Chemical analyses of size-fractionated particle samples collected during the BIOS-SCOPE cruise AE1819 in the Sargasso Sea in July 2018

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Data Type: Cruise Results
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Project
» Bermuda Institute of Ocean Sciences Simons Collaboration on Ocean Processes and Ecology (BIOSSCOPE)

Contributors	Affiliation	Role
Carlson, Craig A.	University of California-Santa Barbara (UCSB)	Principal Investigator
Close, Hilary G.	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Principal Investigator
Garley, Rebecca	Bermuda Institute of Ocean Sciences (BIOS)	Scientist
Henderson, Lillian	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Student
Ortiz, Albert	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Technician
Saied, Amel	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Technician
Halewood, Elisa	University of California-Santa Barbara (UCSB)	Data Manager
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Included in this dataset are chemical analyses of size-fractionated particle samples collected during BIOS-SCOPE project cruises in the Sargasso Sea starting in 2018. Samples were collected using McLane WTS-LV in-situ pumps and analyzed for phytol concentration, bulk particulate organic carbon (POC), stable carbon isotope composition, and nitrogen and carbon isotope composition of amino acids.

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Coverage

Location: North Atlantic Subtropical Gyre - Bermuda Atlantic Time Series (BATS) site
Spatial Extent: **Lat**:31.6667 **Lon**:-64.1667

Temporal Extent: 2018-07-03 - 2018-07-05

Methods & Sampling

Carbon isotopes and concentrations of phytol:
Size-fractionated particle samples were collected using McLane WTS-LV in-situ pumps using four 142-millimeter (mm) diameter filter tiers. Size fractions reported here are as follows: 1.2-6 micrometers (µm) size fraction collected on two pre-combusted, stacked 1.2 µm glass fiber filters and 0.3-1.2 µm size fraction collected on two pre-combusted, stacked 0.3 µm glass fiber filters. Samples were stored at -80 degrees Celsius until processing. Chlorophyll was extracted from frozen or freeze-dried filter splits as part of a total lipid extraction using a mixture of chilled methanol, dichloromethane, and milliQ water (Bligh & Dyer, 1959; Sturt et al., 2004) using freeze/thaw, sonication, and vortexing/shaking to enhance extraction efficiency. Filter material was removed, and the total lipid extract (TLE) was further purified via liquid-liquid extraction against salt water and dried under N2. Lipid classes from each TLE were separated on silica gel mini columns (Bastow et al., 2007); reported here is the sum of the concentrations of phytol from chlorophyll in these fractions and the weighted average d13C value. Lipid classes were aliquoted by volume and saponified to cleave the phytol side chain from intact chlorophyll. Neutral lipids were obtained via liquid-liquid extraction from the basic mixtures and concentrated using a Turbovap evaporator. Quantitative aliquots were derivatized to trimethylsilyl (TMS) ethers and analyzed via gas chromatography mass spectrometry with a TG-5MS column. Samples containing sufficient phytol were analyzed for stable carbon isotope composition via gas chromatography-isotope ratio mass spectrometry equipped with a TG-5MS column. Phytol standards of a known δ13C value were derivatized alongside samples to account for isotope fractionation during the derivatization reaction as well as the δ13C value of added derivative carbon.

Carbon isotopes and bulk particulate organic carbon (POC, d13C POC):
Size-fractionated particle samples were collected using McLane WTS-LV in-situ pumps using four 142 mm diameter filter tiers. Size fractions reported here are as follows: 1.2-6 µm size fraction collected on two pre-combusted, stacked 1.2 µm glass fiber filters and 0.3-1.2 µm size fraction collected on two pre-combusted, stacked 0.3 µm glass fiber filters. Samples were stored at -80 degrees Celsius until processing. Filter splits were then freeze-dried, and carbonates were removed via acidification. Bulk POC concentration and isotope composition were measured using a Thermo Flash elemental analyzer coupled to a Conflo IV and MAT 253 Plus isotope ratio mass spectrometer (EA-IRMS, Thermo Scientific). These data are not blank corrected, but blanks were measured and are negligible relative to measured POC and d13C values.

