

Abundance and biomass of protists from epifluorescence counts and bulk biomass from extracted chl-a from samples from R/V Atlantic Explorer cruises AE1102, AE1118, AE1206, AE1219 in the Sargasso Sea, Bermuda Atlantic Time-Series Station in 2011-12

Website: <https://www.bco-dmo.org/dataset/4019>

Data Type: Cruise Results

Version: 1

Version Date: 2015-01-13

Project

» [Plankton Community Composition and Trophic Interactions as Modifiers of Carbon Export in the Sargasso Sea](#) (Trophic BATS)

Program

» [Ocean Carbon and Biogeochemistry](#) (OCB)

Contributors	Affiliation	Role
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Abstract

Abundance and biomass of protists from epifluorescence counts and bulk biomass from extracted chl-a from samples from R/V Atlantic Explorer cruises AE1102, AE1118, AE1206, AE1219 in the Sargasso Sea, Bermuda Atlantic Time-Series Station in 2011-12.

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Coverage

Spatial Extent: N:33.5 E:-63.48 S:30.05 W:-65.75

Temporal Extent: 2011-02-25 - 2012-07-30

Dataset Description

Protist abundance and biomass based on epifluorescence counts and bulk biomass based on extracted

chlorophyll-a measurements. Samples were collected during four cruises in the Sargasso Sea during spring and summer 2011-2012.

Methods & Sampling

Water Column Sampling:

Water column sampling was performed on four cruises during the spring and the summer of 2011 and 2012 at the Bermuda Atlantic Time-series Study station (31°40'N 64°10'W, BATS) and in the mesoscale eddies found in the surrounding area of the Sargasso Sea. For each cruise, two stations were sampled, usually in the center of a mesoscale eddy and at BATS. The edge of the eddy was sampled two times, as well. To be able to get a better reproducibility of data, each experiment was replicated.

For each experiment, seawater samples were collected pre-dawn (on deck 2:30-4:00, local time) at four different depths within the euphotic zone (20m, 50m, 80m and the Deep Chlorophyll Maximum, DCM). Twenty-one 10L Niskin bottles were attached to a rosette with conductivity, temperature, depth sensors (CTD), and an *in vivo* fluorometer. This sensor allowed for recording in real time of chlorophyll fluorescence and the DCM for each station. The water that was collected from the 10L Niskin bottles was sampled for abundance and biomass of the plankton community.

Bulk measurements:

Chlorophyll-a was extracted from seawater (250 ml and 400 ml depending on the dilution), with 90% acetone and measured after 24hrs at 4 degrees C in the dark onboard the ship using a TD 700 Laboratory Fluorometer using the non-acidification technique (Welschmeyer 1994). These data were used as a proxy for the phytoplankton biomass in the water column and to calculate the bulk growth and grazing rates of the phytoplankton community.

Microscopy Analyses:

To determine cell abundance and the biomass of the protist community (other than ciliates), epifluorescence microscopy was used. Ciliate abundance and biomass was determined using bright-field inverted microscopy (Amacher et al. 2009; Neuer and Cowles 1994). *Epifluorescence microscopy*: 25-50ml of seawater from each depth was filtered onto black membrane filters with 0.2 um pore size. Each sample was fixed first with 0.1 ml of 50% of cold glutaraldehyde, stored for 24 hours at 4 degrees C, and then filtered after addition of 0.2 ml of 1% 4', 6-diamino-2-phenylindole (DAPI). Slides were stored frozen at -20 degrees C onboard ship until transport back to the laboratory at ASU, and stored at -40 degrees C until analysis. The organisms were counted using a ZEISS Axioplan Epifluorescence Microscope equipped with a 100x Plan-NEOFLUAR 100x/1.30 oil, objective lens. Pico, nano and micro plankton were identified and separated in categories based on their approximate geometric shape, size, and on their fluorescence under blue and UV light excitation as described in [Table 1](#) (Amacher et al. 2009, Hansen et al. in prep). Organisms were counted in one to several stripes across the slide. Abundance was then calculated based on number of counted cells, fraction of slide area counted and sample volume. The 95% confidence interval of each organismal count was determined as a function of total cells counted in a given category, according to Lund et al. (1958). The following equations were applied, where x stands for the number of cells counted on each slide:

$LL = x + 1.42 - 1.960 (\sqrt{x + 0.5})$ [Lower limit]

$UL = x + 2.42 - 1.960 (\sqrt{x + 1.5})$ [Upper limit]

Biomass calculations were done for each category of organism counted. Biovolume for each group was determined based on size and shape of the organism by approximating the closest geometric shape (Hillebrand et al. 1999) and then converted into units of carbon based on the carbon to volume ratio (Menden-Deuer and Lessard 2000).

