Size fractionated Amino Acid data collected in the Sargasso Sea during BIOS-SCOPE cruises AE2114 and AE2123 in August and November 2021

Website: https://www.bco-dmo.org/dataset/964684
Data Type: Cruise Results
Version: 1
Version Date: 2025-06-13

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
English, Chance	University of California-Santa Barbara (UCSB)	Scientist
Henderson, Lillian	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Scientist
Popendorf, Kimberly	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Scientist
Jeng, Dailen	University of Miami Rosenstiel School of Marine and Atmospheric Science (UM-RSMAS)	Student
Halewood, Elisa	University of California-Santa Barbara (UCSB)	Data Manager
Gerlach, Dana Stuart	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 (2021). Samples were collected using McLane WTS-LV in-situ pumps and analyzed for individual amino acid concentrations.

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Coverage

Location: North Atlantic Subtropical Gyre - Bermuda Atlantic Time Series (BATS) site
Spatial Extent: **N**:32.17 **E**:-64.08 **S**:30.75 **W**:-64.5
Temporal Extent: 2021-08-05 - 2021-11-13

Methods & Sampling

Samples were collected during August 2021 and November 2021 at or near the BATS site (31°40’ N, 64°10’ W) or at Hydrostation S (32°10’ N, 64°30’ W) on R/V Atlantic Explorer cruises AE2114 and AE2123.

Size-fractionated particle samples were collected using McLane WTS-LV *in-situ* pumps (4 L min^{-1} maximum pumping rate; McLane Research Laboratories, Inc.) during all sampling periods. Five to eight depths were sampled between the surface and 200 meters during each cruise. Most pumps were dual-flow, collecting water through two filter holders simultaneously for geochemical and taxonomic analyses, as described by Henderson et al. (2024) and Comstock et al. (2024). Each filter holder was a vertical-intake (McLane) or mini-MULVFS style and contained four 142 mm diameter filter tiers equipped as follows (from top to bottom) for the geochemical analyses reported here: [1] 20 µm Nitex filter, [2] 6 µm Nitex filter (5 µm polyester filter), [3] two stacked 1.2 µm glass fiber filters (GF/C), [4] two stacked 0.3 µm glass fiber filters (GF75). A 150 µm Nitex backing filter was placed beneath the filter(s) of interest on the first three tiers of all filter holders to ensure filter structural integrity. Nitex filters were acid-and methanol-washed before use, and glass fiber filters were pre-combusted (450°C) for 5 hours. After pump recovery, filter holders were drained with a weak vacuum to remove excess seawater. Filters were photographed, removed and folded with clean forceps, stored in combusted foil, and transported and stored at -80°C. Flow meters were placed in-line on each flow path of the pumps, and exact filtered volumes for each flow path were determined; flow rates through filter stacks used for organic analyses averaged <3 Liters per minutes (L/min). We collected dip blanks – filters that did not have any water pumped through them, but were submerged in natural seawater – along with our samples.

Processing of large particle (>20 µm) samples
Samples were stored at -80°C until processing. Once in the lab, particles collected on 20 µm Nitex filters were rinsed off the filters onto 47-mm diameter, pre-combusted (450°C, for 5 hr) glass fiber filters with a nominal pore size of 0.7 µm (GF/F) using 0.2 µm-filtered seawater and combusted glass filter towers. Briefly, particles were rinsed from the Nitex filters using an acid-clean squirt bottle to spray across the filter. The Nitex mesh was then sonicated for three minutes in an acid-clean polypropylene Nalgene bottle with more filtered seawater. After sonication, this water was poured into the filter tower. The process was repeated three times, with all filtered seawater being drained from the filter tower with gentle vacuum after each rinse and sonication onto the same GF/F filter. Samples were then freeze-dried and inspected under a dissecting microscope to visually characterize the particles and remove intact zooplankton swimmers or contaminant fibers, which were both rare in the samples.

