qPCR data from the B/O Hermano Gines cruises in the CARIACO Basin Time Series Station from May to November 2014 (CariacoMetaOmics project)

Website: https://www.bco-dmo.org/dataset/652366
Data Type: Cruise Results
Version: final
Version Date: 2016-07-22

Project
» Genetic and Metabolic Signatures of Marine Microorganisms in Oxygen Depleted and Varying Geochemical Seascapes (CariacoMetaOmics)

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Table of Contents

Dataset Description

Quantitative reverse transcription polymerase chain reaction (RTqPCR) data collected from RNA samples on 1 leg of each of the CAR212 and CAR216 cruises.

Methods & Sampling

All samples were collected via a Microbial Sampler in situ Incubation Device (MS-SID).

RNA samples for RTqPCR were size-fractionated during collection by the MS-SID into a 2.7um fraction and 0.2-2.7um fraction using using a glass fiber filter pre filter in-line with 0.2um polysulfone filter membrane. RNA was preserved with RNAlater, stored frozen, and transported back to the home laboratory. RNA was extracted according to Stewart et al. (2012) using the *mir*Vana miRNA Isolation kit (Ambion), purified with the RNeasy MinElute Cleanup kit (Qiagen), and reverse-transcribed to cDNA with the QuantiTect Reverse Transcription kit (Qiagen). RTqPCR assays were then carried in the same manner as qPCR assays.

Data Processing Description

All data were normalized to volume of seawater.

DMO Notes:

-transferred each RTqPCR data section into separate a data object.
-reformatted the date to comply with BCO-DMO standards.
-reformatted some column names to comply with BCO-DMO standards.

[table of contents | back to top]

Data Files

File
RTqPCR.csv (Comma Separated Values (.csv), 4.48 KB) MD5:308781189ccbfaf5731217185b9d4e5e Primary data file for dataset ID 652366

[table of contents | back to top]

Parameters

Parameter	Description	Units
cruise_id	cariaco cruise number and leg number	unitless
date_start	start date; mm/dd/yyyy	unitless
depth	depth	meters
bac16S_rna	copies of the bacterial 16S gene	x10^7/L
bac16S_rna_sd	standard deviation of the copies of the bacterial 16S gene	x10^7/L
bac16S_rna_particulate	fraction of bacterial 16S genes in the greater than 2.7 um fraction	dimensionless
bac16S_rna_particulate_sd	standard deviation of the fraction of bacterial 16S genes in the greater than 2.7 um fraction	dimensionless
arch16S_rna	copies of the archaeal 16S gene	x10^8/L
arch16S_rna_sd	standard deviation of the copies of the archaeal 16S gene	x10^8/L
arch16S_rna_particulate	fraction of archaeal 16S genes in the greater than 2.7 um fraction	dimensionless
arch16S_rna_particulate_sd	standard deviation of the fraction of archaeal 16S genes in the greater than 2.7 um fraction	dimensionless

sqrG1_rna	copies of the sqrG1 gene	x10^3/L
sqrG1_rna_sd	standard deviation of the copies of the sqrG1 gene	x10^3/L
sqrG1_rna_particulate	fraction of sqrG1 genes in the greater than 2.7 um fraction	dimensionless
sqrG1_rna_particulate_sd	standard deviation of the fraction of sqrG1 genes in the greater than 2.7 um fraction	dimensionless
sqrG4_rna	copies of the sqrG4 gene	x10^0/L
sqrG4_rna_sd	standard deviation of the copies of the sqrG4 gene	x10^0/L
sqrG4_rna_particulate	fraction of sqrG4 genes in the greater than 2.7 um fraction	dimensionless
sqrG4_rna_particulate_sd	standard deviation of the fraction of sqrG4 genes in the greater than 2.7 um fraction	dimensionless
nirS_rna	copies of the nirS gene	x10^3/L
nirS_rna_sd	standard deviation of the copies of the nirS gene	x10^3/L
nirS_rna_particulate	fraction of nirS genes in the greater than 2.7 um fraction	dimensionless
nirS_rna_particulate_sd	standard deviation of the fraction of nirS genes in the greater than 2.7 um fraction	dimensionless
hzo_rna	copies of the hzo gene	x10^3/L
hzo_rna_sd	standard deviation of the copies of the hzo gene	x10^3/L
hzo_rna_particulate	fraction of hzo genes in the greater than 2.7 um fraction	dimensionless
hzo_rna_particulate_sd	standard deviation of the fraction of hzo genes in the greater than 2.7 um fraction	dimensionless
dsrA_rna	copies of the dsrA gene	x10^5/L
dsrA_rna_sd	standard deviation of the copies of the dsrA gene	x10^5/L

