Pico- and Nanoplankton concentrations from CTD cast deployments collected from the R/V Endeavor (EN532, EN538) cruises in the subarctic Atlantic Ocean from 2013-2014

Website: https://www.bco-dmo.org/dataset/651890
Data Type: Cruise Results
Version: 2
Version Date: 2025-01-08

Project
» Functional diversity of marine eukaryotic phytoplankton and their contributions to the C and N cycling (DimBio NABE)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
Ward, Bess B.	Princeton University	Principal Investigator, Contact
Allen, Andrew E.	J. Craig Venter Institute (JCVI)	Co-Principal Investigator
Sigman, Daniel M.	Princeton University	Scientist
Van Oostende, Nicolas C.	Princeton University	Contact
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset includes pico- and nanoplankton concentrations from CTD cast deployments collected from the R/V Endeavor (EN532, EN538) cruises in the subarctic Atlantic Ocean from 2013-2014.

Table of Contents

Coverage

Spatial Extent: **N**:60 **E**:-19.988 **S**:35.547 **W**:-73.265
Temporal Extent: 2013-08-23 - 2014-05-20

Dataset Description

This dataset includes pico- and nanoplankton cell concentrations from CTD casts made during the August-September 2013 EN532 and April-May 2014 EN358 cruises aboard R/V Endeavor. Study sites were located in the subarctic Atlantic Ocean along the 20 °W meridian between 50 °N and 60 °N in September 2013 and May 2014. Two transects from the US East coast to the subarctic study sites were performed as well.

See the "Related Datasets" section for several related BCO-DMO datasets from the same cruises.

Methods & Sampling

The cell abundance of pico- and nanophytoplankton (<~14 micrometers (µm) cell diameter) was determined by flow cytometric analysis of 1500 microliters (µl) of glutaraldehyde-preserved (1% v/v) (Marie et al. 1997) samples using a BD Accuri C6 flow cytometer equipped with a blue laser (488 nanometers (nm)), at a flow rate of 100 µl per minute, and a core diameter of 22 µm. Standard fluorescent bead solutions were prepared daily and used as an internal standard to assess instrument performance, to standardize scatter and fluorescence measurements (Rainbow Calibration Particles (8 peaks), BD Biosciences), and to validate the flow rate (TruCount, BD Biosciences) for quantitative applications. Each sample was run with fluorescent beads (YG beads, 0.94 µm Fluoresbrite® Yellow Green Microspheres, Polysciences, Inc.) as an internal standard for forward scatter measurements.

We distinguished several phytoplankton groups based on their forward (FSC) and side scatter (SSC), Chla, and phycoerythrin (PE) fluorescence signals: the picophytoplankton (<~2.5 µm) group comprised PE-containing *Synechococcus* and non-PE-containing picoeukaryotes (picoEuk), the nanophytoplankton groups (nanoEuk, >~2.5 - 14 µm) included PE-containing nanophytoplankton (PE_Euk), non-PE-containing phytoplankton, and coccolithophores (Cocco) (the latter group was identified based on their enhanced side scatter signal). The total concentration of nanoeukaryote phytoplankton (totnanoEuk) is the sum of PE_Euk, Cocco, and non-PE-containing phytoplankton other than Cocco.

The picoplanktonic *Prochlorococcus* cells were counted in SYBR Green I-stained samples (Marie et al. 1997), according to (Heywood et al. 2006), because of the difficulty of discriminating unstained cells from background noise. The concentration of heterotrophic bacterial cells was determined by flow cytometric analysis of 250 µl of glutaraldehyde-preserved (1% v/v) and SYBR Green I-stained (1:7500) samples according to Marie et al. (1997) and Gasol and Del Giorgio (2000). The *Prochlorococcus* and heterotrophic bacteria samples were analysed using a BD Accuri C6 flow cytometer, at a flow rate of 35 µl per minute, and a core diameter of 16 µm. All plankton groups were gated and their abundance quantified using FlowJo software (Tree Star, Inc., www.flowjo.com).