Analysis of individual amino acids
Freeze-dried filters of the 0.3 µm, 1.2 µm, and 20 µm size fractions were quantitatively split radially by weight for analysis of amino acid content for selected samples from August and November 2021.

For amino acid analysis, one filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections). Filter splits were hydrolyzed (20 h, 110°C) using trace metal grade 6 N hydrochloric acid. Hydrolysate was separated from filter material using combusted glass syringes with glass wool in the tip and syringe-tip 0.2 µm polyethersulfone filters. Samples were neutralized by evaporating acid under nitrogen (N_2), reconstituted in 0.1 N hydrochloric acid, and purified via cation exchange chromatography. Notably, we found that cation exchange chromatography was crucial in achieving acceptable yields; trial samples analyzed without undergoing this purification step resulted in yields much lower than expected and much lower than when analyzed after the purification procedure, likely due to chromatographic interference from compound(s) that were effectively removed via the cation exchange procedure. Samples were aliquoted into individual 2 mL HPLC vials, and known quantities of the synthetic amino acid aminoadipic acid were added as an internal standard to confirm accurate analysis. Samples were then dried under N_2, reconstituted in 60/40 ultrapure water/methanol (v/v), and derivatized with *o*-phthaldialdehyde and 2-mercaptoethanol 2 minutes before injection for analysis via reverse-phase high performance liquid chromatography (HPLC, Agilent 1100) with fluorescence detection (Agilent G1321A FLD; excitation 250 nm, emission 410 nm). The mobile phase was as follows: eluent A was 50 mmol L^{-1} sodium acetate (HPLC-grade; adjusted to pH 5.7), and eluent B was 100% methanol (HPLC-grade). The stationary phase was a C18 column (Kinetex™ EVO-C18, 5 µm, 100 Å, 4.6x250 mm) with a C18 guard column (EVO-C18 ULTRA cartridge, 4.6 mm) at 20°C. The flow rate was constant at 0.9 mL min^{-1} and the elution gradient of eluent B added to eluent A was as follows:

- -12 min to 0 min: 5% eluent B
- 4 min: 23% eluent B
- 8 min: 29% eluent B
- 24 min: 44% eluent B

- 37 to 44 min: 60% eluent B
- 52 min: 77% eluent B
- 57 to 62 min: 100% eluent B

A standard curve was analyzed alongside samples during each run. The standard used was a mixed amino acid standard solution initially prepared in 0.1 N hydrochloric acid. We measured the following amino acids: alanine, arginine, aspartic acid, glutamic acid, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, serine, threonine, tyrosine, valine, γ-aminobutyric acid, and β-alanine. The standard also included cysteine and proline, though these amino acids are not detectable with the OPA derivatization method. The standard was prepared from the Pierce amino acid calibration standard H with the addition of non-protein forming amino acids γ-aminobutyric acid and β-alanine. The standard solution was prepared to a concentration of 92 µmol L^{-1} for all amino acids except for γ-aminobutyric acid and β-alanine, which were prepared to concentrations of 30 and 34 µmol L^{-1}, respectively. The standard solution was aliquoted by weight to exact concentrations targeting a range of 0.2 to 50 µmol L^{-1} for the protein-forming amino acids. As with the samples, standards were aliquoted directly into individual 2 mL HPLC vials, supplemented with known quantities of aminoadipic acid as an internal standard, dried under N_2, and reconstituted in 60/40 ultrapure water/methanol (v/v). The effect of cation exchange chromatography on measured amino acid yields in the standard was determined by subjecting two aliquots of the standard mixture to the procedure; average yields for each amino acid were 87-98% with the exception of arginine (40%) and lysine (71%). Yields were consistent for each amino acid across the duplicate standard aliquots. Sample concentrations were corrected assuming a yield of 40% for arginine, 71% for lysine, and 91% (average) for all other amino acids. Sample peak areas were converted to molar quantities using the calibration from the standard curve. Blanks of ultrapure water and full process blanks were analyzed alongside samples to check for any background amino acid content in reagents or contamination. Full process blanks consisted of dip blank filter splits that were processed exactly as sample filter splits. Seawater particulate amino acid concentrations (nmol L^{-1}) were calculated based on the original volume of seawater filtered through the portion of sample analyzed during each run (material extracted from 0.7 to 10.5 L of seawater injected for a single run). We report concentrations here as (1) total amino acid carbon as a proportion of POC, where carbon from individual amino acids was calculated (via the molecular formula for each monomer), summed, and divided by the total POC concentration in that particle size fraction, and (2) individual amino acids as mol%, where the concentrations (in nmol L^{-1}) of individual amino acids were each divided by the total amino acid concentration in that sample (sum of individual concentrations in nmol L^{-1}).

