18S rRNA gene sequence from the euphotic zone at Station ALOHA from near-monthly samples collected during Hawaii Ocean Time-series (HOT) program cruises 230-252 between 2011 and 2013 (PhytoNsubResponse project)

Website: https://www.bco-dmo.org/dataset/722731
Version:
Version Date: 2017-08-25

Project
» Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity (PhytoNsubResponse)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
Church, Matthew J.	University of Montana	Principal Investigator, Contact
Arrigo, Kevin R.	Stanford University	Co-Principal Investigator
Kolber, Zbigniew	University of California-Santa Cruz (UCSC)	Co-Principal Investigator
Zehr, Jonathan P.	University of California-Santa Cruz (UCSC)	Co-Principal Investigator
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Coverage

Spatial Extent: **Lat**:22.75 **Lon**:-158

Dataset Description

18S rRNA gene sequences from the euphotic zone (0-175 m) at Station ALOHA. Samples were collected at near-monthly intervals over ~2 year period (2011-2013); the V9 region of the 18S rRNA gene was PCR amplified and sequenced on an Illumina MiSeq.

Methods & Sampling

Sampling and Analytical Methodology:

Seawater was collected in 12-L polyvinylchloride bottles affixed to a 24-bottle rosette

sampler, equipped with a Sea-Bird 911+ conductivity, temperature, and pressure profiler. Seawater samples were sequentially filtered using a peristaltic pump onto 25-mm diameter, 3-µm pore size polycarbonate membranes (Millipore IsoporeTM), followed by filtration through 25-mm diameter, 0.2-µm pore size polyethersulfone filters (Pall Supor®). After filtration, filters were placed in sterile 1.5-mL microcentrifuge tubes, immediately flash-frozen in liquid nitrogen, and stored at -80°C until analysis. Back in the shore-based laboratory, DNA from the 0.2-µm filter membranes was extracted and purified using the QIAGEN DNeasy Plant Mini Kit including a bead-beating step (with 0.1- and 0.5-mm beads) and Proteinase K (QIAGEN) for additional cell disruption and lysing. Extracts were eluted in 200 µL of nuclease-free PCR grade water and quantified using the Qubit® fluorometer. Triplicate PCR products were pooled, fragment size was determined using 1.5% agarose gel electrophoresis, and quantity was measured with the Qubit® 2.0 fluorometer with Qubit® dsDNA High Sensitivity Assay kit (Molecular Probes). From each sample, ~50 ng of PCR product was combined and purified using the UltraClean PCR Clean-Up Kit (MoBio).

Data Processing:

Sequences were merged using PEAR (Zhang et al., 2014) and quality-filtered with reads trimmed to 100-150 bp, a maximum expected error of 1%, no ambiguous bases allowed, and an

average Phred quality threshold >34. Reference-based and de novo 70 chimeras were detected using

USEARCH v7.0.1090 (Edgar et al., 2011) with the SILVA 119 database pre-clustered at 97% sequence identity (Quast et al., 2013) and removed. Sequences were deposited into

NCBI’s Sequence Read Archive as BioProject ID PRJNA351881 (accession SRP092782).

Data Processing Description

BCO-DMO Data Manager Processing Notes:
* added column biosample link which is the direct link to the accession at NCBI
* added lat/lon of Station ALOHA 22.75,-158

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Data Files

File
sequences.csv (Comma Separated Values (.csv), 37.40 KB) MD5:5e5644a7c02a49882d002ed5d784cc5c Primary data file for dataset ID 722731

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

HOT_cruises

Website	https://www.bco-dmo.org/deployment/58879
Platform	Multiple Vessels
Report	http://hahana.soest.hawaii.edu/hot/
Start Date	1988-10-31
Description	Since October 1988, the Hawaii Ocean Time-series (HOT) program has investigated temporal dynamics in biology, physics, and chemistry at Stn. ALOHA (22°45' N, 158°W), a deep ocean field site in the oligotrophic North Pacific Subtropical Gyre (NPSG). HOT conducts near monthly ship-based sampling and makes continuous observations from moored instruments to document and study NPSG climate and ecosystem variability over semi-diurnal to decadal time scales. **Methods & Sampling** Hawaii Ocean Time-series (HOT) program cruises 230-252

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Project Information

Oligotrophic phytoplankton community response to changes in N substrates and the resulting impact on genetic, taxonomic and functional diversity (PhytoNsubResponse)

Coverage: North Pacific Subtropical Gyre at Station ALOHA, and a transect from San Diego, CA to Hawaii

(Extracted from NSF award abstract)

Marine phytoplankton are a diverse group of Prokaryotic and Eukaryotic unicellular organisms that account for approximately 50% of global carbon fixation. Nitrogen (N) is an essential element for microbial growth, but concentrations of bioavailable nitrogen in vast regions of subtropical ocean gyres are extremely low (submicromolar to nanomolar concentrations), and generally limit phytoplankton growth. Phytoplankton taxa differ in their genetic capabilities to take up and assimilate nutrients, and thus competition for different chemical forms of N (NH4+, NO3- and urea) and supply of these N-containing compounds are important controls on phytoplankton growth, productivity, and ultimately ecosystem function. The form and supply of N to phytoplankton have already been altered by anthropogenic activities, and with increasing environmental perturbations the effects will accelerate. To date however, there is limited information on how the N forms and fluxes impact the marine phytoplankton community composition and primary production. Similarly, determining the mechanisms of the response are crucial to assessing how ocean ecosystem function will respond to global climate change.

This project seeks to determine how taxonomic, genetic and functional dimensions of phytoplankton diversity are linked with community-level responses to the availability of different N substrates (NH4+, NO3-, and urea) in one of Earth's largest aquatic habitats, the North Pacific Subtropical Gyre. The project will characterize phytoplankton community composition change and gene expression, photosynthetic performance, carbon fixation, and single-cell level N and C uptake in different taxa within the phytoplankton assemblage in response to different N compounds. The research project is unique in investigating community-to-single-cell level function and species (strain)-specific gene expression patterns using state-of-the-art methods including fast repetition rate fluorometry, nanoscale secondary ion mass spectrometry and a comprehensive marine microbial community microarray. The results will provide predictive understanding of how changes in the availability of key nitrogen pools (N) may impact phytoplankton dynamics and function in the ocean.

References:

Karl, D. M., Bjorkman, K. M., Dore, J. E., Fujieki, L., Hebel, D. V., Houlihan, T., Letelier, R. M., Tupas, L. M. 2001. Ecological nitrogen-to-phosphorus stoichiometry at station ALOHA. Deep-Sea Research II. 48:1529 - 1566.

Karl, D. M., Letelier, R., Tupas, L., Dore, J., Christian, J. & Hebel, D. 1997. The role of nitrogen fixation in biogeochemical cycling in the subtropical North Pacific Ocean. Nature. 388:533-538.

McCarthy, J., Taylor, W. R., Taft, J. 1997. Nitrogenous nutrition of the plankton in the Chesapeake Bay. Limnology and Oceanography. 35:822 - 829.

Letelier, R., Karl, D. M. 1996. Role of Trichodesmium spp. in the productivity of the subtropical North Pacific Ocean. Marine Ecology Progress Series. 133:263 - 273.

Lipschultz, F. 1995. Nitrogen-specific uptake rates of marine phytoplankton isolated from natura populations of particles by flow cytometry. Marine Ecology Progress Series. 123:245-258.

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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-1241263

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