Transcriptome data for bacteria collected eight hours after individual inoculation into a diatom Thalassiosira psuedonana culture

Website: https://www.bco-dmo.org/dataset/818765
Data Type: experimental
Version: 1
Version Date: 2020-07-16

Project
» Metabolic Currencies of the Ocean Carbon Cycle (Metabolic Currencies)

Contributors	Affiliation	Role
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Abstract

Transcriptome data for bacteria Ruegeria pomeroyi DSS-3, Stenotrophomonas sp. SKA14, Polaribacter dokdonensis MED152, and Dokdonia MED134 collected eight hours after individual inoculation into a diatom Thalassiosira psuedonana culture. The sequence data description for PRHNA448168 is at https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA448168.

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Coverage

Temporal Extent: 2017-02 - 2017-12

Dataset Description

Transcriptome data for bacteria Ruegeria pomeroyi DSS-3, Stenotrophomonas sp. SKA14, Polaribacter dokdonensis MED152, and Dokdonia MED134 collected eight hours after individual inoculation into a diatom Thalassiosira psuedonana culture. The sequence data description for PRHNA448168 is at https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA448168.

Methods & Sampling

Thalassiosira pseudonana were removed from the co-cultures by pre-filtration through 2.0 µm pore-size filters, and bacteria were collected on 0.2 µm pore-size filters. Filters were incubated in SDS (0.6% final concentration) and proteinase K (120 ng µl -1 final concentration). RNA was extracted from duplicates of each treatment by adding an equal volume of acid phenol:chloroform:isoamyl-alcohol, followed by shaking, centrifugation, and collection of the supernatant. A second extraction was carried out by the addition of an equal volume of chloroform:isoamyl-alcohol. RNA was recovered from the supernatant, treated to remove rRNA, and

sequenced.

Each sequence library is from four independent bacterial samples that were pooled for sequencing. The data are assigned to one of the four samples post-sequencing by mapping to the genomes of each of the four bacteria. The data table provides the accession numbers of the bacterial genomes to be used for mapping in the final column.

Data Processing Description

BCO-DMO Processing Notes:
- data submitted in Excel file "Diatom matrix data table.xlsx" sheet "Sheet1" extracted to csv
- added conventional header with dataset name, PI name, version date
- NCBI_Genome_Accession data were split into separate rows
- Replicate number and Taxon were put into their own columns

Data Files

File
diatom_matrix_accessions.csv(Comma Separated Values (.csv), 2.07 KB) MD5:4ab90a4446050be36eeffa680522a363 Primary data file for dataset ID 818765

Related Publications

Ferrer-González, F. X., Widner, B., Holderman, N. R., Glushka, J., Edison, A. S., Kujawinski, E. B., & Moran, M. A. (2020). Resource partitioning of phytoplankton metabolites that support bacterial heterotrophy. The ISME Journal. doi:10.1038/s41396-020-00811-y
Results

Related Datasets

IsSupplementTo

Moran Research Group. Ruegeria pomeroyi DSS-3, Stenotrophomonas sp. SKA14, Polaribacter sp. MED152, Dokdonia sp. MED134, Co-culture transcript expression of Thalassiosira pseudonana CCMP1335 with Ruegeria pomeroyi DSS-3, Stenotrophomonas sp. SKA14, Polaribacter sp. MED152, or Dokdonia sp. MED134 Raw sequence reads. 2018/03. 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/PRJNA448168. NCBI:BioProject: PRJNA448168. https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA448168

Parameters

Parameter	Description	Units
Sample_Name	sample identifier	unitless
NCBI_Bioproject_Accession	NCBI Bioproject accession number	unitless
BioSample	NCBI Biosample accession number	unitless
Description	Description of sample	unitless
replicate	Replicate number	unitless
NCBI_Genome_Accession	NCBI Genome accession number	unitless
taxon_microbe	Microbial identification	unitless

Instruments

Dataset-specific Instrument Name	HiSeq Illumina 2500
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.

Project Information

Metabolic Currencies of the Ocean Carbon Cycle (Metabolic Currencies)

NSF Award Abstract:
The roles of microbes in cycling carbon and nutrients in the ocean - the largest biological system on Earth - were initially described about 40 years ago. Now, it is known that half of Earth's primary production is carried out by marine phytoplankton, and half of that is recycled within weeks by marine bacteria. This proposal is a collaboration between microbiologists and chemists to identify the specific compounds that pass between phytoplankton and bacteria in surface ocean waters. Identifying the key chemicals of the ocean's microbial food web will provide insights into how the marine carbon cycle is regulated, generate data to improve ocean carbon models, and train new scientists at the interface of microbiology and chemistry. Hands-on learning opportunities in microbial ecology will be provided for high school students, both in the classroom and in marine ecosystems of the Georgia coast.

Phytoplankton metabolites that sustain the flow of carbon between microbial autotrophs and heterotrophs in the surface ocean carbon cycle will be identified in this project. A matrix of model systems consisting of bacteria-phytoplankton co-cultures will be used as biological assays for key metabolites based on expression patterns of bacterial transporter genes. The chemical identity of candidate metabolites and evaluation of their potential ecological role will be carried out by exometabolomic analysis of co-cultures with bacterial transporter mutants. Both advanced mass spectrometry and NMR will be used for metabolomics analysis, taking advantage of the sensitivity and compound identification strengths of each. The distribution of candidate

metabolites in the ocean microbiome and other microbial systems will be characterized by mining environmental sequence datasets for orthologous transporter genes. This project represents a novel approach to identifying metabolites important in microbiome function, compounds often difficult to address with standard chemical approaches because of their low concentrations and high biological demand.

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Funding

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