BCO-DMO Processing Description

- Imported data from source file "SizeFrac_AminoAcids_BIOSSCOPE_2021.xlsx" into the BCO-DMO data system.
- Modified parameter (column) names to conform with BCO-DMO naming conventions.
- Converted latitude and longitude columns to decimal degrees
- Changed date format to ISO format of yyyy-mm-dd
- Moved standard deviation values to be adjacent to the associated amino acid values
- Rounded values according to submitter's indicated precision

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Data Files

File	
964684_v1_amino_acids_biosscope_2021.csv	(Comma Separated Values (.csv), 7.21 KB) MD5:fb0116b4260c6bea7669dd7f3446fc3a
Primary data file for dataset ID 964684, version 1. Amino Acid concentrations for size fractionated pump samples on BIOSSCOPE cruises AE2114 and AE2123	

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Related Publications

Bishop, J. K. B., Lam, P. J., & Wood, T. J. (2012). Getting good particles: Accurate sampling of particles by large volume in-situ filtration. Limnology and Oceanography: Methods, 10(9), 681–710. doi:10.4319/lom.2012.10.681
Methods

Comstock, J., Henderson, L. C., Close, H. G., Liu, S., Vergin, K., Worden, A. Z., Wittmers, F., Halewood, E., Giovannoni, S., & Carlson, C. A. (2024). Marine particle size-fractionation indicates organic matter is processed by differing microbial communities on depth-specific particles. ISME Communications, 4(1). https://doi.org/10.1093/ismeco/ycae090
Methods

Doherty, S. C., Maas, A. E., Steinberg, D. K., Popp, B. N., & Close, H. G. (2021). Distinguishing zooplankton fecal pellets as a component of the biological pump using compound-specific isotope analysis of amino acids. Limnology and Oceanography, 66(7), 2827–2841. Portico. https://doi.org/10.1002/lno.11793
Methods

Hannides, C. C. S., Popp, B. N., Choy, C. A., & Drazen, J. C. (2013). Midwater zooplankton and suspended particle dynamics in the North Pacific Subtropical Gyre: A stable isotope perspective. Limnology and Oceanography, 58(6), 1931–1946. doi:10.4319/lo.2013.58.6.1931
Methods

Henderson, L.C., Wittmers, F., Carlson, C. A., Worden, A.Z., & Close, H. G. (2024. Variable carbon isotope fractionation of photosynthetic communities over depth in an open-ocean euphotic zone. Proceedings of the National Academy of Sciences, 121(10). https://doi.org/10.1073/pnas.2304613121
Results

Kaiser, K., & Benner, R. (2005). Hydrolysis-induced racemization of amino acids. Limnology and Oceanography: Methods, 3(8), 318–325. doi:10.4319/lom.2005.3.318
Methods

Lindroth, Peter., & Mopper, Kenneth. (1979). High performance liquid chromatographic determination of subpicomole amounts of amino acids by precolumn fluorescence derivatization with o-phthaldialdehyde. Analytical Chemistry, 51(11), 1667–1674. https://doi.org/10.1021/ac50047a019
Methods

