

CTD data from station N-1200 collected in August 2017 from a cruise aboard R/V Mediterranean Explorer

Website: <https://www.bco-dmo.org/dataset/874728>

Data Type: Cruise Results

Version: 1

Version Date: 2022-05-24

Project

» [Microbial ecosystems in silico, in the lab and in the field: understanding interactions between abundant marine bacterial taxa](#) (HADFBA)

Contributors	Affiliation	Role
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Abstract

This dataset contains CTD (Conductivity, Temperature, Depth) from a cruise to station N-1200 to study the photic zone in the Eastern Mediterranean at high depth resolution. Data were collected on August 7, 2017 from the R/V Mediterranean Explorer.

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Coverage

Spatial Extent: Lat:32.456 Lon:34.3745

Temporal Extent: 2017-08-07

Methods & Sampling

Cruises and sample collection

A cruise was carried out on August 7, 2017 on R/V Mediterranean Explorer to study the photic zone in the Eastern Mediterranean at high depth resolution. Genetic data and nano-SIMS measurements were used to infer and quantify mixotrophy by *Prochlorococcus* at the base of the photic zone.

Water samples were collected using a 12-bottle rosette with 8 L Niskin bottles. Sampling depths were selected based on real-time data from a Conductivity, Temperature, Depth (CTD) profiler (Seabird 19 Plus) from the down-cast before each sample collection in the up-cast. The continuous data were processed using custom Excel files taking into account the location of each sensor and the sensor delay, and binned over 1-meter intervals.

Data Processing Description

The whole dataset has undergone quality control and has no known errors. Gaps in data are represented by

the value 'nd' (no data).

BCO-DMO Processing:

- renamed fields;
- added columns for Latitude, Longitude, and Date.

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Related Publications

Wu, Z., Aharonovich, D., Roth-Rosenberg, D., Weissberg, O., Luzzatto-Knaan, T., Vogts, A., Zoccarato, L., Eigemann, F., Grossart, H.-P., Voss, M., Follows, M. J., & Sher, D. (2022). Significant organic carbon acquisition by Prochlorococcus in the oceans. <https://doi.org/10.1101/2022.01.14.476346>
Results

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Related Datasets

IsRelatedTo

Sher, D. (2022) **Nutrients and flow cytometry from station N-1200 collected in August 2017 from a cruise aboard R/V Mediterranean Explorer**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-05-24 <http://lod.bco-dmo.org/id/dataset/874805> [[view at BCO-DMO](#)]

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Parameters

Parameter	Description	Units
Binned_depth	Depth (1m bins)	meters (m)
Mean_Temp	TV290C; Mean temperature over 1m bin ITS-90	degrees Celsius
Mean_Sal	Mean salinity over 1m depth bin	PSU
Mean_FISP	In-situ chlorophyll autofluorescence, mean over 1m bin	AU (Seapoint)
Mean_PAR	PAR/irradiance, Biospherical/LiCor, mean over 1m bin	MicroEinsteins
Mean_Oxygen	Oxygen (SBE 63) % saturation	percent
Latitude	Latitude of sampling location	degrees North
Longitude	Longitude of sampling location	degrees East
Date	Sample date in format YYYY-MM-DD	unitless

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Instruments

Dataset-specific Instrument Name	Seabird 19 Plus
Generic Instrument Name	CTD Sea-Bird
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	8 L Niskin bottles
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.

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Project Information

Microbial ecosystems in silico, in the lab and in the field: understanding interactions between abundant marine bacterial taxa (HADFBFA)

Coverage: Eastern Mediterranean Sea

Every drop of seawater contains around one million microorganisms (bacteria, small algae and other organisms such as ciliates and diatoms). These marine microbes feed the entire marine ecosystem, modulate global cycles of carbon and other elements, and impact climate. With the advances in genome-sequencing technology, we can now identify the microbes and assess their genetic and metabolic capacities, yet we still cannot deduce from the genomes of these organisms how they will grow - and interact - in nature. The proposed project will tackle this challenge through a tightly integrated combination of mathematical modeling, laboratory experiments and field work in the Eastern Mediterranean, to identify genes and pathways dictating how environmentally-relevant microbes grow and interact in the sea. We will produce genome-scale mathematical models of the metabolism of *Prochlorococcus*, the numerically-dominant photosynthetic bacteria in large swaths of the ocean, and of *Alteromonas*, abundant marine bacteria which make their living by consuming and respiring organic molecules produced by *Prochlorococcus* and other photosynthetic microbes. We will test these models using laboratory cultures of these organisms grown alone and together, and determine to what extent the models and laboratory cultures represent the growth and death of these organisms in the Eastern Mediterranean. This study will be useful for scientists of many disciplines, including not only marine biology, oceanography and ecology but also genetics, medicine and agriculture. Our results will shed light on the dynamics of some of the most common organisms in the world, responsible for the production of up to 20% of the oxygen we breathe. Our collaborative study will foster the development and training of the next generation of marine scientists, and will be used in outreach activities designed to share with high-school students and the general public the excitement of marine research and the need to responsibly utilize and sustain the oceans for the sake of future generations.

The proposed project will tackle the challenge of understanding microbial interactions from the underlying genetic data through a tightly integrated combination of genome scale modeling, laboratory experiments and

field work in the Eastern Mediterranean. We aim to identify genomic traits dictating how environmentally-relevant primary producers and heterotrophic bacteria interact. Genome-scale (dynamic flux balance analysis, dFBA) models of *Prochlorococcus* MED4 and of *Alteromonas* HOT1A3 will be produced and calibrated using high-throughput measurements of growth and physiological parameters in laboratory batch cultures, combined with detailed analysis of specific metabolites; The dFBA models will be combined *in-silico* and the results compared to laboratory co-cultures. Model-data discrepancies will provide opportunities to revisit the models, suggesting the mediation of alternative processes such as allelopathy or other types of chemical signaling. Finally, time-series data on the community composition and function during the summer/fall *Prochlorococcus* bloom in the hyper-oligotrophic Eastern Mediterranean, combined with field experiments (microcosms), will provide a test of hypotheses generated in the lab. This study will provide the first detailed "roadmap" linking genomic traits (genes and metabolic pathways) and rate measurements with species interactions in environmentally-relevant marine microbes. Genome-scale models will likely be embedded in a not-so-distant future in global-scale models of the Earth System, and the proposed study will provide a critical stepping-stone towards predicting how marine microbial systems will evolve in a changing world. The strong human impact on marine ecosystems, and the need for quantitative and predictive understanding of how they will respond to a changing environment, calls for interdisciplinary research and training for the next generation of scientists and decision makers. Models and data generated by our work will be integrated into a novel educational exploration-focused, web- and field-based educational module. This module will introduce key concepts in microbiology, environmental sciences and oceanography to intermediate- and high-school students.

(Note: acronym HADFBA = Heterotroph-Autotroph Dynamic Flux Balance Analysis)

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635070

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