Taxonomic binning of transcripts from samples collected during the SIMCO1 (July 2014) and SIMCO2 (Oct 2014) incubation experiments on the linkage between DOM changes and microbial transcription patterns at Sapelo Island, GA.

Website: https://www.bco-dmo.org/dataset/661835
Data Type: Other Field Results
Version:
Version Date: 2016-10-26

Project
» High Resolution Linkages Between DOC Turnover and Bacterioplankton in a Coastal Ocean (SIMCO)

Contributors	Affiliation	Role
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Dataset Description

Incubation experiments examining concurrent changes in DOC composition and microbial transcription patterns were carried out in July 2014 (SIMCO1) and October 2014 (SIMCO2) at Sapelo Island, GA. This dataset contains the taxonomic assignments of transcripts to reference genome bins. Cells were collected by filtration at the time of initial surface water collection (Time 0) and after a 24 hr incubation (Time 24) for both high and low tide water collections on each of the two sample dates. Filters were processed for RNA extraction and mRNA-enriched material was sequenced on an Illumina HiSeq2500 run to produce single-end 250 bp reads.

Methods & Sampling

Water samples were collected from Marsh Landing Dock on Sapelo Island GA, prefiltered through a 3 micron membrane filter to remove most eukaryotic microbes, and incubated in 10 L carboys in situ in the dark for 24 h. At the beginning and end of the incubation, three carboys were sacrificed for nucleic acid extraction on 0.2 micron membrane filters, and microbial transcripts were analyzed from two of the three replicates according to methods in Satinsky et al. 2013 and 2014 and protocols.io (https://www.protocols.io/g/moran-lab).

Data Processing Description

Reads were put through a quality control pipeline that removed rRNAs and internal standards added for quantification (Satinsky et al. 2013). Putative protein encoding reads were analyzed by RAPSearch2 (http://omics.informatics.indiana.edu/mg/RAPSearch2/) against a custom reference database of genomes and transcriptomes compiled from marine bacteria, archaea, and microbial eukaryotes; the database is available for download at: http://ssharma.marsci.uga.edu/Lab/MarineRef2/.

References:
Brandon M. Satinsky, Scott M. Gifford, Byron C. Crump, Mary Ann Moran, 2013. Chapter 12: "Use of Internal Standards for Quantitative Metatranscriptome and Metagenome Analysis" in Methods in Enzymology, Vol. 531. ISSN 0076-6879, http://dx.doi.org/10.1016/B978-0-12-407863-5.00012-5.

Brandon M. Satinskya, Byron C. Crumpb, Christa B. Smithc, Shalabh Sharmac, Brian L. Zielinskid, Mary Dohertye, Jun Mengc, Shulei Sunf, Patricia M. Medeirosc, John H. Pauld, Victoria J. Colese, Patricia L. Yagerc, and Mary Ann Moranc. 2014. Microspatial gene expression patterns in the Amazon River Plume. PNAS 111(30):11085-11090. www.pnas.org/cgi/doi/10.1073/pnas.1402782111

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- column names reformatted to comply with BCO-DMO standards
- replaced spaces with underscores
- replaced commas with semi-colons
- replaced str. and Strain with strain

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Data Files

File
taxonomy_all.csv (Comma Separated Values (.csv), 505.85 KB) MD5:8069efbcc4773c86c673e0c6135eee95 Primary data file for dataset ID 661835

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Parameters

Parameter	Description	Units
sample	sample identification: S1 or S2 = SIMCO experiment 1 or 2; L = low tide; H = high tide; 0 = 0 hour incubation; 24 = 24 hour incubation	unitless
organism_strain	description of organism and strain	unitless
transcripts_per_L	number of transcripts per liter	transcripts/liter

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq2500
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	mRNA-enriched material was sequenced
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.

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Deployments

Moran_Sapelo_2012-14

Website	https://www.bco-dmo.org/deployment/661864
Platform	Univ_Georgia
Start Date	2012-09-01
End Date	2014-10-31
Description	Microbial 'omics studies

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Project Information

High Resolution Linkages Between DOC Turnover and Bacterioplankton in a Coastal Ocean (SIMCO)

Coverage: Southeastern U.S. coastal ocean, 31.4° N Lat, 81.3° W Lon

Description from NSF award abstract:
Long-standing questions regarding the fate of dissolved organic carbon (DOC) in coastal oceans require a better understanding of the network that links bacterioplankton metabolism with carbon transformation. These questions address uncertainties about the composition of the bioreactive DOC components transformed in ocean margins, and the role of bacterial taxonomic and genetic composition in determining the fate of DOC.

This project will infuse a new type of data into coastal carbon cycle research based on high-resolution chemical analysis coupled with bacterial gene expression measures. It will extend DOC process studies down to the single-compound level and bacterial activity studies down to the single-gene level, and integrate this information into existing bioinformatic resources for biogeochemical and modeling applications.

The specific goals of this project are:
1) To reconstruct major components of the network linking DOC composition, DOC turnover, and bacterial heterotrophy in the coastal ocean (the composition of the DOC pool, the major bioreactive components, the bacterioplankton taxa mediating transformations, and the bacterial genes and pathways responsible).

2) To test hypothesized network links for selected DOC compounds using a simplified system that queries individual DOC compounds against a complex natural microbial community.

3) To test hypothesized network links for marine bacteria using a simplified system that queries a single generalist heterotrophic bacteria against a complex natural DOC pool.

4) To verify predicted DOC-gene linkages that are most informative about heterotrophic activities of bacterioplankton.

This research addresses fundamental questions on bacterial mediation of organic carbon fate in the ocean and atmosphere. As such, these investigations linking the chemical changes in dissolved organic carbon with patterns of gene expression in coastal bacterioplankton communities will be of interest to scientists across several disciplines.

Note: The project acronym, SIMCO, means "Sapelo Island Microbial Carbon Observatory".

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1356010

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