Liu, S., Longnecker, K., Kujawinski, E. B., Vergin, K., Bolaños, L. M., Giovannoni, S. J., Parsons, R., Opalk, K., Halewood, E., Hansell, D. A., Johnson, R., Curry, R., & Carlson, C. A. (2022). Linkages Among Dissolved Organic Matter Export, Dissolved Metabolites, and Associated Microbial Community Structure Response in the Northwestern Sargasso Sea on a Seasonal Scale. Frontiers in Microbiology, 13. https://doi.org/10.3389/fmicb.2022.833252
Methods

Wojtal, P. K., Doherty, S. C., Shea, C. H., Popp, B. N., Benitez-Nelson, C. R., Buesseler, K. O., Estapa, M. L., Roca-Martí, M., & Close, H. G. (2023). Deconvolving mechanisms of particle flux attenuation using nitrogen isotope analyses of amino acids. Limnology and Oceanography. Portico. https://doi.org/10.1002/lno.12398
Results

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Related Datasets

IsRelatedTo

Carlson, C. A., Giovannoni, S., Liu, S., Halewood, E. (2025) **BIOS-SCOPE survey biogeochemical data as collected on Atlantic Explorer cruises (AE1614, AE1712, AE1819, AE1916) from 2016 through 2019.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-10-17 doi:10.26008/1912/bco-dmo.861266.1 [view at BCO-DMO]

Henderson, L., Close, H. G., Carlson, C. A., Saied, A., Ortiz, A., Garley, R., Halewood, E. (2024) **Chemical analyses of size-fractionated particle samples collected during the BIOS-SCOPE cruise AE1819 in the Sargasso Sea in July 2018.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-02-22 doi:10.26008/1912/bco-dmo.920443.1 [view at BCO-DMO]

Henderson, L., English, C., Jeng, D., Popendorf, K., Carlson, C. A., Close, H. G. (2025) **Size fractionated carbohydrate data collected in the Sargasso Sea during BIOS-SCOPE cruises AE2114 and AE2123 in August and November 2021.** Biological and Chemical Oceanography Data Management Office (BCO-

DMO). (Version 1) Version Date 2025-06-13 doi:10.26008/1912/bco-dmo.964801.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Sample_ID	Internal sample ID	unitless
Cruise	BIOSSCOPE cruise identifier	unitless
Latitude	Latitude of sample collection	decimal degrees
Longitude	Longitude of sample collection	decimal degrees
Date	Date of sample collection	units
Size_fraction	Particle size range for water fraction	micrometers (um)
Filter_type	Filter type used for particle fraction (Nitex, GF/C ,GF75)	unitless
Depth	Water column depth of sample	meters (m)
Asp	average amino acid concentration: Aspartic Acid. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Asp_sd	standard deviation of Aspartic Acid concentration	nanomoles carbon per liter
Glu	average amino acid concentration: Glutamic Acid. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Glu_sd	standard deviation of Glutamic Acid concentration	nanomoles carbon per liter
HisSer	average amino acid concentration: Histidine+Serine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
HisSer_sd	standard deviation of Histidine+Serine amino acid concentration	nanomoles carbon per liter

Arg	average amino acid concentration: Arginine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Arg_sd	standard deviation of Arginine concentration	nanomoles carbon per liter
Thr	average amino acid concentration: Threonine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Thr_sd	standard deviation of Threonine concenctration	nanomoles carbon per liter
Gly	average amino acid concentration: Glycine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Gly_sd	standard deviation of Glycine concentration	nanomoles carbon per liter
Bala	average amino acid concentration: Beta-alanine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Bala_sd	standard deviation of Beta-alanine concentration	nanomoles carbon per liter
Tyr	average amino acid concentration: Tyrosine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Tyr_sd	standard deviation of Tyrosine concentration	nanomoles carbon per liter
Ala	average amino acid concentration: Alanine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Ala_sd	standard deviation of Alanine concentration	nanomoles carbon per liter
GABA	average amino acid concentration: Gamma-aminobutyric acid. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
GABA_sd	standard deviation of Gamma-aminobutyric acid concentration	nanomoles carbon per liter

