Of this, 25 billion metric tons participate in a rapid cycle in which biologically reactive material is released into seawater and converted back into carbon dioxide by marine bacteria within hours to days. The chemical-microbe network at the heart of this fast cycle remains poorly constrained; consequently, its primary currencies and controls remain elusive; its sensitivities to changing ocean conditions are unknown; and its responses to future climate scenarios are not predictable. The Center for Chemical Currencies of a Microbial Planet (C-CoMP) integrates research, education and knowledge transfer activities to develop a mechanistic understanding of surface ocean carbon flux within the context of a changing ocean and through increased participation in ocean sciences. C-CoMP supports science teams that merge biology, chemistry, modeling, and informatics to close long-standing knowledge gaps in the identities and dynamics of organic molecules that serve as the currencies of elemental transfer between the ocean and atmosphere. C-CoMP fosters education, outreach, and knowledge transfer activities that engage students of all ages, broaden participation in the next generation of ocean scientists, and extend novel open-science approaches into complementary academic and industrial communities. The Center framework is critical to this mission, uniquely facilitating an open exchange of experimental and computational science, methodological and conceptual challenges, and collaborations that establish integrated science and education partnerships. With expanded participation in ocean science research and ocean literacy across the US society, the next generation of ocean scientists will better reflect the diverse US population.

Climate-carbon feedbacks on the marine carbon reservoir are major uncertainties for future climate projections, and the trajectory and rate of ocean changes depend directly on microbial responses to temperature increases, ocean acidification, and other perturbations driven by climate change. C-CoMP research closes an urgent knowledge gap in the mechanisms driving carbon flow between ocean and atmosphere, with global implications for predictive climate models. The Center supports interdisciplinary science teams following open and reproducible science practices to address: (1) the chemical currencies of surface ocean carbon flux; (2) the structure and regulation of the chemical-microbe network that mediates this flux; and (3) sensitivity of the network and its feedbacks on climate. C-CoMP leverages emerging tools and technologies to tackle critical challenges in these themes, in synergy with existing ocean programs and consistent with NSF’s Big Ideas. C-CoMP education and outreach activities seek to overcome barriers to ocean literacy and diversify participation in ocean research. The Center is developing (1) initiatives to expand ocean literacy in K-12 and the broader public, (2) ocean sciences undergraduate curricula and research opportunities that provide multiple entry points into research experiences, (3) post-baccalaureate programs to transition undergraduates into graduate education and careers in ocean science, and (4) interdisciplinary graduate student and postdoctoral programs that prepare the next generation of ocean scientists. The C-CoMP team includes education faculty who evaluate the impacts of education and outreach activities and export successful STEM initiatives to the education community. C-CoMP is revolutionizing the technologies for studying chemical transformations in microbial systems to build understanding of the outsized impact of microbes on elemental cycles. Open science, cross-disciplinary collaborations, community engagement, and inclusive practices foster strategic advances in critical science problems and STEM initiatives. C-CoMP science, education, and knowledge-transfer themes are efficiently addressed through a sustained network of scientists addressing critical research challenges while broadening the workforce that will tackle multi-disciplinary problems with academic, industrial and policy partners.

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.

The Program's Data Management Plan (DMP) is available as a PDF document.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2019589

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