Links to accessions for 18S rDNA, chloroplast and metagenomics (picoeukaryote) data from multiple cruises from the Sargasso Sea and CalCOFI line 67 from 2001-2009 (PHYTO_GENOME project)

Website: https://www.bco-dmo.org/dataset/3373
Version: 18 January 2011
Version Date: 2011-01-18

Project
» Unveiling the contributions and regulation of picoeukaryotic phytoplankton in oceanic environments (PHYTO_GENOME)

Contributors	Affiliation	Role
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Dataset Description

Accessions for 18S rDNA , chloroplast and metagenomics data

Biliphyte sequences from this study have been deposited in GenBank under Accession No. EU368003-EU368039

Cuvelier ML, Ortiz A, Kim E, Moehlig H, Richardson DE, Heidelberg JF, Archibald JM, Worden AZ (2008). Widespread distribution of a unique marine protistan lineage. Environmental Microbiology. Vol. 10:1621-1634.

Prymnesiophyte sequences from this study have been deposited in GenBank under Accession Nos. HM581528-HM581638 and HM565909-HM565914. Other scaffolds with predicted genes from this Whole Genome Shotgun/454 project have been deposited at DNA Data Bank of Japan/European Molecular Biology Laboratory/GenBank under the accession no. AEAR00000000. The version described in this paper is the first version, AEAR01000000.

Cuvelier ML, Allen* AE, Monier* A, McCrow JP, Messie M, Tringe SG, Woyke T, Welsh RM, Ishoey T, Lee JH, Binder BJ, DuPont CL, Latasa M, Guigand C, Buck KR, Hilton J, Thiagarajan M, Caler E, Read B, Lasken RS, Chavez FP & AZ Worden (2010). Targeted metagenomics and ecology of globally important uncultured eukaryotic phytoplankton. Proceedings of the National Academy of Sciences USA.

Alveolate sequences from this study have been deposited in GenBank under: EU818567-EU818691, EU836584-EU836597, EU818578-EU818566, EU817966-EU818077, EU836613-EU836615; EU817882-EU817965; EU836616-EU816617

Guillou L, Viprey M, Chambouvet A, Welsh RM, Kirkham AR, Massana R, Scanlan DJ and AZ Worden (2008). Widespread occurrence and genetic diversity of marine parasitoids belonging to Syndiniales (Alveolata). Environmental Microbiology. DOI: 10.1111/j.1462-2920.2008.01731.x

Methods & Sampling

Samples were typically taken at the surface and deep chlorophyll maximum using a niskin rosette, all contextual data available (typically temperature and salinity) was deposited with the GenBank Submission for each sequence.

Field sites and sample collection
Five cruises were conducted, two transects from coastal New England to the BATS site (R/V Endeavor cruise EN351 and R/V Oceanus cruise OC413) and three transects across the Florida Straits (R/V Walton Smith cruises WS0503, WS0518, WS0528) with characteristics as in Table 1. Samples were collected in surface and DCM waters using a Sea-Bird Niskin Rosette equipped with standard CTD and PAR detectors (see also below). For DNA extraction samples, 1 l of seawater was gravity filtered through 2 um pore size filters (GE Osmonics, Minnetonka, MN, USA) and then onto a 0.45 um pore size (2001) or 0.2 um pore size (2005) Supor filter (Pall Gelman, Ann Arbor, MI, USA) using vacuum. For FISH samples whole seawater (no size fractionation) was preserved with 1% paraformaldahyde (final concentration) for at least 1 h in the dark at 4°C. For each replicate, volumes of 180 ml or more of seawater were gently filtered onto a 25 mm, 0.2 um Anodisc filter (Whatman, Maidstone, England). The filters were then subjected to an ethanol dehydration series at 50%, 80%, 100% (diluted in sterile, 18.2 ° H2O) for 3 min each and stored at -80°C. Flow cytometry samples were preserved with 0.25% (final concentration) fresh electron microscopy grade glutaraldehyde (Tousimis, Rockville, MD, USA), flash frozen in liquid nitrogen and moved to -80°C for long-term storage.

Data Processing Description

PCR, cloning and Sanger sequencing for all 18S rDNA sequences; metagenomic data was produced by multiple displacement amplification of flow cytometrically sorted cells with subsequent Sanger and 454-FLX sequencing. See Cuvelier et al. 2008 and Cuvelier et al. 2010 for greater detail if desired.

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Data Files

File
Accessions.csv (Comma Separated Values (.csv), 58.00 KB) MD5:72fa4b13eeba13438129bd5d0e6d330f Primary data file for dataset ID 3373

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Parameters

Parameter	Description	Units
Sequence	Environmental DNA sequencing type	text
Accession_Number_Series	GenBank Start-End accession numbers of sequence	text
Accession_Number_Link	Link to accession number at GenBank	text

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Instruments

Dataset-specific Instrument Name	CTD Sea-Bird
Generic Instrument Name	CTD Sea-Bird
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	Niskin bottle
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	Photosynthetically Available Radiation Sensor
Generic Instrument Name	Photosynthetically Available Radiation Sensor
Generic Instrument Description	A PAR sensor measures photosynthetically available (or active) radiation. The sensor measures photon flux density (photons per second per square meter) within the visible wavelength range (typically 400 to 700 nanometers). PAR gives an indication of the total energy available to plants for photosynthesis. This instrument name is used when specific type, make and model are not known.

