Diel metatranscriptome study in Monterey Bay, California, USA from August to September 2012 (C-MORE project, CANON project)

Website: https://www.bco-dmo.org/dataset/555991
Data Type: Cruise Results
Version: 16 April 2015
Version Date: 2015-04-16

Project
» Center for Microbial Oceanography: Research and Education (C-MORE)
» Controlled, Agile, and Novel Observing Network (CANON)

Contributors	Affiliation	Role
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Dataset Description

Diel metatranscriptome study in Monterey Bay, 2012.

Data from the accession numbers listed below can be accessed from NCBI (http://www.ncbi.nlm.nih.gov/).

GenBank accession numbers
BioProject: PRJNA268385 (http://www.ncbi.nlm.nih.gov/bioproject/PRJNA268385)
SRP: SRP050269 (http://www.ncbi.nlm.nih.gov/sra/?term=SRP050269)

Data Processing Description

C-MORE Monterey Bay diel metatranscriptome study
DeLong Lab - Massachusetts Institute of Technology
Ed DeLong
CMORE/MontereyBay
Date ingested into BCO-DMO: April 16 2015

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Data Files

File
diel_metatrans.csv (Comma Separated Values (.csv), 9.30 KB) MD5:6c22dce891af73ad13b43a67260abd59 Primary data file for dataset ID 555991

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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	Environmental Sample Processor (ESP)
Generic Instrument Name	Environmental Sample Processor
Dataset-specific Description	Environmental Sample Processor (ESP)

Generic Instrument Description	The MBARI Environmental Sample Processor—the ESP—provides on-site (in situ) collection and analysis of water samples from the subsurface ocean. The instrument is an electromechanical/fluidic system designed to collect discrete water samples, concentrate microorganisms or particles, and automate application of molecular probes and qPCR which identify microorganisms and their gene products. The ESP also archives samples so that further analyses may be done after the instrument is recovered. Environmental Sample Processor See references below for methodology used on the ESP: Greenfield, D.I., R. Marin III, S. Jensen, E. Massion, B. Roman, J. Feldman, C. Scholin (2006). Application of the Environmental Sample Processor (ESP) methodology for quantifying Pseudo-nitzschia australis using ribosomal RNA-targeted probes in sandwich and fluorescent in situ hybridization. Limnology and Oceanography: Methods 4: 426-435. Greenfield, D., R. Marin III, G.J. Doucette, C. Mikulski, S. Jensen, B. Roman, N. Alvarado, and C.A. Scholin (2008). Field applications of the second-generation Environmental Sample Processor (ESP) for remote detection of harmful algae: 2006-2007. Limnology and Oceanography: Methods 6: 667-679. Marin III, R., and C. Scholin (2010). Sandwich Hybridization. In: Microscopic and molecular methods for quantitative phytoplankton analysis (Chapter 12), edited by B. Karlson, C. Cusack, and E. Bresnan, E.. IOC Manuals and Guides, no. 55. (IOC/2010/MG/55) Paris, UNESCO. 110 pp. Ottesen, E.A., R. Marin III, C.M. Preston, C.R. Young, J.P. Ryan, C.A. Scholin, and E.F. DeLong (2011). Metatranscriptomic analysis of autonomously collected and preserved marine bacterioplankton. The ISME Journal, 5: 1881-1895, doi: 10.1038/ismej.2011.70. Ottesen, E.A., C.R. Young, J.M. Eppley, J.P. Ryan, F.P. Chavez, C.A. Scholin, and E.F. DeLong (2013). Pattern and synchrony of gene expression among sympatric marine microbial populations. Proceedings of the National Academy of Sciences, 110: E488-E497, doi: 10.1073/pnas.1222099110. Ottesen, E.A., C.M. Young, S.M. Gifford, J.M. Eppley, R. Marin III, S.C. Schuster, C.A. Scholin, and E.F. DeLong (2014). Multispecies diel transcriptional oscillations in open ocean heterotrophic bacterial assemblages. Science, 345: 207-212, 10.1126/science.1252476. Preston, C.M., A. Harris, J.P. Ryan, B. Roman, R. Marin III, S. Jensen, C. Everlove, J. Birch, J.M. Dzenitis, D. Pargett, M. Adachi, K. Turk, J.P. Zehr, and C.A. Scholin (2011). Underwater application of quantitative PCR on an ocean mooring. PLoS ONE, 6:e22522, doi: 10.1371/journal.pone.0022522. Robidart, J.C., C.M. Preston, R.W. Paerl, K.A. Turk, A.C. Mosier, C.A. Francis, C.A. Scholin, and J.P. Zehr (2011). Seasonal Synechococcus and Thaumarchaeal population dynamics examined with high resolution with remote in situ instrumentation. The ISME Journal, 6: 513-523, doi: 10.1038/ismej.2011.127. Robidart, J., M.J. Church, J.P. Ryan, F. Ascani, S.T. Wilson, D. Bombar, R. Marin III, K.J. Richards, D.M. Karl, C.A. Scholin, and J.P Zehr (2014). Ecogenomic sensor reveals controls on N2-fixing microorganisms in the North Pacific Ocean. The ISME Journal, 8: 1175-1185, 10.1038/ismej.2013.244. Saito, M.A., V.V. Bulygin, D.M. Moran, C. Taylor, and C. Scholin (2011). Examination of microbial proteome preservation techniques applicable to autonomous environmental sample collection. Frontiers in Aquatic Microbiology, 2: doi: 10.3389/fmicb.2011.00215. Scholin, C.. (2010). What are “ecogenomic sensors?” A review and thoughts for the future. Ocean Science 6: 51-60. Ussler III, W., C.M. Preston, P. Tavormina, D. Pargett, S. Jensen, B. Roman, R. Marin III, S.R. Shah, P.R. Girguis, J.M. Birch, V.J. Orphan, and C. Scholin (2013). Autonomous application of quantitative PCR in the deep sea: In situ surveys of aerobic methanotrophs using the deep-sea Environmental Sample Processor. Environmental Science and Technology, 47: 9339–9346, doi: 10.1021/es4023199. Varaljay, V.A, J. Robidart, C.M. Preston, S.M. Gifford, B. Durham, A.S. Burns, J.P. Ryan, R. Marin III, R.P. Kiene, J.P Zehr, C.A. Scholin, M. Moran. 2015. Single-taxon field measurements of bacterial gene regulation controlling DMSP fate. ISME Journal, doi:10.1038/ismej.2015.23|

