

Five year time-series of Prochlorococcus ecotype abundance at HOT and BATS sites from 2002-2008 (C-MORE project, Prochlorococcus project)

Website: <https://www.bco-dmo.org/dataset/3381>

Version:

Version Date: 2014-11-26

Project

» [Center for Microbial Oceanography: Research and Education](#) (C-MORE)

» [The Ecology of Prochlorococcus: Toward a Model System for Microbial Oceanography](#) (Prochlorococcus)

Contributors	Affiliation	Role
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Dataset Description

The goal was to collect long-term, high-resolution data on the temporal and spatial variability of Prochlorococcus ecotypes in the Pacific and Atlantic Oceans. The abundance of five Prochlorococcus ecotypes was determined by quantitative PCR at 12 depths every month for 5 years at two locations:

BATS location (5 nautical mile radius around 31 40'N, 64 10'W)

HOT Station ALOHA (5 nautical mile radius around 22 45'N, 158 00' W)

Methods & Sampling

Sample processing and analyses are detailed in the publication listed below. Briefly, 100ml of seawater was collected onto 25mm dia polycarbonate filters (0.22um pore size), rinsed with Tris-buffered saline, flash frozen in liquid N₂, and stored at -80C until extraction. DNA was extracted using a combination of 5min of bead beating and 15min heat lysis at 95C. Extracted DNA was used as template of quantitative PCR reactions using primers specifically designed to target different Prochlorococcus ecotypes. Standard curves used for quantitation of field data were derived from DNA extracted from cultured representatives belonging to each ecotype.

Malmstrom, RR, A Coe, GC Kettler, AC Martiny, J Frias-Lopez, ER Zinser, and SW Chisholm. 2010. Temporal dynamics of Prochlorococcus ecotypes in the Atlantic and Pacific oceans. The ISME Journal. 4(10): 1252-1264

Data Processing Description

Estimated abundances that fell below the lowest value of the standard curve were set to the theoretical detection limit of 0.65 cells/mL. Samples were excluded if their melt curves contained multiple peaks or peaks different from those in the DNA standards. Missing data points were determined by linear interpolation when abundance estimates were available for the depths immediately above and below the missing value.

In November 2014, the online data were updated to correct relatively minor errors from HOT cruises 187 and 188. The "no data" value in the original data (-9999) was replaced with the "nd" string.

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Data Files

File
hot_bats_2014.csv (Comma Separated Values (.csv), 750.67 KB) MD5:3447a8d3c816d659e27e8666793855a2
Primary data file for dataset ID 3381

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Parameters

Parameter	Description	Units
ecotype	A group of organisms, normally a subdivision of a species, that is adapted to a specific environment	
site	Location of the measurement, in this case one of two sites located at the HOT and BATS sites.	
lat	Latitude, north is positive	decimal degrees
lon	Longitude, east is positive	decimal degrees
year	Year the measurement was taken	
month	Month the measurement was taken	
day	Day the measurement was taken	
abundance	Number of bacteria counted	cells/milliliter
temp	Temperature at the sample location	degrees centigrade
sal	Salinity measured at the sample location	PSS-78
depth	Depth at which the sample was taken	meters
sigma_0	Potential density	kilograms/cubic meter
standard_deviation	Standard deviation of the abundance measurement	cells/milliliter
date	Date the sample was taken, in the form of mm/dd/yy	
yday_gmt	The year day the sample was taken, with 1 meaning January 1.	
cruiseid	The cruise identification	

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Deployments

HOT_Prochlorococcus

Website	https://www.bco-dmo.org/deployment/58143
Platform	Hawaii Ocean Time-series Vessel
Start Date	2002-11-13
End Date	2007-12-06
Description	Long-term, high-resolution data on the temporal and spatial variability of Prochlorococcus ecotypes in the Pacific and Atlantic Oceans. The abundance of five Prochlorococcus ecotypes was determined by quantitative PCR at 12 depths every month for 5 years at two locations.

BATS_Prochlorococcus

Website	https://www.bco-dmo.org/deployment/58144
Platform	Bermuda Atlantic Time Series Vessel
Start Date	2002-11-13
End Date	2007-12-06
Description	Long-term, high-resolution data on the temporal and spatial variability of Prochlorococcus ecotypes in the Pacific and Atlantic Oceans. The abundance of five Prochlorococcus ecotypes was determined by quantitative PCR at 12 depths every month for 5 years at two locations.

