

# Radioisotope 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/652461>

**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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## Dataset Description

Dark DIC assimilation and bacterial net productivity data measured from incubation experiments on 1 leg of each of the CAR212 and CAR216 cruises.

## Methods & Sampling

All samples were collected via Niskin bottles.

Dark DIC assimilation, a proxy for chemoautotrophy, and bacterial net productivity, BNP, were determined by incorporation of  $^{14}\text{C}$ - bicarbonate and  $^3\text{H}$ -leucine into microbial biomass, respectively, according to Taylor et al. (2001) and Kirchman (1993). Incubations were done at *in situ* temperatures and oxygen concentrations. After incubations were terminated, the microbial biomass was collected onto filters, stored in scintillation cocktail (Hionic-Fluor, Perkin Elmer) and activity was measured on a Tri-Carb 2810TR (Perkin Elmer) scintillation counter.

## Data Processing Description

All data were normalized to volume of seawater.

DMO Notes:

-transferred radioisotope 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
<b>Radioisotope_rate.csv</b> (Comma Separated Values (.csv), 1.61 KB) MD5:c051dfb75b0fe2966eee34984c4e4aff Primary data file for dataset ID 652461

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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
dark_DIC_assim	dark DIC assimilation	micrograms of C per liter per day
dark_DIC_assim_sd	standard deviation of the dark DIC assimilation	micrograms of C per liter per day
bac_net_productivity	bacterial net productivity by leucine incorporation	micrograms of C per liter per day
bac_net_productivity_sd	standard deviation of the bacterial net productivity by leucine incorporation	micrograms of C per liter per day

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## Instruments

<b>Dataset-specific Instrument Name</b>	Tri-Carb 2810TR (Perkin Elmer) scintillation counter
<b>Generic Instrument Name</b>	Liquid Scintillation Counter
<b>Dataset-specific Description</b>	Activity was measured on this scintillation counter
<b>Generic Instrument Description</b>	Liquid scintillation counting is an analytical technique which is defined by the incorporation of the radiolabeled analyte into uniform distribution with a liquid chemical medium capable of converting the kinetic energy of nuclear emissions into light energy. Although the liquid scintillation counter is a sophisticated laboratory counting system used to quantify the activity of particulate emitting ( $\beta$ and $\alpha$ ) radioactive samples, it can also detect the Auger electrons emitted from $^{51}\text{Cr}$ and $^{125}\text{I}$ samples. Liquid scintillation counters are instruments assaying alpha and beta radiation by quantitative detection of visible light produced by the passage of rays or particles through a suitable scintillant incorporated into the sample.

<b>Dataset-specific Instrument Name</b>	Niskin bottle
<b>Generic Instrument Name</b>	Niskin bottle
<b>Dataset-specific Description</b>	All samples were collected via Niskin bottles.
<b>Generic Instrument Description</b>	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.

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## Deployments

### CAR212\_2

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

### CAR216\_2

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/652494">https://www.bco-dmo.org/deployment/652494</a>
<b>Platform</b>	B/O Hermano Gines
<b>Start Date</b>	2014-11-05
<b>End Date</b>	2014-11-07
<b>Description</b>	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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1335436</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1336082</a>

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