Metadata for transcriptomic expression data from cultures of Ruegeria pomeroyi DSS-3 and Alteromonas macleodii MIT1002 grown in defined culture media with either glucose, acetate, or a mix of both as carbon substrates

Website: https://www.bco-dmo.org/dataset/916134
Data Type: experimental
Version: 1
Version Date: 2023-12-06

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 includes metadata for transcriptomic expression data from cultures of Ruegeria pomeroyi DSS-3 and Alteromonas macleodii MIT1002. These model marine bacteria were grown in defined culture media with either glucose, acetate, or a mix of both as carbon substrates. The data are sampled so as to capture the metabolic differences the bacteria employ when catabolizing these different substrates and when switching between them. The raw RNA sequences (50 bp reads in fastq format) have been submitted to the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under BioProject PRJNA972985 (https://www.ncbi.nlm.nih.gov/bioproject/972985).

Table of Contents

Coverage

Temporal Extent: 2022-02-22 - 2022-07-17

Methods & Sampling

This lab study took place in Athens, Georiga (GA), USA within the Department of Marine Sciences at the

University of Georgia. Experiments were conducted on several dates: samples ending in _glc_a/b/c (samples grown with glucose only) were collected February 22-23, 2022; samples ending in _ac_a/b/c (samples grown with acetate only) were collected June 24-25, 2022; and the rest of the samples ending with _glc_ac_5/8/19/34_a/b/c (grown with both glucose and acetate) were collected July 16-17, 2022.

Samples were collected for transcriptomic analysis during exponential growth phase from liquid cultures, and samples were pelleted and immediately frozen at -80°C. RNA was extracted from thawed samples using the Zymo Quick-RNA Fungal/Bacterial Microprep kit (Irvine, CA, USA). Ribosomal RNAs were depleted using NEBNext® rRNA Depletion Kit (Ipswich, MA, USA), and the remaining RNA was purified using the Zymo RNA Clean and Concentrator-5 kit (Irvine, CA, USA). RNA concentration was quantified using Qubit fluorometry (Invitrogen, Waltham, MA, USA), and libraries were prepped using the NEBNext® Ultra™ II Directional RNA Library Prep kit (Ipswich, MA, USA). Sequencing was conducted at the Georgia Genomics and Bioinformatics Center (Athens, GA, USA) using the Illumina NextSeq 2000 platform to obtain 50-bp single-end reads.

Data Processing Description

The submitted data are raw RNA sequences in 50 bp reads in fastq format and are otherwise unprocessed. RNA sequences can be accessed on the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) under BioProject PRJNA972985 (https://www.ncbi.nlm.nih.gov/bioproject/972985).

Within this dataset, transcripts from *Ruegeria pomeroyi* DSS-3 are included in the *Ruegeria pomeroyi* DSS-3 Digital Microbe data package that is currently available on the C-CoMP Zenodo Community page (doi: 10.5281/zenodo.7888446).

BCO-DMO Processing Description

- Imported original file "CCoMPmodelbacteria_metabolicresponses_primarydatafile.csv" into the BCO-DMO system.
- Renamed fields to comply with BCO-DMO naming conventions.
- Saved the final file as "916134_v1_transcriptomic_expression_metadata.csv".

[table of contents | back to top]

Data Files

File	
916134_v1_transcriptomic_expression_metadata.csv	(Comma Separated Values (.csv), 4.34 KB) MD5:98986a18324d7463c6fcbca225e7de19
Primary data file for dataset ID 916134, version 1	

[table of contents | back to top]

Related Publications

University of Georgia. Substrate-specific metabolic responses of model marine bacteria. 2023/05. 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/PRJNA972985. NCBI:BioProject: PRJNA972985.
IsRelatedTo

Veseli, I., & Cooper, Z. (2023). Ruegeria pomeroyi digital microbe databases (Version 04) [Data set]. Zenodo. https://doi.org/10.5281/ZENODO.7888446
IsRelatedTo

[table of contents | back to top]

Related Datasets

IsRelatedTo

Saito, M. A., Moran, M. A., Cooper, Z. S. (2024) **Normalized protein abundance data and protein annotations for proteomic data from laboratory cultures of Ruegeria pomeroyi DSS-3 and Alteromonas macleodii MIT1002 in 2022.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-05-14 doi:10.26008/1912/bco-dmo.927507.1 [view at BCO-DMO] *Relationship Description: These transcriptomic expression data accompany the proteomic data "Substrate-specific metabolic responses of model marine bacteria using proteomics" https://www.bco-dmo.org/dataset/927507).*

[table of contents | back to top]

Parameters

Parameter	Description	Units
Sample_Name	Name of sample used during the experiment	unitless
Accession	NCBI BioSample Accession Number	unitless
BioProject	NCBI BioProject Accession Number	unitless
Organism	Type of model marine bacteria used in this experiment	unitless
Strain	Strain number for the referenced bacteria	unitless
Tax_ID	NCBI Taxonomy ID	unitless
Glucose_initial_concentration_uM	Initial concentration of glucose	micromolar concentration
Acetate_initial_concentration_uM	Initial concentration of acetate	micromolar concentration
Sample_description	Description of growth and collection conditions	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina NextSeq 2000
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Qubit Fluorometer
Generic Instrument Name	Fluorometer
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

[table of contents | back to top]

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.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]