Flow cytometry analyses:

Collection and fixation of flow cytometry samples was carried out according to established methods of the BATS program (<http://www.bios.edu/research/projects/bats/>) and analyzed by the group of Co-PI Dr. Mike Lomas.

Refer to the original [dataset legend](#) (PDF) for more information.

Data Processing Description

BCO-DMO Processing Notes:

- Added lat and lon for each station & cast from the metadata form.
- Replaced spaces with underscores.
- Replaced blanks with 'nd' to indicate 'no data'.
- Dates/times assumed to be in UTC/GMT, based on comparison with other Trophic BATS datasets.

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Data Files

File
protists_biomass.csv (Comma Separated Values (.csv), 49.93 KB) MD5:caa79be2b667f68687497c90b30c7deb Primary data file for dataset ID 4019

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Supplemental Files

File
Neuer protist abundance and biomass original legend filename: Biomass_Neuer_Legend_011315.pdf (Portable Document Format (.pdf), 188.74 KB) MD5:9e324c51c01d3fea977aba9403158a87 Neuer protist abundance and biomass original legend (supplemental doc)
Neuer Table 1 protist abundance and biomass supplemental doc filename: Table1_methodology_neuer.pdf (Portable Document Format (.pdf), 102.51 KB) MD5:607ba2501ae7a30149c9172d4b246dbe Neuer Table 1 protist abundance and biomass supplemental doc

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Related Publications

Agatha S. (2004). A Cladistic Approach for the Classification of Oligotrichid Ciliates (Ciliophora: Spirotricha). *Acta protozoologica*, 43(3), 201–217. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2854820/>
General

Agatha, S., & Strüder-Kypke, M. C. (2007). Phylogeny of the order Choreotrichida (Ciliophora, Spirotricha, Oligotricha) as inferred from morphology, ultrastructure, ontogenesis, and SSrRNA gene sequences. *European Journal of Protistology*, 43(1), 37–63. doi:[10.1016/j.ejop.2006.10.001](https://doi.org/10.1016/j.ejop.2006.10.001)
General

Amacher, J., Neuer, S., Anderson, I., & Massana, R. (2009). Molecular approach to determine contributions of the protist community to particle flux. *Deep Sea Research Part I: Oceanographic Research Papers*, 56(12), 2206–2215. doi:[10.1016/j.dsr.2009.08.007](https://doi.org/10.1016/j.dsr.2009.08.007)
General

Hillebrand, H., Dürselen, C.-D., Kirschtel, D., Pollinger, U., & Zohary, T. (1999). Biovolume calculation for pelagic and benthic microalgae. *Journal of Phycology*, 35(2), 403–424. doi:[10.1046/j.1529-8817.1999.3520403.x](https://doi.org/10.1046/j.1529-8817.1999.3520403.x)
Methods

Landry, M. R., & Hassett, R. P. (1982). Estimating the grazing impact of marine micro-zooplankton. *Marine Biology*, 67(3), 283–288. doi:10.1007/bf00397668 <https://doi.org/10.1007%2Fbfb00397668>
Methods

Landry, M. R., Brown, S. L., Rii, Y. M., Selph, K. E., Bidigare, R. R., Yang, E. J., & Simmons, M. P. (2008). Depth-stratified phytoplankton dynamics in Cyclone Opal, a subtropical mesoscale eddy. *Deep Sea Research Part II: Topical Studies in Oceanography*, 55(10-13), 1348–1359. doi:[10.1016/j.dsr2.2008.02.001](https://doi.org/10.1016/j.dsr2.2008.02.001)
General

