Chromophoric dissolved organic matter (CDOM) from two microcosm incubation experiments conducted under three light treatments using water originating from West Bay of the Neuse River Estuary, North Carolina USA in 2021 and 2022

Website: https://www.bco-dmo.org/dataset/908572
Data Type: experimental
Version: 1
Version Date: 2023-09-18

Project
» Bacteria as Biosensors of Carbon and Energy Flow in Marine Ecosystems: Quantitative Links Between Substrates, Transcripts, and Metabolism (Bacterial DOC Sensor)

Contributors	Affiliation	Role
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Abstract
Chromophoric dissolved organic matter (CDOM) was collected for two microcosm incubation experiments. Sample water originated from West Bay of the Neuse River Estuary, North Carolina USA in 2021 and 2022. The microcosms were 60 liters, conducted in biological duplicates under three light treatment incubations: 12-hour light-dark cycle of photosynthetically active radiation (PAR), 12-hour light-dark cycle of UV-B radiation, or darkness. Samples were collected from the microcosms in duplicate every few days for over one month to examine how light and the resulting microbial activity altered the dissolved organic carbon (DOC) pool over time. Absorbance spectra of 0.2 micron filtered estuarine water was measured from 190 - 1100 nanometers (nm) on a Genesys 10S UV-Vis spectrophotometer for the calculation of absorbance coefficients, spectral slopes, and slope ratio which describe the organic matter complexity as it develops throughout the incubations.

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Coverage

Spatial Extent: **Lat**:34.925672 **Lon**:-76.365069
Temporal Extent: 2021-09-02 - 2022-05-28

Methods & Sampling

Surface water samples for these experiments were collected from West Bay of the Neuse River Estuary, North

Carolina USA (34°55'32.42" N, 76°21'54.25" W). The microcosms were 60 liters. The experiments were conducted in biological duplicates under three light treatment incubations: 12-hour light-dark cycle of photosynthetically active radiation (PAR), 12-hour light-dark cycle of UV-B radiation, or darkness. Samples were collected from the microcosms in duplicate every few days for over one month to examine how light and the resulting microbial activity altered the DOC pool over time.

For each 60-liter microcosm, water was sampled daily to weekly at the University of North Carolina over the month-long (September 2021) experiment or two-month-long experiment (April 2022). Water was sampled from the microcosms using a peristaltic pump (Masterflex) under gentle (75%) pressure through in-line 3 micron and 0.2 micron, 47-millimeter (mm) polycarbonate filters (Millipore Sigma) which were flushed with 250 milliliters (mL) of Milli-Q water. All tubing, filter holders and 60-mL HDPE collection bottles (Fisher Scientific) were acid washed in 10% (v/v) HCl for six hours and triple rinsed with Milli-Q water. The collection bottles were twice rinsed with c.a. 10 mL of 0.2 micron-filtered sample water then filled to 40 mL and immediately placed in the fridge (4 degrees Celsius). At the conclusion of the experiment (after two months), the samples were run on a Genesys 10S UV-Vis spectrophotometer (ThermoFisher) in scanning mode at 1 nanometer (nm) intervals from 190 - 1100 nm using quartz cuvettes. The spectrophotometer was regularly blanked using Milli-Q water every c.a. 15 samples.

Instruments and Materials:
L/S Peristaltic Pump (Masterflex EW-07557-10) and 1/4 inch Masterflex L/S Platinum-Cured Silicone Tubing: Estuarine water sampled from microcosm tank at 75% speed.

Millipore SX0004700 Polypropylene Swinnex Filter Holder (47 mm) used in-line with the tubing to pump sample water from the microcosm tank through a 3.0 micron and 0.2 micron polycarbonate filter (Millipore Sigma, 47 mm).

Hydrochloric acid (36% w/w, ThermoFisher) was diluted to 10% (v/v) with Milli-Q water for acid washing procedures.

60-mL HDPE dark bottle (Fisher Scientific, 029235B): 0.2 micron filtered water was collected into these acid washed and rinsed bottles and stored at 4 deg. C until analysis.

Genesys 10S UV-Vis Spectrophotometer (ThermoFisher): used in scanning mode, fast, at 1 nm intervals to measure the absorbance of the filtrate.

Quartz Cuvettes, 1-centimeter (cm) pathlength, 3.5 mL (VWR): 2 mL of filtrate was added to the cuvette for absorbance measurements.

BCO-DMO Curation Notes

- Imported original file named "Results_CDOM.csv" into the BCO-DMO system.
- Flagged '-9999' and 'NA' as missing data values; missing data are blank/empty in the final CSV file.
- Renamed fields to comply with BCO-DMO naming conventions.
- Created the 'Start_date' column and added the dates for each experiment.
- Saved the final file as "908572_v1_cdom.csv".

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Data Files

File	
908572_v1_cdom.csv	(Comma Separated Values (.csv), 6.21 MB) MD5:076576e2f8949df8249311b87401abcb
Primary data file for dataset ID 908572, version 1.	

