Metagenomic, metatranscriptomic, and single cell sequencing data from an Environmental Sample Processor deployment in Monterey Bay, CA in 2016.

Website: https://www.bco-dmo.org/dataset/753343
Data Type: Other Field Results
Version: 2
Version Date: 2020-03-20

Project
» Bacterial Taxa that Control Sulfur Flux from the Ocean to the Atmosphere (OceanSulfurFluxBact)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
Moran, Mary Ann	University of Georgia (UGA)	Principal Investigator
Nowinski, Brent	University of Georgia (UGA)	Co-Principal Investigator
Biddle, Mathew	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
These metagenomic and metatranscriptomic time-series data cover a 52-day period in the fall of 2016 during an intense bloom of the dinoflagellate Akashiwo sanguinea in Monterey Bay, CA, USA. The dataset comprises 84 metagenomes, 82 metatranscriptomes, and 88 16S rRNA amplicon libraries that capture the functions and taxonomy the bacterial and archaeal community. In addition, 88 18S rRNA amplicon libraries describe the taxonomy of the eukaryotic community during the bloom. Microbial cells were collected at station M0 using the moored autonomous robotic Environmental Sample Processor (ESP) instrument and preserved with RNAlater in the instrument until retrieval.

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Coverage

Spatial Extent: **Lat**:36.835 **Lon**:-121.901
Temporal Extent: 2016-09-26 - 2016-11-16

Dataset Description

These metagenomic and metatranscriptomic time-series data cover a 52-day period in the fall of 2016 during an intense bloom of the dinoflagellate Akashiwo sanguinea in Monterey Bay, CA, USA. The dataset comprises 84 metagenomes, 82 metatranscriptomes, and 88 16S rRNA amplicon libraries that capture the functions and taxonomy the bacterial and archaeal community. In addition, 88 18S rRNA amplicon libraries describe the taxonomy of the eukaryotic community during the bloom. Microbial cells were collected at station M0 using the moored autonomous robotic Environmental Sample Processor (ESP) instrument and preserved with RNAlater in the instrument until retrieval.

Methods & Sampling

The Environmental Sample Processor (ESP) filtered seawater sequentially through 5.0 um and 0.2 um pore size polyvinylidene fluoride filters. Seawater was evacuated from filters and followed twice with a 2 minute incubation with 1 ml of RNAlater™. RNAlater was evacuated, and filters were stored in the ESP until they were transferred to -80 C upon instrument recovery.

Grab samples for sequencing while the ESP was not deployed were taken using Niskin bottles that collected seawater at the same depth and location of the ESP. Water was transferred to a low-density polyethylene cubitainer and maintained at ambient temperature until return to lab within 30 min. Seawater was filtered as above with vacuum filtration and preserved immediately in liquid nitrogen and transferred to -80 C.

Single-cell sequencing: Seawater was transferred directly from the Niskin bottle to a 50 ml Falcon tube and placed on ice until brought back to lab. Each sampling day, 3 x 1 ml of seawater was preserved in cryovials using 100 ul of glyTe (5 ml glycerol, 3 ml Milli-Q H2O, 1 ml 100 x TE pH 8.0, 0.2 um filter sterilized after mixing the above, and stored in -20 C freezer). Preserved samples were then placed in a -80 C freezer. Samples were processed and sequenced at JGI

Data Processing Description

ESP and grab sample filters were processed for DNA and RNA using the Zymobiomics DNA/RNA Mini Kit. Turbo DNase and RiboZero were performed on RNA samples. Illumina HiSeq-2500 1TB 2 x 151 bp sequencing was performed at the Joint Genome Institute (JGI).

BBtools was used to trim and screen reads, followed by read correction using bfc (version r181). Reads with no mate pair were removed. Metagenomes were assembled using SPAdes assembler 3.11.1. The entire filtered read set was mapped to the final assembly and coverage information generated using bbmap (version 37.78). Metatranscriptomes were assembled using MEGAHIT v1.1.2 and reads were mapped to the assembly using BBMap. The JGI Integrated Microbial Genomes System (IMG) was used for annotation of the metagenomes and metatranscriptomes.