dsrA_rna_particulate	fraction of dsrA genes in the greater than 2.7 um fraction	dimensionless
dsrA_rna_particulate_sd	standard deviation of the fraction of dsrA genes in the greater than 2.7 um fraction	dimensionless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Microbial Sampler in situ Incubation Device (MS-SID)
Generic Instrument Name	Submersible Incubation Device-In Situ Microbial Sampler
Dataset-specific Description	Samples size-fractionated during collection by the MS-SID
Generic Instrument Description	The Submersible Incubation Device-In Situ Microbial Sampler (SID-ISMS) system was developed for the 2011 NSF funded DHAB Metazoans Mediterranean Brine research project and first used on cruise AT18-14. The system includes several integrated components including: a 2 liter incubation chamber; fixation filters and water sample bottles; a High Range CTD (Neil Brown Ocean Sensors, Inc., USA) equipped with two turbidity sensors (Wet Labs ECOView); an Aanderra 2808F oxygen optode; an SDSL-data link; and a sonardyne beacon, a pinger and a 24 volt deep-sea battery. The sensors and sampling devices are mounted on a frame that is attached to the hydro-wire. Lowering rate and recovery speed are controlled by a winch mounted on the surface vessel.

[table of contents | back to top]

Deployments

CAR212_2

Website	https://www.bco-dmo.org/deployment/652493
Platform	B/O Hermano Gines
Start Date	2014-05-07
End Date	2014-05-09
Description	These deployments are part of the MetaOmics studies in the Cariaco Basin

CAR216_2

Website	https://www.bco-dmo.org/deployment/652494
Platform	B/O Hermano Gines
Start Date	2014-11-05
End Date	2014-11-07
Description	These deployments are part of the MetaOmics studies in the Cariaco Basin.

[table of contents | back to top]

Project Information

Genetic and Metabolic Signatures of Marine Microorganisms in Oxygen Depleted and Varying Geochemical Seascapes (CariacoMetaOmics)

Coverage: Southern Caribbean Sea - 10" 30' N, 64" 40' W (CARIACO Ocean Time Series Station)

Oxygen depleted water columns (ODWCs) appear to be expanding in response to global climate change. This alters trophic structure, compresses habitat and modifies geochemical cycles of major elements. Oxygen depletion can vary in intensity and duration from seasonal hypoxia to permanent anoxia. The focus of this study is a classic example of the anoxic end-member, the Cariaco Basin. The overall goal is to examine how microbial functional potential (metagenomic), activity (metatranscriptomic), taxonomic diversity (based on SSU rRNA) and the ecological/geochemical consequences (in terms of measured rates of key processes) relate along vertical oxygen/geochemical gradients and between seasons in the Cariaco Basin. This will reveal relationships between expression of particular sets of genes, environmental differences in nutrients, energy substrates and oxidant availabilities.

The objectives are to: (1) Integrate hydrographic, geochemical and microbial ecological data with metagenomic and metatranscriptomic profiles to understand regulatory and metabolic networks defining microbial community responses to environmental forcing during high and low productivity periods. This will help to understand the importance of processes, such as anaerobic oxidation of methane, utilization of redox-sensitive metals, the cryptic sulfur cycle in this ODWC, and the impacts of oxygen depletion on nitrogen transformations. (2) Determine the importance of associations between microbial eukaryotes (mEuks) and prokaryotes in this ODWC. (3) Identify "indicator" genes of known or unknown function that may be relevant to major elemental and trace gas cycling as targets for further biochemical characterization and molecular probe development, and quantify a key subset of these genes and transcripts across redox gradients using qPCR. (4) Provide a basis for developing monitoring tools using expressed genes indicative of important elemental transformations and fluxes for diagnosing the health status of natural and human engineered ecosystems. (5) Compare results with recent and ongoing studies of other ODWCs to discern shared and unique attributes of these systems.

Intellectual Merit: Previous studies of ODWCs have underscored the need for more data on microbial community structure and functionality in ODWCs, particularly biochemical rate measurements and other data on community responses to changing conditions. Better predictive models of responses of marine microbial communities and biogeochemical processes to global climate change are essential for informing future policy and management decisions. Data from an anoxic end-member ODWC like Cariaco Basin are critically needed to compare with data from other recent and ongoing studies of seasonally-depleted coastal systems and permanently-depleted deep basin and western boundary oxygen minimum zones (OMZs) to construct more skillful models. This study will advance the understanding of impacts of expanding ODWCs around the world, moving beyond assessments based only on taxonomic diversity, to yield new insights into the ecology and physiology of major microbial groups in these environments and interactions among Bacteria, Archaea and microbial eukaryotes.

Broader Impacts: The PIs and their collaborators will train one Research Associate, one postdoctoral investigator, a graduate student, and numerous undergraduates from SBU. All personnel will be trained in various aspects of microbial ecology and oceanography, with an emphasis on both traditional (e.g., microscopy) and "cutting edge" (e.g. metagenomics/transcriptomics) techniques. The PIs will also involve the Zephyr Education Foundation's marine science literacy and education program, located in Woods Hole, MA. The PIs will work with this organization to educate inner city K-12 students using local boat field trips organized by Zephyr, and lectures, and classroom laboratory exercises designed by the PIs. Additionally, this project will have broad implications for understanding how ODWCs affect marine ecosystems, and may influence future management strategies and models describing the cycling of C and N between the ocean and atmosphere.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1335436
NSF Division of Ocean Sciences (NSF OCE)	OCE-1336082

[table of contents | back to top]