The biovolume of phytoplankton cells analyzed by flow cytometry was derived from forward scatter measurements of individual cells based on the polynomial relationship between the log10 of measured biovolumes of pico- and nanophytoplankton cells and the log10 of the peak area of their forward scatter signal (FSC-A) (Laney & Sosik 2014). A calibration procedure, using bead stocks and an unidentified cultured picoeukaryote from the Sosik Lab at Woods Hole Oceanographic Institution, confirmed the inter-lab agreement of flow cytometry-derived biovolume estimates. Since the largest phytoplankton cell in the empirical relationship of Laney & Sosik (2014) had a cell diameter of 14 µm and the number of cells larger than this in our samples was negligible, only cells up to ~14 µm in diameter were included in the cell abundance and biovolume calculations. Cellular biomass was estimated according to the relationship between cellular biovolume (cubic micrometers per cell (µm3 cell-1)) and carbon content (picomoles per cell (pmol cell-1)) for glutaraldehyde preserved pico- and nanophytoplankton cells from (Verity et al. 1992): $C = (0.433 / 12) \times \text{biovolume}^{0.863}$.

Although *Synechococcus* cells could readily be counted based on their size and their characteristic PE fluorescence the high signal-to-noise ratio in the FSC-A channel of the Accuri precluded a reliable cell size estimate for particles smaller than 1 µm. Therefore, the biomass of *Synechococcus* was estimated using a conversion factor of 140 femtograms carbon per cell (fg C cell-1) assuming a cell diameter of 1 µm and 270 fg C µm-3 (Bertilsson et al. 2003). The biomass of *Prochlorococcus* cells was calculated by using an average cellular carbon content of 53.5 fg C cell-1 (Bertilsson et al. 2003), which is very similar to the range of cellular carbon content determined by Casey et al. (2013) for *Prochlorococcus* in the euphotic zone.

Data Processing Description

Quality Flags:

The data quality flag scheme used is that of SEADATANET, where:
no quality control = 0
good value = 1
probably good value = 2
probably bad value = 3
bad value = 4
changed value = 5
value below detection = 6
value in excess = 7
interpolated value = 8
missing value = 9
value phenomenon uncertain = A

BCO-DMO Processing & Version History:
Version 1 (date: 2016-07-15)
- added conventional header with dataset name, PI name, version date.
- renamed parameters to BCO-DMO standard.
- replaced blank cells with "nd".
- replaced blanks with underscores.
- formatted lat and long to 4 decimal places.
Version 1 contained some incorrect values in column "totnanoEuk_biomass_nMC". These values have been corrected in version 2.

Version 2 (date: 2025-01-08)
- Imported original file "FCM_Ward_Dimensions_2024.xlsx" into the BCO-DMO system.
- Marked "nd" as a missing data identifier; all missing data are empty/blank in the final csv file.
- Added a trailing "Z" to the ISO_DateTime_UTC column to indicate UTC time zone.
- Added column for longitude in -180 to 180 degrees; renamed the original longitude column "lon_360"
- Saved the final file as "651890_v2_pico_nano_abund_fcm_en532_en538.csv".
In this version, values in the column "totnanoEuk_biomass_nMC" have been corrected.

[table of contents | back to top]

Data Files

File	
651890_v2_pico_nano_abund_fcm_en532_en538.csv	(Comma Separated Values (.csv), 34.71 KB) MD5:11c6e86cf4ef06412fb913f0f8d01f54
Primary data file for dataset ID 651890, version 2	

[table of contents | back to top]

Related Publications

Bertilsson, S., Berglund, O., Karl, D. M., & Chisholm, S. W. (2003). Elemental composition of marine Prochlorococcus and Synechococcus: Implications for the ecological stoichiometry of the sea. Limnology and Oceanography, 48(5), 1721–1731. Portico. https://doi.org/10.4319/lo.2003.48.5.1721
Methods

Casey, J. R., Aucan, J. P., Goldberg, S. R., & Lomas, M. W. (2013). Changes in partitioning of carbon amongst photosynthetic pico- and nano-plankton groups in the Sargasso Sea in response to changes in the North Atlantic Oscillation. Deep Sea Research Part II: Topical Studies in Oceanography, 93, 58–70. doi:10.1016/j.dsr2.2013.02.002
Methods

Gasol, J. M., & Del Giorgio, P. A. (2000). Using flow cytometry for counting natural planktonic bacteria and understanding the structure of planktonic bacterial communities. Scientia Marina, 64(2), 197–224. doi:10.3989/scimar.2000.64n2197
Methods

Heywood, J. L., Zubkov, M. V., Tarran, G. A., Fuchs, B. M., & Holligan, P. M. (2006). Prokaryoplankton standing

stocks in oligotrophic gyre and equatorial provinces of the Atlantic Ocean: Evaluation of inter-annual variability. Deep Sea Research Part II: Topical Studies in Oceanography, 53(14–16), 1530–1547. https://doi.org/10.1016/j.dsr2.2006.05.005
Methods