BCO-DMO Processing notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- reformatted date from Mon-DD (Oct-04) to YYYYMMDD (20141004)

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Data Files

File
seq_2016.csv (Comma Separated Values (.csv), 144.91 KB) MD5:545b78c80171b46fefa0feef7bea41d4 Primary data file for dataset ID 753343

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Parameters

Parameter	Description	Units
GOLD_Project_ID	Accession number at DOE JGI IMG database: https://img.jgi.doe.gov	unitless

Analysis_Project_Name	Name of sequencing project	unitless
Type	Material type sequenced	unitless
Assembly_Method	assembly method	unitless
Collection_Date	collection date of samples	unitless
Instrument	instrument	unitless
JGI_Contigs_Link	JGI Contigs Link	unitless
JGI_Project_ID	JGI Project ID	unitless
JGI_Sample_ID	JGI Sample ID	unitless
JGI_Sequencing_Project_ID	JGI Sequencing Project ID	unitless
JGI_Sequencing_Project_Name	JGI Sequencing Project Name	unitless
Latitude_and_Longitude	Latitude and Longitude	unitless
NCBI_BioProject_Accession	NCBI BioProject Accession	unitless
NCBI_BioSample_Accession	NCBI BioSample Accession	unitless
NCBI_Project_ID	NCBI Project ID	unitless
NCBI_SRA_Accession_ID	NCBI SRA Accession ID	unitless
Sample_Name	sample name	unitless
Sequencing_Run_Mode	sequencing run mode	unitless
Total_Bases	total bases	unitless
Volume_Seawater_Filtered	Volume Seawater Filtered	milliliters (mL)

env_biome	environmental biome	unitless
env_feature	environmental feature	unitless
env_material	environmental material	unitless
geo_loc_name	location name	unitless
lat	latitude with positive values indicating North	decimal degrees
lon	longitude with negative values indicating West	decimal degrees

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Deployments

Moran_Monterey_2016

Website	https://www.bco-dmo.org/deployment/755677
Platform	Environmental Sample Processor
Start Date	2016-09-23
End Date	2016-11-16

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Project Information

Bacterial Taxa that Control Sulfur Flux from the Ocean to the Atmosphere (OceanSulfurFluxBact)

Surface ocean bacterioplankton preside over a divergence point in the marine sulfur cycle where the fate of dimethylsulfoniopropionate (DMSP) is determined. While it is well recognized that this juncture influences the fate of sulfur in the ocean and atmosphere, its regulation by bacterioplankton is not yet understood. Based on recent findings in biogeochemistry, bacterial physiology, bacterial genetics, and ocean instrumentation, the microbial oceanography community is poised to make major advances in knowledge of this control point. This research project is ascertaining how the major taxa of bacterial DMSP degraders in seawater regulate DMSP transformations, and addresses the implications of bacterial functional, genetic, and taxonomic diversity for global sulfur cycling.

The project is founded on the globally important function of bacterial transformation of the ubiquitous organic sulfur compound DMSP in ocean surface waters. Recent genetic discoveries have identified key genes in the two major DMSP degradation pathways, and the stage is now set to identify the factors that regulate gene expression to favor one or the other pathway during DMSP processing. The taxonomy of the bacteria mediating DMSP cycling has been deduced from genomic and metagenomic sequencing surveys to include four major groups of surface ocean bacterioplankton. How regulation of DMSP degradation differs among these groups and maps to phylogeny in co-occurring members is key information for understanding the marine sulfur cycle and predicting its function in a changing ocean. Using model organism studies, microcosm experiments (at Dauphin Island Sea Lab, AL), and time-series field studies with an autonomous sample collection instrument (at Monterey Bay, CA), this project is taking a taxon-specific approach to decipher the

regulation of bacterial DMSP degradation.

This research addresses fundamental questions of how the diversity of microbial life influences the geochemical environment of the oceans and atmosphere, linking the genetic basis of metabolic potential to taxonomic diversity. The project is training graduate students and post-doctoral scholars in microbial biodiversity and providing research opportunities and mentoring for undergraduate students. An outreach program is enhance understanding of the role and diversity of marine microorganisms in global elemental cycles among high school students. Advanced Placement Biology students are participating in marine microbial research that covers key learning goals in the AP Biology curriculum. Two high school students are selected each year for summer research internships in PI laboratories.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1342694

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