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Deployments

EN351

Website	https://www.bco-dmo.org/deployment/58128
Platform	R/V Endeavor
Start Date	2001-03-28
End Date	2001-04-10

EN360

Website	https://www.bco-dmo.org/deployment/58129
Platform	R/V Endeavor
Start Date	2001-09-16
End Date	2001-09-27

OC374

Website	https://www.bco-dmo.org/deployment/58126
Platform	R/V Oceanus
Start Date	2002-03-01
End Date	2002-03-14
Description	Cruise Objective: Examine the relationships between growth rate, grazing mortality, and relative abundance for two pico-phytoplankton groups (Prochlorococcus and Synechococcus) over the well-defined seasonal cycle these two groups experience in surface waters of the Sargasso Sea. Science Activities: - CTD - Drogue Deployments Operations Area: - 32N 64W - Vicinity of BATS - 0-200m, occasional deep casts to 3km Cruise information and original data are available from the NSF R2R data catalog.

OC413

Website	https://www.bco-dmo.org/deployment/58127
Platform	R/V Oceanus
Start Date	2005-05-23
End Date	2005-06-12
Description	Cruise Objective: The primary objective of the project is to examine the relationships between growth rate, grazing mortality, and relative abundance for two pico-phytoplankton groups (Prochlorococcus and Synechococcus) in surface waters of the Sargasso Sea. On-board flow cytometry will be used to assess the abundance of these phytoplankton. A suite of experimental approaches for measuring growth and grazing mortality in natural picoplankton populations will also be applied. Science Activities: This work will involve both on-deck incubations and intensive water- column sampling. For incubations, trace metal-clean Go-Flo samples will be required (see Other Comments, below). For the water-column measurements, CTD casts will be repeatedly made in the vicinity of a free-drifting drogue (see Other Comments); drogue deployments will last ~36 hr. Operations Area: We plan to occupy 2 or 3 major stations, with 1 or 2 drogue deployments and experimental series at each. Additional short stations along the transect from WHOI to BATS will also be made. Cruise information and original data are available from the NSF R2R data catalog.

WS0503

Website	https://www.bco-dmo.org/deployment/58125
Platform	R/V F.G. Walton Smith
Start Date	2005-01-01
End Date	2005-01-01
Description	Only year of cruise known at this time BCO-DMO Staff 13Oct2010

WS0518

Website	https://www.bco-dmo.org/deployment/58131
Platform	R/V F.G. Walton Smith
Start Date	2005-11-01
End Date	2005-11-15
Description	Cruise dates estimated. Month/Year known but exact dates unknown at this time BCO-DMO Staff, 13Oct2010

WS0528

Website	https://www.bco-dmo.org/deployment/58132
Platform	R/V F.G. Walton Smith
Start Date	2005-12-01
End Date	2005-12-01
Description	Cruise dates estimated. BCO-DMO Staff, 13Oct2010

WS0705

Website	https://www.bco-dmo.org/deployment/58130
Platform	R/V F.G. Walton Smith
Start Date	2007-02-27
End Date	2007-02-27
Description	Cruise information and original data are available from the NSF R2R data catalog.

CN207

Website	https://www.bco-dmo.org/deployment/58139
Platform	R/V C_N
Start Date	2009-01-01
End Date	2009-01-01
Description	Vessel name unknown at this time "R/V C_N" is only a place holder based on the cruise id supplied in the metadata form Cruise dates unkown except for year. BCO-DMO Staff, 26Oct2010

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Project Information

Unveiling the contributions and regulation of picoeukaryotic phytoplankton in oceanic environments (PHYTO_GENOME)

Website: http://www.mbari.org/phyto-genome/research.htm

Coverage: Sargasso Sea, Gulf Stream, Florida Straits and eastern North Pacific (CalCOFI line 67)

The growth rates and fate of primary producers in the oceans are key factors regulating carbon flux in the biosphere. While resource limitation is known to

play a major regulatory role, the specific factors controlling growth and mortality of picophytoplankton (<2 microm diameter) are poorly understood. In particular, due to the small size and low sinking quotient of these dominant primary producers, determinants of their fate and transport in the water column are critical to the development of predictive models of carbon flux and its likely perturbation due to climate change. Picophytoplankton is composed of cyanobacteria, (Prochlorococcus and Synechococcus) and small eukaryotes. While the picocyanobacteria have received much attention, little is known about the distribution and dynamics of picophytoeukaryotes, particularly in oceanic settings. The few comparative measurements made to date indicate that the productivity of picophytoeukaryotes can rival that of picocyanobacteria. Hence, knowledge regarding the role of picophytoeukaryotes in open ocean environments is urgently needed. However, this knowledge is only valuable when put in the context of the total picophytoplankton community and, therefore, quantification of picocyanobacteria must also be included.

The overall goal is to develop a method for determining underlying physiological controls of picophytoeukaryotes. A targeted approach will be used, combining flow sorting, cDNA libraries and Expressed Sequence Tags (EST), allowing real-time expressional responses to be identified. This knowledge will highlight key physiological constraints and information on molecular underpinnings of picoeukaryotic population dynamics as well as aiding future efforts to isolate open-ocean picoeukaryotes. This is an important additional benefit from the work since environmental clone library data has demonstrated that such picoeukaryotes are poorly represented in culture collections. Long-term, the environmental genomic approach developed will also provide a high throughput mechanism for profiling expressional responses (mRNA) in the field. In the proposed work, expressional responses will be evaluated in two ocean basins, the equatorial Atlantic and the South Pacific.

PUBLICATIONS PRODUCED AS A RESULT OF THIS RESEARCH
Cuvelier et al. "Widespread distribution of a unique marine protistan lineage.," Environmental Microbiology, 2008.

Note:
All contextual data available (typically temperature and salinity) was deposited with the GenBank Submission for each sequence.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0623928
NSF Division of Ocean Sciences (NSF OCE)	OCE-0836721

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