Landry, M., Haas, L., & Fagerness, V. (1984). Dynamics of microbial plankton communities: experiments in Kaneohe Bay, Hawaii. Marine Ecology Progress Series, 16, 127–133. doi:[10.3354/meps016127](https://doi.org/10.3354/meps016127)
General

Lund, J. W. G., Kipling, C., & Le Cren, E. D. (1958). The inverted microscope method of estimating algal numbers and the statistical basis of estimations by counting. Hydrobiologia, 11(2), 143–170. doi:10.1007/bf00007865 <https://doi.org/10.1007/BF00007865>
Methods

Menden-Deuer, S., & Lessard, E. J. (2000). Carbon to volume relationships for dinoflagellates, diatoms, and other protist plankton. Limnology and Oceanography, 45(3), 569–579. doi:[10.4319/lo.2000.45.3.0569](https://doi.org/10.4319/lo.2000.45.3.0569)
Methods

Neuer, S., & Cowles, T. (1994). Protist herbivory in the Oregon upwelling system. Marine Ecology Progress Series, 113, 147–162. doi:[10.3354/meps113147](https://doi.org/10.3354/meps113147)
General

Putt, M., & Stoecker, D. K. (1989). An experimentally determined carbon : volume ratio for marine “oligotrichous” ciliates from estuarine and coastal waters. Limnology and Oceanography, 34(6), 1097–1103. doi:[10.4319/lo.1989.34.6.1097](https://doi.org/10.4319/lo.1989.34.6.1097)
General

Selph, K. E., Landry, M. R., Taylor, A. G., Yang, E.-J., Measures, C. I., Yang, J., ... Bidigare, R. R. (2011). Spatially-resolved taxon-specific phytoplankton production and grazing dynamics in relation to iron distributions in the Equatorial Pacific between 110 and 140°W. Deep Sea Research Part II: Topical Studies in Oceanography, 58(3-4), 358–377. doi:[10.1016/j.dsr2.2010.08.014](https://doi.org/10.1016/j.dsr2.2010.08.014)
General

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Parameters

Parameter	Description	Units
cruise_id	Official cruise identifier e.g. AE1102 = R/V Atlantic Explorer cruise number 1102.	dimensionless
cast	Cast number.	dimensionless
station	Station number.	dimensionless
location_description	Description of sampling location.	dimensionless
lat	Latitude. Positive values = North.	decimal degrees
lon	Longitude. Positive values = East.	decimal degrees
depth	Sample depth.	meters
taxon	Name of the taxonomic group. Codes: H_dinos = Heterotrophic dinoflagellates H_nano = Heterotrophic nanoflagellates Mixo_dino = Mixotrophic dinoflagellates Nano_Photo_Eukaryotes = Nano Phototrophic Eukaryotes Pico_Photo_Eukaryotes = Pico Phototrophic Eukaryotes Photo_Eukaryotes = Phototrophic Eukaryotes	dimensionless
total_biomass_per_taxon	Total biomass (pg C/mL) at the particular cast and depth for the taxonomic group.	picograms C per milliliter
length	Length/diameter (in um).	micrometers
width	Width/height (in um).	micrometers
shape	Description of the 3D shape.	dimensionless
abundance	Abundance (cells/mL).	cells per milliliter
abund_lower_95pcnt_CI	Upper 95% confidence interval for abundance.	cells per milliliter
abund_upper_95pcnt_CI	Lower 95% confidence interval for abundance.	cells per milliliter
cells_counted	Number of cells counted.	dimensionless
biovolume	Biovolume (um ³ /mL).	cubic micrometers per milliliter
dino_biomass	Dinoflagellate biomass (pg C/cell).	picograms C per cell
diatoms_biomass	Diatom biomass (pg C/cell).	picograms C per cell
protists_biomass	Protist biomass (pg C/cell).	picograms C per cell
date	2-digit month, 2-digit day, and 4-digit year of sampling. Reported in UTC. Format: mmddYYYY	unitless
experiment_num	Experiment number.	dimensionless
season_year	Sampling season and year.	text

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Instruments

Dataset-specific Instrument Name	Fluorescence Microscope Image Analysis System
Generic Instrument Name	Fluorescence Microscope Image Analysis System
Dataset-specific Description	The organisms were counted using a ZEISS Axioplan Epifluorescence Microscope equipped with a 100x Plan-NEOFLUAR 100x/1.30 oil, objective lens
Generic Instrument Description	A Fluorescence (or Epifluorescence) Microscope Image Analysis System uses semi-automated color image analysis to determine cell abundance, dimensions and biovolumes from an Epifluorescence Microscope. An Epifluorescence Microscope (conventional and inverted) includes a camera system that generates enlarged images of prepared samples. The microscope uses excitation ultraviolet light and the phenomena of fluorescence and phosphorescence instead of, or in addition to, reflection and absorption of visible light.

