

“Collaborative Research: Genetic and Metabolic Signatures of Marine Microorganisms in Oxygen Depleted and Varying Geochemical Seascapes (MetaOmics in the Cariaco Basin)”

OCE-1335436 (V. Edgcomb & C Taylor (WHOI), G. Taylor (Stony Brook University, co-PIs), 08/01/13-07/31/16

Data Management Plan

We have read and agree to abide by NSF guidelines and award conditions for scientific conduct and data management. Results, data, and collections will be made available to qualified researchers upon request, provided that the quantities and time requirements for compliance do not compromise our research objectives. We will also address data sharing issues in annual and final reports.

Primary Investigators: Virginia P. Edgcomb (WHOI), Co-PI: Gordon T. Taylor (Stony Brook Univ.), Co-I Craig Taylor (WHOI)

Project: Collaborative Research: Genetic and Metabolic Signatures of Marine Microorganisms in Oxygen Depleted and Varying Geochemical Seascapes (MetaOmics in the Cariaco Basin)

Scientific Collaborators: Walter Betancourt (IVIC-W, our Venezuelan local collaborator), Maria Pachiadaki (bioinformatic analyses), David Beaudoin (molecular analyses)

Solicitation Info: NSF BIO-OCE

Overview

Our overall goal is to examine the genetic, functional and phylogenetic signatures of microbial communities (Bacteria, Archaea, and Eukarya) in response to oxygen depletion in a well-constrained ecosystem (Cariaco Basin, Venezuela).

Data description

Environmental data, microbial community ribosomal RNA sequence data, metatranscriptome and metagenome data, microbial cell abundances, productivity measurements and copy numbers of selected functional genes and their transcripts.

Description of fieldwork

Year 1: Two 3-day sampling trips into Cariaco Basin (Venezuela) for collection of water samples.

Expected data product #1: CTD data

Responsible investigators: G. T. Taylor

Product description: Continuous profiles of temperature and conductivity from dual sensors, depth/pressure, O₂, optical properties (turbidity from 2 turbidity sensors), from the General Oceanics water column rosette sampler.

Preservation and dissemination plan: Within 12 months of completing both cruises in year 1, the underway data collected from the ship's CTD system will be contributed by us to BCO-DMO.

These measurements will be managed by the Biological and Chemical Oceanography Data Management Office (BCO-DMO) as we provide them to BCO-DMO, and the data sets will be available online from the BCO-DMO data system (<http://bco-dmo.org/data/>).

A full synthesis of the data will be presented in a publication along with a synopsis of key results and how they might be applied to policy decisions. All products will be made available to our collaborators on this project.

Expected data product #2: Analytical/Microbial population diversity data

Responsible investigator: Edgcomb

Product description: MiSeq ribosomal RNA amplicon profiles of Bacteria, Archaea and Eukarya diversity in all water samples collected in two seasons and at 6 depths selected along the TPI 7334735 oxygen gradient at the CARIACO time series station A. Data will be binned taxonomically, and clustered according to sequence identity (clustering ranging from 90-99%). This will be used to compare community composition in different samples using analyses that include Principal Component Analysis, UniFrac, etc. qPCR data will also be generated for populations of interest and for functional genes and transcripts.

Preservation and dissemination plan: A data synthesis will be presented in a publication; results disseminated through collaborations described above. Amplicon and qPCR data will be stored indefinitely on our laboratory computers (these are backed up daily via the WHOI automated backup system) and with BCO-DMO and the Short Read Archive at NCBI within 2 years of acquisition.

Timeline for data release: Upon publication

Expected data product #3: Analytical/metatranscriptome data

Responsible investigator: Edgcomb

Product description: Sequences (Illumina HiSeq metatranscriptome and metagenome data)

Preservation and dissemination plan: All assembled, annotated and taxonomically-assigned Illumina metatranscriptome and metagenome data will be stored indefinitely on our laboratory computers and through the WHOI backup system, and with BCO-DMO, and will be uploaded to NCBI Short Read Archive within 2 years of acquisition.

Timeline for data release: Upon publication

Expected data product #4: Contextual Data

Responsible investigator: G. T. Taylor

Product description: Depth profiles of nutrients (nitrogen species, phosphate, sulfide), microbial cell abundances, heterotrophic and chemoautotrophic production, FISH community analysis from Niskin bottle casts.

Preservation and dissemination plan: Samples will be transported back to Stony Brook University after both cruises for analyses that should be completed 12 months after the last cruise. All data will be stored indefinitely on our laboratory computers, and submitted to BCO-DMO for archiving and online availability (<http://bco-dmo.org/data/>). A full data synthesis will be presented in a publication along with a synopsis of key results and how they might be applied to policy decisions. All products will be made available to our collaborators on this project.

Timeline for data release: Upon publication