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Related Publications

Helms, J. R., Stubbins, A., Ritchie, J. D., Minor, E. C., Kieber, D. J., & Mopper, K. (2008). Absorption spectral slopes and slope ratios as indicators of molecular weight, source, and photobleaching of chromophoric dissolved organic matter. Limnology and Oceanography, 53(3), 955–969. doi:10.4319/lo.2008.53.3.0955
Methods

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Parameters

Parameter	Description	Units
Experiment_Name	Name of incubation experiment; either "Eco1" or "Eco2".	unitless
Start_date	Date the experiment was initiated. Eco1 was initiated September 2, 2021 and Eco2 was initiated April 4, 2022.	unitless
Treatment	Light treatment applied to incubation: "L" = 12 h PAR/dark; "V" = 12 h UV-B/dark; "D" = dark; and "in situ" = at time of collection.	unitless
Incubation_day	Days elapsed since incubation initiation	days
Tank_ID	Identifier for microcosm replicate (two tanks per light treatment)	unitless
nm	Wavelength of absorption measurement	nanometers (nm)
absp_coef	Absorption coefficient	unitless

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Instruments

Dataset-specific Instrument Name	Peristaltic Pump
Generic Instrument Name	Pump
Dataset-specific Description	L/S Peristaltic Pump (Masterflex EW-07557-10) and 1/4 inch Masterflex L/S Platinum-Cured Silicone Tubing: Estuarine water sampled from microcosm tank at 75% speed.
Generic Instrument Description	A pump is a device that moves fluids (liquids or gases), or sometimes slurries, by mechanical action. Pumps can be classified into three major groups according to the method they use to move the fluid: direct lift, displacement, and gravity pumps

Dataset-specific Instrument Name	Genesys 10S UV-Vis Spectrophotometer
Generic Instrument Name	Spectrophotometer
Dataset-specific Description	Genesys 10S UV-Vis Spectrophotometer (ThermoFisher): used in scanning mode, fast, at 1 nm intervals to measure the absorbance of the filtrate.
Generic Instrument Description	An instrument used to measure the relative absorption of electromagnetic radiation of different wavelengths in the near infra-red, visible and ultraviolet wavebands by samples.

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Project Information

Bacteria as Biosensors of Carbon and Energy Flow in Marine Ecosystems: Quantitative Links Between Substrates, Transcripts, and Metabolism (Bacterial DOC Sensor)

Coverage: Estuaries and Coastal Ecosystems of North Carolina

NSF Award Abstract:
The formation and flux of organic material is the foundation of ocean ecosystems, which in turn, substantially influences the global carbon cycle. As such, a fundamental goal in the ocean sciences is increasing our ability to identify marine organic matter's sources, transformations, and sinks, as well as how these components may change due to anthropogenic activities. Understanding these components is especially important in estuarine and coastal systems given these ecosystems are critical zones of organic carbon transformations. However, the dissolved organic carbon (DOC) pool in these systems consists of numerous different compounds from a multitude of sources that can turn over at vastly different rates (minutes to millennia). This makes it difficult to identify which DOC compounds support microbial growth, limiting the incorporation of microbial metabolism into predictive ecosystem models. Novel approaches are therefore needed to identify the DOC substrates driving microbial metabolism in ocean ecosystems. This project is premised on the idea that the bacterial cellular system is the ultimate chemical sensor of the organic environment and that the information recorded in the cell's active gene pool (transcripts) can be leveraged to make insights into DOC composition when the relationships between organic substrate availability, gene activity, and metabolism are known. This project identifies substrate-transcript relationships for a model marine bacterium, as well as the growth and metabolic outcomes of substrate availability. These insights are used to identify the biologically active DOC substrates in coastal environments when the model organism is added directly to coastal samples, and to interpret both historical and current environmental RNA and DNA data sets. This work provides novel insights into the substrates driving the ocean's carbon cycle and how marine bacterial cellular systems are regulated. Bioassays are developed that can be applied in many different aquatic environment settings. The project trains graduate and undergraduate students directly involved in the research and minority undergraduates will be recruited to use research modules for hands-on study of cell cultivation, bioinformatics, and microbial metabolism. High school students will be engaged through a module developed for an aquatic microbiology field trip and subsequent sample and data analysis.

Bacterial processing of dissolved organic carbon (DOC) mediates the flux of gigatons of carbon in the ocean, yet a significant hurdle to incorporating bacterial metabolism into ocean models is the inability to quantify the DOC substrates supporting bacterial metabolism and their transformation. Metatranscriptomics (sequencing of community mRNAs) has the potential to be a sensitive method for surveying bacterioplankton responses to the DOC pool and making insights into its composition but is currently limited by insufficient knowledge as to how transcriptional patterns relate to substrate availability. This project will identify carbon substrates supporting microbial metabolism and their transformation in estuarine-coastal ecosystems by elucidating the relationships between transcript abundances and carbon substrate availability. It aims to bridge the gap between model organism and environmental -omic studies by creating quantitative inventories of transcripts in response to defined substrates, and then using these calibrated transcriptional signals to interpret environmental DOC bioassays and metatranscriptomes. The first component of the project will establish

genome-wide transcript-substrate relationships in a model marine bacterium in response to individual, environmentally-relevant carbon substrates. The second component will determine the extent to which transcription and metabolism are altered when the bacterium is exposed to complex mixtures of defined and undefined substrates, revealing the potential for transcription to identify individual substrates within a complex DOC pool and how metabolic processing may shape the DOC pools labile and refractory components. Finally, these calibrated transcriptional responses will be used to identify the DOC substrates driving bacterial metabolism in an estuarine-coastal system via DOC drawdown bioassays in which the model organism is added to natural seawater samples, as well as community wide bacterioplankton responses to the extant DOC pool via metatranscriptomics.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1850692

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