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Samples were collected using 10-Liter Niskin bottles attached to a CTD rosette.
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	TD 700 Laboratory Fluorometer
Generic Instrument Name	Turner Designs 700 Laboratory Fluorometer
Dataset-specific Description	Chlorophyll a was extracted from seawater (250 ml and 400 ml depending on the dilution), with 90% acetone and measured after 24hrs at 4 degrees C in the dark onboard ship using a TD 700 Laboratory Fluorometer using the non-acidification technique (Welschmeyer 1994).
Generic Instrument Description	The TD-700 Laboratory Fluorometer is a benchtop fluorometer designed to detect fluorescence over the UV to red range. The instrument can measure concentrations of a variety of compounds, including chlorophyll-a and fluorescent dyes, and is thus suitable for a range of applications, including chlorophyll, water quality monitoring and fluorescent tracer studies. Data can be output as concentrations or raw fluorescence measurements.

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Deployments

AE1102

Website	https://www.bco-dmo.org/deployment/58672
Platform	R/V Atlantic Explorer
Start Date	2011-02-23
End Date	2011-03-07
Description	This cruise was the first in a series of four cruises planned to study the trophic interactions and particle export during the winter season in the Sargasso Sea. The researchers focused on several sampling locations including an anticyclonic eddy, slope waters of the eddy, and repeated visits to the Bermuda Atlantic Time Series (BATS) study site. The research focus for the cruise included phytoplankton production, microzooplankton grazing, mesozooplankton grazing and particle export. This process cruise was designed to quantify stocks and rate processes in the Sargasso Sea food web. Work entailed CTD casts, over the stern deployment of in situ primary production arrays and surface tethered sediment traps. Until 26 November 2012 this cruise was identified by BIOS and R2R as AE-X1101. On 26 November 2012, the cruise ID was corrected to AE1102. Original cruise data are available from the NSF R2R data catalog

AE1118

Website	https://www.bco-dmo.org/deployment/58934
Platform	R/V Atlantic Explorer
Start Date	2011-07-22
End Date	2011-08-04
Description	AE1118 was a process cruise aboard the R/V Atlantic Explorer to quantify stocks and rate processes in the Sargasso Sea food web. This was the second in a series of cruises for the Trophic BATS project. On each cruise, sampling was conducted at three stations: the center and edge of a mesoscale eddy and at one station outside of the eddy. Core CTD casts to ~2000 meters and pre-dawn 'Productivity' CTD casts were made at each station. Original cruise data are available from the NSF R2R data catalog.

AE1206

Website	https://www.bco-dmo.org/deployment/58935
Platform	R/V Atlantic Explorer
Start Date	2012-03-14
End Date	2012-03-23
Description	AE1206 was the third in a series of four cruises for the Trophic BATS project. On each cruise, sampling was conducted at three stations: the center and edge of a mesoscale eddy and at one station outside of the eddy. Core CTD casts to ~2000 meters and pre-dawn 'Productivity' CTD casts were made at each station. Cruise information and original data are available from the NSF R2R data catalog.