Laney, S. R., & Sosik, H. M. (2014). Phytoplankton assemblage structure in and around a massive under-ice bloom in the Chukchi Sea. Deep Sea Research Part II: Topical Studies in Oceanography, 105, 30–41. https://doi.org/10.1016/j.dsr2.2014.03.012
Methods

Marie, D., Partensky, F., Jacquet, S., & Vaulot, D. (1997). Enumeration and Cell Cycle Analysis of Natural Populations of Marine Picoplankton by Flow Cytometry Using the Nucleic Acid Stain SYBR Green I. Applied and Environmental Microbiology, 63(1), 186–193. doi:10.1128/aem.63.1.186-193.1997
Methods

Verity, P. G., Robertson, C. Y., Tronzo, C. R., Andrews, M. G., Nelson, J. R., & Sieracki, M. E. (1992). Relationships between cell volume and the carbon and nitrogen content of marine photosynthetic nanoplankton. Limnology and Oceanography, 37(7), 1434–1446. Portico. https://doi.org/10.4319/lo.1992.37.7.1434
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

Ward, B. B., Allen, A. E., Sigman, D. M. (2015) **CTD data from the R/V Endeavor (EN532) cruise in the subarctic Atlantic Ocean during 2013 (DimBio NABE project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2015-07-31) Version Date 2015-07-31 http://lod.bco-dmo.org/id/dataset/563684 [view at BCO-DMO]

Ward, B. B., Allen, A. E., Sigman, D. M. (2015) **CTD data from the R/V Endeavor (EN538) cruise in the subarctic Atlantic Ocean during 2014 (DimBio NABE project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2015-07-31) Version Date 2015-07-31 http://lod.bco-dmo.org/id/dataset/564097 [view at BCO-DMO]

Ward, B. B., Allen, A. E., Sigman, D. M. (2016) **Dissolved inorganic nutrient concentrations from ctd cast deployments and underway seawater inflow from Endeavor 532 and Endeavor 538.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). Version Date 2016-07-14 http://lod.bco-dmo.org/id/dataset/651816 [view at BCO-DMO]

Ward, B. B., Allen, A. E., Sigman, D. M. (2016) **Particulate nitrogen concentrations, N isotopic composition, and nitrate isotopic composition from EN532.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2) Version Date 2016-07-15 http://lod.bco-dmo.org/id/dataset/652025 [view at BCO-DMO]

Ward, B. B., Allen, A. E., Sigman, D. M. (2022) **Chlorophyll-a concentrations from CTD cast deployments and underway seawater inflow from Endeavor 532 and Endeavor 538 cruises in 2013 and 2014.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2) Version Date 2017-07-17 doi:10.26008/1912/bco-dmo.651784.2 [view at BCO-DMO]

[table of contents | back to top]

Parameters

Parameter	Description	Units
cruise_id	cruise identification	unitless

cast	cast number	unitless
ISO_DateTime_UTC	Date and time (UTC) in ISO 8601 format	unitless
lat	latitude; positive values = North	decimal degrees
lon	longitude; negative values = West	decimal degrees
lon_360	longitude from 0 to 360 degrees	decimal degrees
depth_w	depth of the water	meters
depth	sample depth	meters
Syn_biomass_nMC	concentration of Synechococcus carbon biomass	nanomoles Carbon per liter (nmol C/liter)
Syn_cells_per_ml	concentration of Synechococcus cells	cells/milliliter
Syn_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
picoEuk_biomass_nMC	concentration of picoeukaryote phytoplankton carbon biomass	nanomoles Carbon per liter (nmol C/liter)
picoEuk_cells_per_ml	concentration of picoeukaryote phytoplankton cells	cells/milliliter
picoEuk_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
PE_Euk_biomass_nMC	concentration of phycoerythrin-containing nanoeukaryote phytoplankton carbon biomass	nanomoles Carbon per liter (nmol C/liter)
PE_Euk_cells_per_ml	concentration of phycoerythrin-containing nanoeukaryote phytoplankton cells	cells/milliliter
PE_Euk_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
totnanoEuk_biomass_nMC	concentration of nanoeukaryote phytoplankton carbon biomass	nanomoles Carbon per liter (nmol C/liter)