Amino Acid analysis (d13C THAA):
Size-fractionated particle samples were collected using McLane WTS-LV in-situ pumps using four 142 mm diameter filter tiers. Size fractions reported here are as follows: 1.2-6 µm size fraction collected on two pre-combusted, stacked 1.2 µm glass fiber filters and 0.3-1.2 µm size fraction collected on two pre-combusted, stacked 0.3 µm glass fiber filters. Samples were stored at -80 degrees Celsius until processing. Quantitative splits were freeze-dried, hydrolyzed, purified, derivatized, and analyzed for nitrogen and carbon isotope composition of individual amino acids. δ13C values of total hydrolysable amino acids (δ13CTHAA) were calculated as in McCarthy et al. (2013): δ13CTHAA = Σ (δ13CAA * mol%AA) where δ13CAA and mol%AA are the δ13C value and the molar percentage contribution of each individual amino acid, respectively. The standard deviation for each sample was calculated as the square root of the weighted average of variances of each individual amino acid.

Trophic Position (TP) from d15N-AA:
Size-fractionated particle samples were collected using McLane WTS-LV in-situ pumps using four 142 mm diameter filter tiers. Size fractions reported here are as follows: 1.2-6 µm size fraction collected on two pre-combusted, stacked 1.2 µm glass fiber filters and 0.3-1.2 µm size fraction collected on two pre-combusted, stacked 0.3 µm glass fiber filters. Samples were stored at -80 degrees Celsius until processing. Quantitative splits were freeze-dried, hydrolyzed, purified, derivatized, and analyzed for nitrogen and carbon isotope composition of individual amino acids. POM trophic position was calculated from measured δ15N values of glutamic acid+glutamine (Glx) and phenylalanine (Phe) as in Chikaraishi et al. (2009): TP = (δ15NGlx - δ15NPhe - 3.4)/7.6 + 1 . TP propagated uncertainty was calculated as in Jarman et al. (2017).

BCO-DMO Processing Description

- Imported original file "BIOSSCOPE_in-situ pump_chem data.xlsx" into the BCO-DMO system.
- Flagged "NaN" and "n/a" as missing data identifiers (missing data are empty/blank in the final CSV).

- Renamed fields (parameters) to comply with BCO-DMO naming conventions.
- Converted dates to YYYY-MM-DD format.
- Added columns for Latitude and Longitude.
- Saved the final file as "920443_v1_biosscope_in_situ_pump_chemical_data.csv".

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Data Files

File	
920443_v1_biosscope_in_situ_pump_chemical_data.csv	(Comma Separated Values (.csv), 1.33 KB) MD5:9a15976e7fef40d5c3f33b226120bd64
Primary data file for dataset ID 920443, version 1	

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Related Publications

Bastow, T. P., van Aarssen, B. G. K., & Lang, D. (2007). Rapid small-scale separation of saturate, aromatic and polar components in petroleum. Organic Geochemistry, 38(8), 1235–1250. https://doi.org/10.1016/j.orggeochem.2007.03.004
Methods

Bligh, E. G., & Dyer, W. J. (1959). A RAPID METHOD OF TOTAL LIPID EXTRACTION AND PURIFICATION. Canadian Journal of Biochemistry and Physiology, 37(8), 911–917. https://doi.org/10.1139/o59-099
Methods

Chikaraishi, Y., Ogawa, N. O., Kashiyama, Y., Takano, Y., Suga, H., Tomitani, A., Miyashita, H., Kitazato, H., & Ohkouchi, N. (2009). Determination of aquatic food-web structure based on compound-specific nitrogen isotopic composition of amino acids. Limnology and Oceanography: Methods, 7(11), 740–750. Portico. https://doi.org/10.4319/lom.2009.7.740
Methods

Henderson, L.C., Wittmers, F., Carlson, C. A., Worden, A.Z., & Close, H. G. (under review). Variable carbon isotope fractionation of photosynthetic communities over depth in a stratified euphotic zone. 10.1073/pnas.2304613121
Results

Jarman, C. L., Larsen, T., Hunt, T., Lipo, C., Solsvik, R., Wallsgrove, N., Ka'apu-Lyons, C., Close, H. G., & Popp, B. N. (2017). Diet of the prehistoric population of Rapa Nui (Easter Island, Chile) shows environmental adaptation and resilience. American Journal of Physical Anthropology, 164(2), 343–361. Portico. https://doi.org/10.1002/ajpa.23273
Methods

