qPCR data from 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/652312
Data Type: Cruise Results
Version: working
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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Abstract
qPCR data from B/O Hermano Gines cruises in the CARIACO Basin Time Series Station from May to November 2014 (CariacoMetaOmics project)

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Dataset Description

Quantitative polymerase chain reaction (qPCR) data collected from molecular samples on the CAR212 and CAR216 cruises.

Methods & Sampling

All samples were collected via Niskin bottles.

DNA samples for qPCR were size fractionated into a >2.7um fraction and 0.2-2.7um fraction using a glass fiber filter pre filter in-line with a sterivex filter. DNA was preserved in lysis buffer, stored frozen, and transported back to the home laboratory. After thawing, DNA was extracted according to Frias-Lopez et al. 2008, modified by Ganesh et al. 2014. All qPCR assays were performed on an Mx3000P thermal cycler (Agilent) using the SYBRgreen filter. Assays were designed for the following genes according to the following references:

Target	Description	Proxy Process or Variable	Reference
sqr-G1	γ- and α-*proteobacteria*- like *sulfide quinone reductase* (group 1)	sulfide oxidation	Pham et al. (2008) Modified by Rodriguez-Mora (2012)
sqr-G4	ε-*proteobacteria*- like *sulfide quinone reductase* (group 4)	sulfide oxidation	Pham et al. (2008) Modified by Rodriguez-Mora (2012)
dsrA	*dissimilatory sulfate reductase A*	sulfate reduction	Wagner et al. (1998) Modified by Rodriguez-Mora (2012)
bacterial 16S *rDNA*	bacterial 16S ribosomal rRNA gene	total bacteria	Nadkarni et al. 2002
achaeal 16S *rDNA*	archaeal 16S ribosomal rRNA gene	total archaea	Takai and Horikoshi 2000
nirS	*nitrite reductase S*	denitrification	Braker et al. 1998
hzo	*hydrazine oxidoreductase*	anammox	Li et al. 2010

Data Processing Description

All data were normalized to volume of seawater.

DMO Notes:

-transferred each qPCR 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.

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Data Files

File
qPCR.csv (Comma Separated Values (.csv), 4.10 KB) MD5:97e1ef8f4b79bed10c67a00fb932a6f4 Primary data file for dataset ID 652312

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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_dna	copies of the bacterial 16S gene	x10^8/L
bac16S_dna_sd	standard deviation of the copies of the bacterial 16S gene	x10^8/L
bac16S_dna_particulate	fraction of bacterial 16S genes in the greater than 2.7 um fraction	dimensionless
bac16S_dna_particulate_sd	standard deviation of the fraction of bacterial 16S genes in the greater than 2.7 um fraction	dimensionless
arch16S_dna	copies of the archaeal 16S gene	x10^8/L
arch16S_dna_sd	standard deviation of the copies of the archaeal 16S gene	x10^8/L
arch16S_dna_particulate	fraction of archaeal 16S genes in the greater than 2.7 um fraction	dimensionless
arch16S_dna_particulate_sd	standard deviation of the fraction of archaeal 16S genes in the greater than 2.7 um fraction	dimensionless
sqrG1_dna	copies of the sqrG1 gene	x10^4/L
sqrG1_dna_sd	standard deviation of the copies of the sqrG1 gene	x10^4/L
sqrG1_dna_particulate	fraction of sqrG1 genes in the greater than 2.7 um fraction	dimensionless
sqrG1_dna_particulate_sd	standard deviation of the fraction of sqrG1 genes in the greater than 2.7 um fraction	dimensionless
sqrG4_dna	copies of the sqrG4 gene	x10^4/L
sqrG4_dna_sd	standard deviation of the copies of the sqrG4 gene	x10^4/L
sqrG4_dna_particulate	fraction of sqrG4 genes in the greater than 2.7 um fraction	dimensionless
sqrG4_dna_particulate_sd	standard deviation of the fraction of sqrG4 genes in the greater than 2.7 um fraction	dimensionless
nirS_dna	copies of the nirS gene	x10^5/L

nirS_dna_sd	standard deviation of the copies of the nirS gene	x10^5/L
nirS_dna_particulate	fraction of nirS genes in the greater than 2.7 um fraction	dimensionless
nirS_dna_particulate_sd	standard deviation of the fraction of nirS genes in the greater than 2.7 um fraction	dimensionless
hzo_dna	copies of the hzo gene	x10^5/L
hzo_dna_sd	standard deviation of the copies of the hzo gene	x10^5/L
hzo_dna_particulate	fraction of hzo genes in the greater than 2.7 um fraction	dimensionless
hzo_dna_particulate_sd	standard deviation of the fraction of hzo genes in the greater than 2.7 um fraction	dimensionless
dsrA_dna	copies of the dsrA gene	x10^7/L
dsrA_dna_sd	standard deviation of the copies of the dsrA gene	x10^7/L
dsrA_dna_particulate	fraction of dsrA genes in the greater than 2.7 um fraction	dimensionless
dsrA_dna_particulate_sd	standard deviation of the fraction of dsrA genes in the greater than 2.7 um fraction	dimensionless

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Instruments

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	All samples were collected via Niskin bottles.
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	Mx3000P thermal cycler (Agilent)
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	All qPCR assays were performed on this thermal cycler using the SYBRgreen filter.
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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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.

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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.

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Funding

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

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