totnanoEuk_cells_per_ml	concentration of nanoeukaryote phytoplankton cells	cells/milliliter
totnanoEuk_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
cocco_biomass_nMC	concentration of coccolithophore carbon biomass	nanomoles Carbon per liter (nmol C/liter)
cocco_cells_per_ml	concentration of coccolithophore cells	cells/milliliter
cocco_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
Prochlor_biomass_nMC	concentration of Prochlorococcus carbon biomass	nanomoles Carbon per liter (nmol C/liter)
Prochlor_cells_per_ml	concentration of Prochlorococcus cells	cells/milliliter
Prochlor_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
total_FC_phyto_biomass_nMC	concentration of total flow cytometrically determined phytoplankton carbon biomass	nanomoles Carbon per liter (nmol C/liter)
total_FC_phyto_cells_per_ml	concentration of total flow cytometrically determined phytoplankton cells	cells/milliliter
total_FC_phyto_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
total_het_bact_cells_per_ml	concentration of non-chlorophyll a containing bacterial cells	cells/milliliter
total_het_bact_cells_per_ml_flag	quality flag - see description in the Data Processing section of metadata	unitless
comment	comments	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird SBE 911plus
Generic Instrument Description	The Sea-Bird SBE 911 plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911 plus includes the SBE 9plus Underwater Unit and the SBE 11plus Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9 plus and SBE 11 plus is called a SBE 911 plus. The SBE 9 plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 plus and SBE 4). The SBE 9 plus CTD can be configured with up to eight auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorescence, light (PAR), light transmission, etc.). more information from Sea-Bird Electronics

Dataset-specific Instrument Name	
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	BD Accuri C6 flow cytometer
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)

Dataset-specific Instrument Name	
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.

[table of contents | back to top]

Deployments

EN532

Website	https://www.bco-dmo.org/deployment/563687
Platform	R/V Endeavor
Report	http://dmoserv3.bco-dmo.org/data_docs/DimBio_NABE/EN532_CruiseReport.pdf
Start Date	2013-08-22
End Date	2013-09-15
Description	Study sites in the subtropical North-Atlantic Ocean near the Bermuda Atlantic Time Series in February 2012 and August 2012, and in the subarctic Atlantic Ocean along the 20W meridian between 50N and 60N in September 2013 and May 2014. Two transects from the US East coast to the subarctic study sites were performed as well.

EN538

Website	https://www.bco-dmo.org/deployment/563697
Platform	R/V Endeavor
Report	http://dmoserv3.bco-dmo.org/data_docs/DimBio_NABE/EN538_CruiseReport.pdf
Start Date	2014-04-29
End Date	2014-05-22
Description	Study sites in the subarctic Atlantic Ocean along the 20 °W meridian between 58 °N and 60 °N in May 2014. A transect from the US East coast (RI) to the subarctic study sites was performed as well.

[table of contents | back to top]

Project Information

Functional diversity of marine eukaryotic phytoplankton and their contributions to the C and N cycling (DimBio NABE)

Coverage: North Atlantic Ocean, transects from southwest to northeast

This project will investigate the taxonomic, genetic and functional diversity of eukaryotic phytoplankton at two North Atlantic sites (subarctic and subtropical) in two seasons. The PIs will use diagnostic microarrays for community analysis based on functional genes (both DNA and RNA) and next generation sequencing (i.e., transcriptomics using 454 technology) to identify the players, both in terms of community composition and activity, and to explore the functional diversity of the natural assemblage. In order to identify which groups are active in C and N assimilation and which N source is being utilized by the different size and functional groups, both filter-separated and flow cytometry-sorted samples will be used to 1) measure 13C primary production and 15N assimilation by incubations with isotope tracers, 2) measure the natural stable N isotope signatures of different taxonomic groups and 3) link the molecular diversity to the functional diversity in C and N transformations. Using flow cytometry linked to mass spectrometry, these investigators have found an unexpectedly strong differentiation in the form of N assimilated by prokaryotes and eukaryotes, with eukaryotes being more dynamic.

This project will investigate the taxonomic, genetic and functional diversity of eukaryotic phytoplankton and to link this diversity and assemblage composition to the carbon and nitrogen biogeochemistry of the surface ocean. Taxonomic diversity will be investigated by identifying the components of the phytoplankton assemblages using molecular, chemical and microscope methods. Genetic diversity will be explored at several levels, including direct sequencing of clone libraries of key functional genes and metatranscriptomic sequencing and microarray analysis of size fractionated/sorted phytoplankton assemblages. Using natural abundance and tracer stable isotope methods, genetic and taxonomic diversity will be linked to functional diversity in C and N assimilation in size- fractionated and taxon-sorted populations.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1136345

[table of contents | back to top]