McCarthy, M. D., Lehman, J., & Kudela, R. (2013). Compound-specific amino acid δ15N patterns in marine algae: Tracer potential for cyanobacterial vs. eukaryotic organic nitrogen sources in the ocean. Geochimica et Cosmochimica Acta, 103, 104–120. https://doi.org/10.1016/j.gca.2012.10.037
Methods

Sturt, H. F., Summons, R. E., Smith, K., Elvert, M., & Hinrichs, K.-U. (2004). Intact polar membrane lipids in prokaryotes and sediments deciphered by high-performance liquid chromatography/electrospray ionization multistage mass spectrometry—new biomarkers for biogeochemistry and microbial ecology. Rapid Communications in Mass Spectrometry, 18(6), 617–628. doi:10.1002/rcm.1378
Methods

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Parameters

Parameter	Description	Units
Sample	Internal sample ID	unitless
Cruise	BIOSSCOPE cruise identifier	unitless
Date	Date (local, Bermuda) of sample collection	unitless
Latitude	Latitude of sample collection	decimal degrees
Longitude	Longitude of sample collection (negative values = West)	decimal degrees
size_fraction_um	particle size range for water fraction	micrometers (um)
split_type	Condition under which filter was stored and split into fractions for analysis (frozen or freeze dried)	unitless
Depth_m	Water column depth of sample	meters (m)
total_phytol_from_chlorophyll_concentration_ng_L	phytol concentration	nanograms per liter (ng/L)
phytol_concentration_sd_ng_L	phytol concentration standard deviation	nanograms per liter (ng/L)
d13C_phytol_corrected_value_per_mil	stable carbon isotope composition of phytol	per mil
d13C_phytol_sd_per_mil	stable carbon isotope composition of phytol standard deviation	per mil
d13C_POC_per_mil	stable carbon isotope composition of bulk particulate organic carbon	per mil
d13C_POC_sd_per_mil	stable carbon isotope composition of bulk particulate organic carbon standard deviation	per mil
POC_concentration_ug_L	bulk particulate organic carbon	micrograms per liter (ug/L)
d13C_THAA_per_mil	d13C values of total hydrolysable amino acids	per mil
d13C_THAA_sd_per_mil	d13C THAA standard deviation	per mil
TP_from_d15N_AA	POM trophic position (TP) calculated from measured d15N values of glutamic acid+glutamine (Glx) and phenylalanine (Phe) as in Chikaraishi et al. (2009): TP = (d15NGlx - d15NPhe - 3.4)/7.6 + 1 . TP propagated uncertainty was calculated as in Jarman et al. (2017).	unitless
TP_sd	Trophic Position (TP) standard deviation	unitless

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Instruments

Dataset-specific Instrument Name	Conflo IV
Generic Instrument Name	Continuous Flow Interface for Mass Spectrometers
Dataset-specific Description	Thermo Flash elemental analyzer coupled to a Conflo IV and MAT 253 Plus isotope ratio mass spectrometer (EA-IRMS, Thermo Scientific).
Generic Instrument Description	A Continuous Flow Interface connects solid and liquid sample preparation devices to instruments that measure isotopic composition. It allows the introduction of the sample and also reference and carrier gases. Examples: Finnigan MATConFlo II, ThermoScientific ConFlo IV, and Picarro Caddy. Note: This is NOT an analyzer

Dataset-specific Instrument Name	Thermo Flash elemental analyzer
Generic Instrument Name	Elemental Analyzer
Dataset-specific Description	Thermo Flash elemental analyzer coupled to a Conflo IV and MAT 253 Plus isotope ratio mass spectrometer (EA-IRMS, Thermo Scientific)
Generic Instrument Description	Instruments that quantify carbon, nitrogen and sometimes other elements by combusting the sample at very high temperature and assaying the resulting gaseous oxides. Usually used for samples including organic material.

Dataset-specific Instrument Name	GC-MS,GC-IRMS
Generic Instrument Name	Gas Chromatograph Mass Spectrometer
Dataset-specific Description	GC-MS,GC-IRMS (gas chromatography-isotope ratio mass spectrometry equipped with a TG-5MS column)
Generic Instrument Description	Instruments separating gases, volatile substances or substances dissolved in a volatile solvent by transporting an inert gas through a column packed with a sorbent to a detector for assay by a mass spectrometer.

