Cariaco metagenomes/metatranscriptomes for samples collected at the CARIACO Basin Time Series Station 10.5˚N, 64.7˚W on CAR212_2 and CAR_216_2

Website: https://www.bco-dmo.org/dataset/716766
Data Type: experimental
Version:
Version Date: 2017-10-12

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

Contributors	Affiliation	Role
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Dataset Description

Description metadata and links for metagenome and metatranscriptome data.

Location: CARIACO Basin Time Series Station 10.5˚N, 64.7˚W.

Methods & Sampling

DNA for metagenomes:

Samples for DNA were collected at 10-12 depths from standard rosette-mounted Niskin bottles. Niskin bottles were slightly pressurized with N2 or argon gas from the top vent to prevent O2 contamination during sample transfer. Eight or 12L samples were filtered directly from Niskin bottles sequentially through a 2.7µm hydrophilic glass fiber filter (EMD Millipore) and then 0.2µm in-line Millipore® Sterivex™ filter units (EMD Millipore) for the particle-associated and free-living fractions, respectively. Filters were immediately treated with lysis buffer (50mM Tris-HCL, 40mM EDTA, 0.73M sucrose) and stored frozen. DNA samples were extracted according to Frias-Lopez et al. (2008) and Ganesh et al. (2014). DNA was purified with the Genomic DNA Clean and Concentrator -25 kit (Zymo Research), eluted into 10mM Tris for qPCR samples or into TE buffer for sequencing samples, and stored at -80˚C for downstream analyses.

RNA for transcriptomes:

For RNA samples ~2L water was filtered and preserved in situ in RNALaterfrom each depth using a custom instrument MS-SID (C. Taylor/V. Edgcomb, WHOI). RNA was isolated using the MirVana MiRNA Isolation kit, and cDNA prepared and libraries constructed with the ScriptSeq RNA Seq library preparation kit.

Data Processing Description

Transcriptome library quality control was performed using Trimmomatic and assembled into contigs using Trinity 2.03.

Metagenome library quality control was performed using Trimmomatic and assembled using IDBA v. 1.11.

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Data Files

File
Genomes_IMG_2017.csv (Comma Separated Values (.csv), 18.91 KB) MD5:6afe970a91b30fff254deade872eef23 Primary data file for dataset ID 716766

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Parameters

Parameter	Description	Units
Library_kind	Library kind	no units
geo_loc_name	Location name	no units
collection_date	collection data	no units
Depth_m	Depth_m	meters
Size_Fraction	Size_Fraction	um
Replicate	Replicate	no units
Sequencing_Center	Seqencing_Center	no units
Genome_Size_assembled	Genome size assembled	no units
Gene_Count_assembled	Genome count assembled	no units
Release_date	Release_date	no units
OID_number	OID number	no units
OID_link	OID link	no units

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird 25
Generic Instrument Description	The Sea-Bird SBE 25 SEALOGGER CTD is battery powered and is typically used to record data in memory, eliminating the need for a large vessel, electrical sea cable, and on-board computer. All SBE 25s can also operate in real-time, transmitting data via an opto-isolated RS-232 serial port. Temperature and conductivity are measured by the SBE 3F Temperature sensor and SBE 4 Conductivity sensor (same as those used on the premium SBE 9plus CTD). The SBE 25 also includes the SBE 5P (plastic) or 5T (titanium) Submersible Pump and TC Duct. The pump-controlled, TC-ducted flow configuration significantly reduces salinity spiking caused by ship heave, and in calm waters allows slower descent rates for improved resolution of water column features. Pressure is measured by the modular SBE 29 Temperature Compensated Strain-Gauge Pressure sensor (available in eight depth ranges to suit the operating depth requirement). The SBE 25's modular design makes it easy to configure in the field for a wide range of auxiliary sensors, including optional dissolved oxygen (SBE 43), pH (SBE 18 or SBE 27), fluorescence, transmissivity, PAR, and optical backscatter sensors. More information from Sea-Bird Electronics: http:www.seabird.com.

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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
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