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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 \(PDF file\)](#)

The Ecology of Prochlorococcus: Toward a Model System for Microbial Oceanography (Prochlorococcus)

Coverage: BATS and HOT station ALOHA

The goal was to collect long-term, high-resolution data on the temporal and spatial variability of Prochlorococcus ecotypes in the Pacific and Atlantic Oceans. The abundance of five Prochlorococcus ecotypes was determined by quantitative PCR at 12 depths every month for 5 years at two locations.

The work was done in coordination with NSF-funded Bermuda Atlantic Time Series (BATS) and Hawaii Ocean Time-series (HOT), but not officially affiliated with these programs.

Geolocation:

BATS location (5 nautical mile radius around 31 40'N, 64 10'W)

HOT Station ALOHA (5 nautical mile radius around 22 45'N, 158 00' W)

References:

Temporal dynamics of Prochlorococcus ecotypes in the Atlantic and Pacific oceans. Rex R Malmstrom, Allison Coe, Gregory C Kettler, Adam C Martiny, Jorge Frias-Lopez, Erik R Zinser, Sallie W Chisholm. The ISME Journal 4, 1252-1264 (13 May 2010) doi:10.1038/ismej.2010.60 [Link to paper](#)

Original Project Abstract:

The power of a model system for advancing our understanding of the natural world has been proven repeatedly in diverse sub-disciplines of science. This approach is equally valuable for the study of marine microbial ecology, either through the sustained study of a particular ecosystem, or through the study of a particular organism at all scales of organization from the genome to the ecosystem level. In this project the investigators will do the latter through a diverse set of laboratory and field studies designed to advance the

understanding of *Prochlorococcus*, the numerically dominant phytoplankter in the world oceans. The objective is to understand what regulates the distribution and abundance of this important primary producer. *Prochlorococcus* has a number of features that make it a useful model organism for understanding the forces that shape marine microbial systems, and for generating hypotheses that will advance the field of Microbial Oceanography. It is the smallest and most abundant photosynthetic cell in the oceans, it can be isolated into culture, and it can be easily enumerated and studied in situ. Furthermore, it has the smallest genome of any known photosynthetic cell -- the minimal phototroph to date. *Prochlorococcus* is really a collection of "ecotypes", i.e., closely related but physiologically distinct populations that co-exist with different distributions along the light, temperature, nutrient, and predator (including viruses) gradients that shape their habitat. These distributions are determined by the relative fitness of the cells, i.e. the balance of growth rates and death rates along these gradients. The broad challenge is to understand the forces that have shaped this microdiversity over evolutionary time, and that guide the self-organization of these populations under different selective regimes. This is a multi-dimensional project designed to understand the "bottom up" (growth limitation by light, temperature, oxygen, and nutrients) and "top down" (mortality from viruses and grazing) influences on the population growth of different *Prochlorococcus* ecotypes through both laboratory and field studies. The project will involve high-throughput studies of the growth of ecotypes along gradients of environmental variables in the laboratory, as well as studies of the distribution of ecotypes along spatial and temporal gradients in the field (at the Hawaii and Bermuda Time Series Stations, along a longitudinal Atlantic transect, and in Oxygen Minimum Zones in the Arabian Sea and Peruvian Upwelling) using Q-PCR to assess their relative abundance. The investigators will also study the life cycle of viruses that infect *Prochlorococcus* and cross infect between ecotypes, and the growth and mortality rates of specific ecotypes in field samples due to grazing pressure. Another set of analyses will measure the full diversity of co-occurring *Prochlorococcus* in selected field samples, and work toward understanding at what level genetic diversity corresponds to ecologically meaningful diversity. Finally, the study will develop statistical methods for the characterization and analysis of *Prochlorococcus* ecotype "fitness spaces" established in the laboratory, and compare them with the distribution of ecotypes along environmental gradients in the field. This will allow a rigorous analysis of the degree to which different selective pressures shape the relative abundance of the different *Prochlorococcus* ecotypes in the oceans, and how they change over time and space.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0425602

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