Marine sediment trap metagenomes from R/V Kilo Moana KM1215, KM1219 in the Station ALOHA, an oligotrophic station 100 miles north of Oahu, Hawaii, July to September 2012 (C-MORE project)

Website: https://www.bco-dmo.org/dataset/559235
Version: 22 May 2015
Version Date: 2015-05-22

Project
» Center for Microbial Oceanography: Research and Education (C-MORE)

Contributors	Affiliation	Role
DeLong, Edward	Massachusetts Institute of Technology (MIT-Dept CEE)	Principal Investigator
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Dataset Description

Marine sediment trap metagenomes

This study explores the taxonomic and metabolic diversity of microbes associated with sinking particles in the North Pacific Subtropical Gyre. Marine particles are hotspots of microbial activity, yet the microbial taxa and biochemical processes involved in carbon and energy cycling on sinking particles are poorly understood. Metagenomes generated in this study revealed new insights into the important taxa and metabolisms involved in microbial processing of marine particles.

NCBI BioProject PRJNA270248

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#  C-MORE sediment trap metagenomes
#  DeLong Lab - MIT
#  Ed DeLong
#  CMORE/HOEDYLAN
#  date ingested into BCO-DMO: May 22 2015
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Methods & Sampling

A HOE-DYLAN 5 sediment trap filled with brine/preservative solution and screened with 335 micron mesh was deployed at station ALOHA in the North Pacific Subtropical Gyre from July 14, 2012 to July 26, 2012. It was filtered onto a 0.2 micron filter, preserved with RNAlater and frozen at -80C. Genomic DNA representing the 0.2-335 micron fraction was isolated from frozen filters using a modified MOBIO Powerwater kit protocol and prepared for sequencing using the Illumina Nextera XT DNA sample preparation protocol. The library was dual-indexed according to Illumina's low-plexity pooling guidelines. This library was pooled with 9 others on a 300 bp paired-end sequencing run on a MiSeq instrument using MiSeq reagent kit version 3.

Seawater at station ALOHA in the North Pacific Subtropical Gyre was collected by CTD during the HOE-DYLAN 9 expedition on 08/26/2012. Seawater was prefiltered with a 5 micron filter and microbial communities were collected on a 0.2 micron filter, preserved with RNAlater and frozen at -80C. Genomic DNA representing the 0.2-5 micron fraction was isolated from frozen filters using a modified MOBIO Powerwater kit protocol and prepared for sequencing using the Illumina Nextera XT DNA sample preparation protocol. The library was dual-indexed according to Illumina's low-plexity pooling guidelines. This library was pooled with 9 others on a 300 bp paired-end sequencing run on a MiSeq instrument using MiSeq reagent kit version 3.

C-MORE DNA Sampling Protocol

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Data Files

File
sedtrap_metagenomes.csv (Comma Separated Values (.csv), 3.25 KB) MD5:f018c0a298deaa4dc3db519050842629 Primary data file for dataset ID 559235

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Parameters

Parameter	Description	Units
lat	latitude (positive north)	decimal degrees
lon	longitude (positive east)	decimal degrees
sample	sample ID	dimensionless
depth	depth	meters
date	date	YYYYMMDD
BioProject	NCBI BioProject accession number	dimensionless
SRX	NCBI SRX accession number	dimensionless
BioSample	NCBI BioSample accession number	dimensionless

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Instruments

Dataset-specific Instrument Name	MOBIO Powerwater
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	MOBIO Powerwater Genomic DNA representing the 0.2-335 micron fraction was isolated from frozen filters using a modified MOBIO Powerwater kit protocol and prepared for sequencing using the Illumina Nextera XT DNA sample preparation protocol.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Illumina Nextera XT
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina Nextera XT Illumina Nextera XT Data Sheet Genomic DNA representing the 0.2-335 micron fraction was isolated from frozen filters using a modified MOBIO Powerwater kit protocol and prepared for sequencing using the Illumina Nextera XT DNA sample preparation protocol.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	MiSeq instrument
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	MiSeq instrument This library was pooled with 9 others on a 300 bp paired-end sequencing run on a MiSeq instrument using MiSeq reagent kit version 3.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird SBE 911plus
Generic Instrument Description	The Sea-Bird SBE 911 plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911 plus includes the SBE 9plus Underwater Unit and the SBE 11plus Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9 plus and SBE 11 plus is called a SBE 911 plus. The SBE 9 plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 plus and SBE 4). The SBE 9 plus CTD can be configured with up to eight auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorescence, light (PAR), light transmission, etc.). more information from Sea-Bird Electronics

Dataset-specific Instrument Name	
Generic Instrument Name	Niskin bottle
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	HOE-DYLAN 5 sediment trap
Generic Instrument Name	Sediment Trap
Dataset-specific Description	A HOE-DYLAN 5 sediment trap filled with brine/preservative solution and screened with 335 micron mesh was deployed at station ALOHA in the North Pacific Subtropical Gyre from July 14, 2012 to July 26, 2012. filled with brine/preservative solution and screened with 335 micron mesh was deployed at station ALOHA in the North Pacific Subtropical Gyre from July 14, 2012 to July 26, 2012.
Generic Instrument Description	Sediment traps are specially designed containers deployed in the water column for periods of time to collect particles from the water column falling toward the sea floor. In general a sediment trap has a jar at the bottom to collect the sample and a broad funnel-shaped opening at the top with baffles to keep out very large objects and help prevent the funnel from clogging. This designation is used when the specific type of sediment trap was not specified by the contributing investigator.