Dataset-specific Instrument Name	MAT 253 Plus isotope ratio mass spectrometer
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	Thermo Flash elemental analyzer coupled to a Conflo IV and MAT 253 Plus isotope ratio mass spectrometer (EA-IRMS, Thermo Scientific).
Generic Instrument Description	The Isotope-ratio Mass Spectrometer is a particular type of mass spectrometer used to measure the relative abundance of isotopes in a given sample (e.g. VG Prism II Isotope Ratio Mass-Spectrometer).

Dataset-specific Instrument Name	McLane WTS-LV
Generic Instrument Name	McLane Large Volume Pumping System WTS-LV
Generic Instrument Description	The WTS-LV is a Water Transfer System (WTS) Large Volume (LV) pumping instrument designed and manufactured by McLane Research Labs (Falmouth, MA, USA). It is a large-volume, single-event sampler that collects suspended and dissolved particulate samples in situ. Ambient water is drawn through a modular filter holder onto a 142-millimeter (mm) membrane without passing through the pump. The standard two-tier filter holder provides prefiltering and size fractioning. Collection targets include chlorophyll maximum, particulate trace metals, and phytoplankton. It features different flow rates and filter porosity to support a range of specimen collection. Sampling can be programmed to start at a scheduled time or begin with a countdown delay. It also features a dynamic pump speed algorithm that adjusts flow to protect the sample as material accumulates on the filter. Several pump options range from 0.5 to 30 liters per minute, with a max volume of 2,500 to 36,000 liters depending on the pump and battery pack used. The standard model is depth rated to 5,500 meters, with a deeper 7,000-meter option available. The operating temperature is -4 to 35 degrees Celsius. The WTS-LV is available in four different configurations: Standard, Upright, Bore Hole, and Dual Filter Sampler. The high-capacity upright WTS-LV model provides three times the battery life of the standard model. The Bore-Hole WTS-LV is designed to fit through a narrow opening such as a 30-centimeter borehole. The dual filter WTS-LV features two vertical intake 142 mm filter holders to allow simultaneous filtering using two different porosities.

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Deployments

AE1819

Website	https://www.bco-dmo.org/deployment/857784
Platform	R/V Atlantic Explorer
Report	https://datadocs.bco-dmo.org/docs/305/BIOSSCOPE/data_docs/AE1819_CS_narrative_v1.pdf
Start Date	2018-07-03
End Date	2018-07-06
Description	Project BIOS-SCOPE

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Project Information

Bermuda Institute of Ocean Sciences Simons Collaboration on Ocean Processes and Ecology (BIOSSCOPE)

Website: http://scope.bios.edu/

Coverage: North Atlantic Subtropical Gyre, Bermuda Atlantic Time Series (BATS) site

The aim of BIOS-SCOPE is to expand knowledge about the BATS ecosystem and achieve a better understanding of ocean food web sources, sinks and transformations of DOM. Advances in knowledge and

technology now poise us to investigate the specific mechanisms of DOM incorporation, oxidation and transformation by zooplankton and the distinct microbial plankton communities that have been discovered at BATS.

The overarching goal of the BIOS-SCOPE is to form and foster collaborations of cross disciplinary science that utilize a broad suite of genomic, chemical, ecological, and biogeochemical approaches to evaluate microbial process, structure and function on various scales. These scales will range from organism-compound and organism-organism interactions to large biogeochemical patterns on the ecosystem scale. For this purpose we have assembled a cross-disciplinary team including microbial oceanographers (Carlson and Giovannoni), a chemical oceanographer (Kujawinski), biological oceanographer / zooplankton ecologists (Maas and Blanco-Bercial) and microbial bioinformatician (Temperton) with the expertise and technical acuity that are needed to study complex interactions between food web processes, microbes and DOM quantity and quality in the oligotrophic ocean. This scientific team has a vision of harnessing this potential to produce new discoveries that provide a mechanistic understanding of the carbon cycle and explain the many emergent phenomenon that have yet to be understood.

For additional details:

- ***BIOS-SCOPE Narrative***: *https://datadocs.bco-dmo.org/docs/302/BIOSSCOPE/data_docs/BIOS-SCOPE_Narrative_FINAL.pdf*
- ***Physical Framework***: *https://datadocs.bco-dmo.org/docs/302/BIOSSCOPE/data_docs/Physical_Framework.pdf*

BIOSSCOPE I: November 1st, 2015 through October 31st, 2020
Current: November 1st, 2020 to October 31st, 2025

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Funding

Funding Source	Award
Simons Foundation (Simons)	409923

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