Met	average amino acid concentration: Methionine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Met_sd	standard deviation of Methionine concentration	nanomoles carbon per liter
Val	average amino acid concentration: Valine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Val_sd	standard deviation of Valine concentration	nanomoles carbon per liter
Phe	average amino acid concentration: Phenylalanine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Phe_sd	standard deviation of Phenylalanine concentration	nanomoles carbon per liter
Ile	average amino acid concentration: Isoleucine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Ile_sd	standard deviation of Isoleucine concentration	nanomoles carbon per liter
Leu	average amino acid concentration: Leucine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Leu_sd	standard deviation of Leucine concentration	nanomoles carbon per liter
Lys	average amino acid concentration: Lysine. One filter split was prepared per sample, and three aliquots from the final prepared solution were analyzed (triplicate injections).	nanomoles carbon per liter
Lys_sd	standard deviation of Lysine concentration	nanomoles carbon per liter

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Instruments

Dataset-specific Instrument Name	(HPLC, Agilent 1100) with fluorescence detection (Agilent G1321A FLD; excitation 250 nm, emission 410 nm).
Generic Instrument Name	Agilent 1100 G1321A FLD Detector
Dataset-specific Description	Samples were injected for analysis via reverse-phase high performance liquid chromatography (HPLC, Agilent 1100) with fluorescence detection (Agilent G1321A FLD; excitation 250 nm, emission 410 nm).
Generic Instrument Description	The Agilent 1100 G1321A FLD Detector is a high-performance fluorescence detector designed for precise and sensitive analysis in HPLC applications. Featuring advanced optical design and variable wavelength settings, this detector enhances fluorescence detection for a wide range of compounds, improving sensitivity and selectivity. Its robust design ensures reliable performance, while seamless integration with Agilent 1100 HPLC systems makes it an excellent choice for laboratories requiring high-quality fluorescence detection.

Dataset-specific Instrument Name	flow meter
Generic Instrument Name	Flow Meter
Dataset-specific Description	Flow meters were placed in-line on each flow path of the pumps, and exact filtered volumes for each flow path were determined.
Generic Instrument Description	General term for a sensor that quantifies the rate at which fluids (e.g. water or air) pass through sensor packages, instruments, or sampling devices. A flow meter may be mechanical, optical, electromagnetic, etc.

Dataset-specific Instrument Name	McLane WTS-LV in-situ pumps (4 L min-1 maximum pumping rate; McLane Research Laboratories, Inc.)
Generic Instrument Name	McLane Large Volume Pumping System WTS-LV
Dataset-specific Description	Size-fractionated particle samples were collected using McLane WTS-LV in-situ pumps (4 L min-1 maximum pumping rate; McLane Research Laboratories, Inc.) during all sampling periods.
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.

Dataset-specific Instrument Name	dissecting microscope
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Samples were inspected under a dissecting microscope to visually characterize the particles and remove intact zooplankton swimmers or contaminant fibers, which were both rare in the samples.
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

Dataset-specific Instrument Name	sonicator
Generic Instrument Name	ultrasonic cell disrupter (sonicator)
Dataset-specific Description	The mesh filter was sonicated for three minutes in an acid-clean polypropylene Nalgene bottle with filtered seawater.
Generic Instrument Description	Instrument that applies sound energy to agitate particles in a sample.

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Deployments

AE2114

Website	https://www.bco-dmo.org/deployment/964699
Platform	R/V Atlantic Explorer
Start Date	2021-08-05
End Date	2021-08-08

AE2123

Website	https://www.bco-dmo.org/deployment/964707
Platform	R/V Atlantic Explorer
Start Date	2021-11-10
End Date	2021-11-13

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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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