AE1219

Website	https://www.bco-dmo.org/deployment/58936
Platform	R/V Atlantic Explorer
Start Date	2012-07-19
End Date	2012-07-31
Description	AE1219 was the final cruise in a series of four for the Trophic BATS project. On each cruise, sampling was conducted at three stations: the center and edge of a mesoscale eddy and at one station outside of the eddy. Core CTD casts to ~2000 meters and pre-dawn 'Productivity' CTD casts were made at each station. Cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Plankton Community Composition and Trophic Interactions as Modifiers of Carbon Export in the Sargasso Sea (Trophic BATS)

Coverage: Sargasso Sea, BATS site

Fluxes of particulate carbon from the surface ocean are greatly influenced by the size, taxonomic composition and trophic interactions of the resident planktonic community. Large and/or heavily-ballasted phytoplankton such as diatoms and coccolithophores are key contributors to carbon export due to their high sinking rates and direct routes of export through large zooplankton. The potential contributions of small, unballasted phytoplankton, through aggregation and/or trophic re-packaging, have been recognized more recently. This recognition comes as direct observations in the field show unexpected trends. In the Sargasso Sea, for example, shallow carbon export has increased in the last decade but the corresponding shift in phytoplankton community composition during this time has not been towards larger cells like diatoms. Instead, the abundance of the picoplanktonic cyanobacterium, *Synechococcus*, has increased significantly. The trophic pathways that link the increased abundance of *Synechococcus* to carbon export have not been characterized. These observations helped to frame the overarching research question, "How do plankton size, community composition and trophic interactions modify carbon export from the euphotic zone". Since small phytoplankton are responsible for the majority of primary production in oligotrophic subtropical gyres, the trophic interactions that include them must be characterized in order to achieve a mechanistic understanding of the function of the biological pump in the oligotrophic regions of the ocean.

This requires a complete characterization of the major organisms and their rates of production and consumption. Accordingly, the research objectives are: 1) to characterize (qualitatively and quantitatively) trophic interactions between major plankton groups in the euphotic zone and rates of, and contributors to, carbon export and 2) to develop a constrained food web model, based on these data, that will allow us to better understand current and predict near-future patterns in export production in the Sargasso Sea.

The investigators will use a combination of field-based process studies and food web modeling to quantify rates of carbon exchange between key components of the ecosystem at the Bermuda Atlantic Time-series Study (BATS) site. Measurements will include a novel DNA-based approach to characterizing and quantifying planktonic contributors to carbon export. The well-documented seasonal variability at BATS and the occurrence of mesoscale eddies will be used as a natural laboratory in which to study ecosystems of different structure. This study is unique in that it aims to characterize multiple food web interactions and carbon export simultaneously and over similar time and space scales. A key strength of the proposed research is also the tight connection and feedback between the data collection and modeling components.

Characterizing the complex interactions between the biological community and export production is critical for predicting changes in phytoplankton species dominance, trophic relationships and export production that might occur under scenarios of climate-related changes in ocean circulation and mixing. The results from this research may also contribute to understanding of the biological mechanisms that drive current regional to basin scale variability in carbon export in oligotrophic gyres.

Program Information

Ocean Carbon and Biogeochemistry (OCB)

Website: <http://us-ocb.org/>

Coverage: Global

The Ocean Carbon and Biogeochemistry (OCB) program focuses on the ocean's role as a component of the global Earth system, bringing together research in geochemistry, ocean physics, and ecology that inform on and advance our understanding of ocean biogeochemistry. The overall program goals are to promote, plan, and coordinate collaborative, multidisciplinary research opportunities within the U.S. research community and with international partners. Important OCB-related activities currently include: the Ocean Carbon and Climate Change (OCCC) and the North American Carbon Program (NACP); U.S. contributions to IMBER, SOLAS, CARBOOCEAN; and numerous U.S. single-investigator and medium-size research projects funded by U.S. federal agencies including NASA, NOAA, and NSF.

The scientific mission of OCB is to study the evolving role of the ocean in the global carbon cycle, in the face of environmental variability and change through studies of marine biogeochemical cycles and associated ecosystems.

The overarching OCB science themes include improved understanding and prediction of: 1) oceanic uptake and release of atmospheric CO₂ and other greenhouse gases and 2) environmental sensitivities of biogeochemical cycles, marine ecosystems, and interactions between the two.

The OCB Research Priorities (updated January 2012) include: ocean acidification; terrestrial/coastal carbon fluxes and exchanges; climate sensitivities of and change in ecosystem structure and associated impacts on biogeochemical cycles; mesopelagic ecological and biogeochemical interactions; benthic-pelagic feedbacks on biogeochemical cycles; ocean carbon uptake and storage; and expanding low-oxygen conditions in the coastal and open oceans.

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1030476