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Deployments

CANON_2012_ESP

Website	https://www.bco-dmo.org/deployment/556018
Platform	Environmental Sample Processor
Start Date	2012-08-31
End Date	2012-09-25
Description	Coordinated Platforms: MBARI R/V Western Flyer: http://www.mbari.org/dmo/vessels_vehicles/western_flyer/flyer.html MBARI long-range AUV (LRAUV): http://www.mbari.org/auv/LRAUVdescription.htm Related files:http://www.mbari.org/news/publications/ar/2012ann_rpt.pdf (pages 4-14)http://odss.mbari.org/canon/stoqs_september2012/query/

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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)

Controlled, Agile, and Novel Observing Network (CANON)

Website: http://www.mbari.org/canon/

Coverage: Coastal California, USA

Growth and death of microorganisms in the sea occur as ephemeral features that continually evolve and interact with the environment. These “booms and busts” reflect the interplay between physics, chemistry, and biology, and represent the core of the oceanic food web. But not all of this activity is benign. Some blooms can be harmful to humans and wildlife, and can bring negative economic consequences. The ability to achieve mechanistic understanding of these phenomena has eluded us because of technical difficulties tracking water masses and the rapidly changing life they carry. The Controlled, Agile, and Novel Observing Network (CANON) team aims to overcome that limitation by creating new ways to remotely assess oceanic conditions and collect samples of microorganisms for in situ analysis as well as for return to shoreside laboratories.

How does the pelagic food web respond to changes in the natural environment? Our ability to answer this question is central to predicting how the oceans will respond to human perturbations such as increasing atmospheric carbon dioxide (CO2) levels, nutrient runoff from agricultural and aquacultural activities, dispersal of various pollutants, and climate change. Yet present-day models are not capable of accurately predicting future consequences because very basic questions about the food web are still unanswered. Further, unexpected but significant events will continue to appear requiring an observing system capable of rapidly responding to these new challenges as well as investigating the basic processes required for accurate environmental prediction.

The food web of interest is much more complex than it might initially appear. Take the marine microorganisms at its core—not composed of one entity, but rather they span a tremendous range of physiological capabilities and mediate many different biogeochemical processes as functionally diverse as that of the full biota on land. Thus, changes such as increased atmospheric CO2 levels, which will reduce ocean pH, will have different consequences for the many organisms in the marine environment, and these in turn will propagate through the food web. While the last decade has seen a revolution in understanding of the diversity and importance of microbial populations in the ocean, our understanding of how those populations respond to changes in their environment—and to other microbes—is rudimentary at best. Developing a better understanding of microbial dynamics through the development of new ocean observation capabilities is the initial thrust of the CANON program.

A key initial premise of CANON is to provide a new class of observation systems that will be able to follow and facilitate the study of organism assemblages and the transitions they undergo in the ocean environment. This is a critical development. The spatial and temporal sampling resolutions currently possible are not relevant to the spatial and temporal scales on which microbial processes occur. A fundamental principle for the initiative is that processes and microbes must be studied at scales relevant to the organisms’ adaptive strategies to determine how metabolism influences larger-scale ecosystem dynamics. The initiative builds on lessons learned from previous multi-platform, multi-institutional field programs of the Autonomous Ocean Sampling Network (AOSN). In contrast to the earlier field programs, which addressed observing and predicting the physical ocean, the AOSN team is further developing the Collaborative Ocean Observatory Portal and other tools and methods to observe marine microorganism populations.

The CANON team aims to merge observation, modeling, and prediction to cast projections of biological, chemical, and physical gradients within a defined region. By directing small fleets of mobile sensors within that domain, they will detect specific phenomena remotely, collect physical samples of microbes, algae, and small invertebrates autonomously, and track the evolution of biological patches over time. The system in its final form will be able to provide scientists and managers with the information required to interpret the mechanisms detected and make decisions as to how to proceed.

CANON will bring the biological insights to the requirements of new sensor development, based on cutting-edge approaches to genomics, transcriptomics, and physiology studies, and the technological innovations necessary to access the environment in unprecedented resolution, letting environmental conditions guide sampling decisions in real time and in situ.

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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

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