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Deployments

KM1215

Website	https://www.bco-dmo.org/deployment/59101
Platform	R/V Kilo Moana
Start Date	2012-07-08
End Date	2012-07-28
Description	In the summer of 2012, C-MORE conducted a "continuous" long-term field experiment at Station ALOHA to observe and interpret temporal variability in microbial processes, and the consequences for ecological dynamics and biogeochemical cycling. Special focus was given to time-space coupling because proper scale sampling of the marine environment is an imperative, but generally neglected aspect of marine microbiology. Hawaii Ocean Experiment - Dynamics of Light and Nutrients (HOE-DYLAN)

KM1219

Website	https://www.bco-dmo.org/deployment/59105
Platform	R/V Kilo Moana
Start Date	2012-08-22
End Date	2012-09-11
Description	In the summer of 2012, C-MORE conducted a "continuous" long-term field experiment at Station ALOHA to observe and interpret temporal variability in microbial processes, and the consequences for ecological dynamics and biogeochemical cycling. Special focus was given to time-space coupling because proper scale sampling of the marine environment is an imperative, but generally neglected aspect of marine microbiology. Hawaii Ocean Experiment - Dynamics of Light and Nutrients (HOE-DYLAN)

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Project Information

Center for Microbial Oceanography: Research and Education (C-MORE)

Website: http://cmore.soest.hawaii.edu/

Coverage: North Pacific Subtropical Gyre (large region around 22 45 N, 158 W)

Project summary

The **Center for Microbial Oceanography: Research and Education** (C-MORE) is a recently established (August 2006; NSF award: EF-0424599) NSF-sponsored Science and Technology Center designed to facilitate a more comprehensive understanding of the diverse assemblages of microorganisms in the sea, ranging from the genetic basis of marine microbial biogeochemistry including the metabolic regulation and environmental controls of gene expression, to the processes that underpin the fluxes of carbon, related bioelements and energy in the marine environment. Stated holistically, C-MORE's primary mission is: *Linking Genomes to Biomes*.

We believe that the time is right to address several major, long-standing questions in microbial oceanography. Recent advances in the application of molecular techniques have provided an unprecedented view of the structure, diversity and possible function of sea microbes. By combining these and other novel approaches with more well-established techniques in microbiology, oceanography and ecology, it may be possible to develop a meaningful predictive understanding of the ocean with respect to energy transduction, carbon sequestration, bioelement cycling and the probable response of marine ecosystems to global environmental variability and climate change. The strength of C-MORE resides in the synergy created by bringing together experts who traditionally have not worked together and this, in turn, will facilitate the creation and dissemination of new knowledge on the role of marine microbes in global habitability.

The new Center will design and conduct novel research, broker partnerships, increase diversity of human resources, implement education and outreach programs, and utilize comprehensive information about microbial life in the sea. The Center will bring together teams of scientists, educators and community members who otherwise do not have an opportunity to communicate, collaborate or design creative solutions to long-term ecosystem scale problems. The Center's research will be organized around four interconnected themes:

- (Theme I) microbial biodiversity,
- (Theme II) metabolism and C-N-P-energy flow,
- (Theme III) remote and continuous sensing and links to climate variability, and
- (Theme IV) ecosystem modeling, simulation and prediction.

Each theme will have a leader to help coordinate the research programs and to facilitate interactions among the other related themes. The education programs will focus on pre-college curriculum enhancements, in service teacher training and formal undergraduate/graduate and post-doctoral programs to prepare the next generation of microbial oceanographers. The Center will establish and maintain creative outreach programs to help diffuse the new knowledge gained into society at large including policymakers. The Center's activities will be dispersed among five partner institutions:

- Massachusetts Institute of Technology,
- Woods Hole Oceanographic Institution,
- Monterey Bay Aquarium Research Institute,
- University of California at Santa Cruz and
- Oregon State University

and will be coordinated at the University of Hawaii at Manoa.

Related Files:

Strategic plan (PDF file)

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Funding

Funding Source	Award
US Department of Energy (DOE)	unknown C-MORE DOE
NSF Division of Biological Infrastructure (NSF DBI)	DBI-0424599
Gordon and Betty Moore Foundation (GBMF)	unknown C-MORE Moore
NSF Division of Biological Infrastructure (NSF DBI)	DBI-1202684
Gordon and Betty Moore Foundation (GBMF)	GBMF3777
Agouron Institute (AI)	AI-MO9.12.1

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