CTD profiles from six cruises to the Eastern Mediterranean from 2014-2016

Website: https://www.bco-dmo.org/dataset/763725
Data Type: Cruise Results
Version: 1
Version Date: 2022-02-03

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 includes CTD profiles from six cruises to the Eastern Mediterranean from 2014-2016.

Table of Contents

Coverage

Spatial Extent: **N**:32.456 **E**:34.3745 **S**:32.43567 **W**:34.3675
Temporal Extent: 2014-12-01 - 2016-07-24

Methods & Sampling

CTD casts were conducted using a Seabird CTD. The data underwent QC including smoothing and binning using SeaBird software.

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added lat, lon, time, and sheet name columns
- combined all data sheets together on column names.

Data Files

File
ctd_combined.csv (Comma Separated Values (.csv), 438.18 KB) MD5:002290352fead4fde4f00a2b20820c0f Primary data file for dataset ID 763725

Supplemental Files

File
2014_Dec_header.txt   (Octet Stream, 7.23 KB) MD5:217a742fdb5747bbfdf30cf002e753d7 CTD header information for 2014_Dec
2015_July_header filename: 2015_July_header.txt   (Octet Stream, 5.81 KB) MD5:c015bbb9bd70db4000498ea60bec043e CTD header for 2015_July
2015_March_header.txt   (Octet Stream, 6.82 KB) MD5:8254a693ab6967a672d1bc9241228b70 CTD header for 2015_March
2015_Nov_header.txt   (Octet Stream, 6.38 KB) MD5:02e634c2bb914629819d25b453a8d86b CTD header for 2015_Nov
2016_July_header.txt   (Octet Stream, 6.53 KB) MD5:3a6e7771bf034be5b24dab9c804225d7 CTD header for 2016_July
2016_March_header.txt   (Octet Stream, 6.61 KB) MD5:f5c12ae9fd74239611e6106844bf2e3b CTD header for 2016_March

Parameters

Parameter	Description	Units
Sheet_Name	Name of the Sheet in the Excel workbook	unitless
ISO_Date_Time_UTC	Date and time of first data scan	unitless
lat	latitude in degrees north	decimal degrees
lon	longitude in degrees east	decimal degrees
Binned_depth	Depth (1m bins)	meter
Mean_Tv290C	Mean temperature over 1m bin	degrees Celsius
Mean_Sal	Mean salinity over 1m depth bin	PSU
Mean_FISP	In-situ chlorophyll autofluorescence; mean over 1m bin	AU (seapoint)
Mean_turb	IN-situ turbidity mean over 1m bin	FTU (seapoint)
Mean_PAR	PAR/irradiance; Biospherical/LiCor; mean over 1m bin	microEinsteins
Density	Calculated density; mean over 1m bin	kilograms per meter cubed (kg/m3)

Instruments

Dataset-specific Instrument Name	Seabird CTD
Generic Instrument Name	CTD Sea-Bird
Dataset-specific Description	CTD casts using Seabird CTD.
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.

Project Information

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

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 *Prochlorococus*, 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 *Prochlorococus* 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)

Funding