The abundance of Prochlorococcus cells containing the nitrate reductase gene (narB) at the HOT and BATS sites in the Pacific and Atlantic Oceans between October 2005 and January 2008

Website: https://www.bco-dmo.org/dataset/641495
Data Type: Cruise Results
Version: final
Version Date: 2016-03-31

Project
» Nitrate Assimilation and the Ecology of Prochlorococcus: Features and Implications of Intraspecific Diversity in a Model Marine Phototroph (Prochloro_ecology)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:31.6667 **E**:-64.1667 **S**:22.75 **W**:-158
Temporal Extent: 2005-10-08 - 2008-01-31

Dataset Description

Two year time series of the abundance of Prochlorococcus cells containing the nitrate reductase gene (narB) at the HOT and BATS sites in the Pacific and Atlantic Oceans. The goal was to collect long-term, high-resolution data on the temporal and spatial variability of Prochlorococcus narB genotypes belonging to the HLII and LLI clades. The abundance of Prochlorococcus cells containing narB for each of these clades was determined by quantitative PCR at 12 depths every month from October 2005 to December 2007 at two locations: BATS location (5 nautical mile radius around 31 40'N, 64 10'W) and HOT Station ALOHA (5 nautical mile radius around 22 45'N, 158 00' W). These field samples are a subset of those utilized in the "Prochlorococcus HOT/BATS" dataset (http://www.bco-dmo.org/dataset/3381).

These data are reported and described in:

Berube, P. M., Coe, A., Roggensack, S. E., & Chisholm, S. W. (2015). Temporal dynamics of Prochlorococcuscells with the potential for nitrate assimilation in the subtropical Atlantic and Pacific oceans. Limnology and Oceanogr

Methods & Sampling

Sample processing and analyses are detailed in the publications 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 the narB gene from the HLII and LLI clades of Prochlorococcus. Standard curves used for quantitation of field data were derived from DNA extracted from defined cell numbers of cultured representatives of each clade.

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. Samples were excluded if the coefficient of variation (standard deviation divided by the mean) was greater than 50%. The no data value "nd" refers to missing or excluded measurements.

Related files and references:

Analysis and data processing used the same field samples and methods as described in the following publication, but with different primer sets:

Malmstrom, R. R., Coe, A., Kettler, G. C., Martiny, A. C., Frias-Lopez, J., Zinser, E. R., & Chisholm, S. W. (2010). Temporal dynamics of Prochlorococcus ecotypes in the Atlantic and Pacific oceans. The ISME Journal, 4(10), 1252–1264. doi:10.1038/ismej.2010.60

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Data Files

File
prochloro_narB.csv(Comma Separated Values (.csv), 128.74 KB) MD5:5bd36164a1ed7345bb923c1cbca70872 Primary data file for dataset ID 641495

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Related Publications

Berube, P. M., Coe, A., Roggensack, S. E., & Chisholm, S. W. (2015). Temporal dynamics of Prochlorococcuscells with the potential for nitrate assimilation in the subtropical Atlantic and Pacific oceans. Limnology and Oceanography, 61(2), 482–495. doi:10.1002/lno.10226
Results

Malmstrom, R. R., Coe, A., Kettler, G. C., Martiny, A. C., Frias-Lopez, J., Zinser, E. R., & Chisholm, S. W. (2010). Temporal dynamics of Prochlorococcus ecotypes in the Atlantic and Pacific oceans. The ISME Journal, 4(10), 1252–1264. doi:10.1038/ismej.2010.60
Methods

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Parameters

Parameter	Description	Units
gene	nitrate reductase gene (narB) in one of two clades (HLII and LLI)	text
site	Location of the measurement at one of two sites located at the HOT and BATS sites	text
lat	Latitude; north is positive	decimal degrees
lon	Longitude; east is positive	decimal degrees
cruiseid	The cruise identification	numeric
year	Year the measurement was taken in YYYY format	unitless
month	Month the measurement was taken	mm
day	Day the measurement was taken	dd
date	Date the sample was taken	mm/dd/yy
yrday_gmt	The year day the sample was taken with 1 meaning January 1	decimal number
abundance	Abundance of HLII or LLI clade Prochlorococcus cells containing the narB gene	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 measurements	cells/milliliter

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Instruments

Dataset-specific Instrument Name	influx flow cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	from Becton Dickinson, Franklin Lakes, NJ, USA
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

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Deployments

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.

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.

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Project Information

Nitrate Assimilation and the Ecology of Prochlorococcus: Features and Implications of Intraspecific Diversity in a Model Marine Phototroph (Prochloro_ecology)

Coverage: BATS station (31.7 N 64.2 W) and HOT station ALOHA (22.75 N 158 W)

Extracted from the NSF award abstract:

First discovered in 1988, Prochlorococcus is now recognized as the most abundant photosynthetic cell in the oceans and is responsible for a significant fraction of global primary productivity. Arguably one of the best studied marine microorganisms to date, Prochlorococcus is well-developed as a model system for advancing our understanding of microbial ecology. It is comprised of a collection of genetically and physiologically distinct populations that co-exist and are differentially distributed along quantifiable gradients of light,

temperature, and inorganic nutrients. Early physiological studies using cultured isolates indicated that this group of cyanobacteria was unable to assimilate nitrate, typically the most abundant inorganic nitrogen source in the open ocean. This observation was supported by the first 12 genome sequences of Prochlorococcus which all lacked the genes necessary for nitrate assimilation. The lack of these genes in Prochlorococcus was puzzling given that closely related, and co-occurring, Synechococcus cells have them, and that nitrogen availability can be a significant limiting factor for primary production in marine ecosystems. Our understanding changed in 2009 with the discovery of nitrate assimilation genes in wild Prochlorococcus genomes and the isolation of an axenic strain capable of growth on nitrate (unpublished data). This discovery has lead to the overarching questions that are the subject of this project:

- What subset of the Prochlorococcus meta-population in the wild contains nitrate assimilation genes and how do the dynamics of this sub-population vary in time and space?

- What features of the environment select for cells with this functional trait?

- Is the phylogeny of Prochlorococcus nitrate assimilation genes better correlated with the local environment or the overall 16S-23S ITS phylogeny of Prochlorococcus?

- Do the genomes of cells that contain nitrate assimilation genes share specific features? What do they tell us about what other environmental variables influence the fitness of nitrate-assimilating cells?

- What are the physiological tradeoffs underlying the loss or gain of assimilation genes in particular strains?

These questions will be addressed using an integrative cross-scale approach to characterize nitrate assimilation by Prochlorococcus at the population, cellular, and genomic levels. Specifically, the distribution and abundance of nitrate assimilating Prochlorococcus will be measured at two contrasting open ocean time-series stations (HOT and BATS), and along a longitudinal gradient in the Atlantic (AMT). The PI will examine the regulation of nitrate assimilation, the kinetics of growth on nitrate, and the ability of Prochlorococcus to compete with Synechococcus under nitrogen limiting conditions. Further, they will use a culture independent single cell genomics approach to assess the phylogenetic diversity of nitrate assimilation genes within the genomic context of several ribotypes. These studies will advance our understanding the biogeography of functional traits in microbes, how it is shaped by selection, and the role of intra-species functional diversity in the overall population dynamics of Prochlorococcus.

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Funding

Funding Source	Award
NSF Division of Biological Infrastructure (NSF DBI)	DBI-0424599
NSF Division of Ocean Sciences (NSF OCE)	OCE-1153588
Gordon and Betty Moore Foundation (GBMF)	GBMF495

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