Oceanographic data from 12 monthly cruises off the Israeli coast in the east Mediterranean conducted between Feb 2018 and Jan 2019 at a continental shelf station (~140m depth) and an open-deep water station.

Website: https://www.bco-dmo.org/dataset/866995
Data Type: Cruise Results
Version: 1
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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
Oceanographic data from 12 monthly cruises off the Israeli coast in the east Mediterranean. Cruises where conducted between Feb 2018 and Jan 2019. Data was collected from 2 stations, a continental shelf station (~140m depth) and an open-deep water station (~1450m depth) (THEMO1 station 33.040 N, 34.950 E, THEMO2 station 32.820 N, 34.380 E).

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Coverage

Spatial Extent: **N**:33.04 **E**:34.95 **S**:32.82 **W**:34.38
Temporal Extent: 2018-02-07 - 2019-01-22

Dataset Description

The Levantine basin of the Eastern Mediterranean Sea (EMS) is one of the most oligotrophic regions of the world ocean, yet supports relatively diverse populations of organisms from microbes to fish. In this ecosystem, processes involving both seasonal bottom up control (nutrient limitation) and biotic interactions (such as coupling of primary productivity to heterotrophic growth and grazing) likely control community structure and function. The EMS, despite being an inland sea, has many of the characteristics of a major ocean gyre, while being highly accessible - only a few hours by ship from shore. Thus, the EMS is an accessible natural laboratory to study biotic and a-biotic processes affecting oligotrophic seas.

Methods & Sampling

Cruises and sample collection

Water samples were collected as part of the SoMMoS project during twelve cruises, from February 2018 until January 2019. Each cruise took samples at two THEMO (Texas-Haifa Eastern Mediterranean Observatory) stations.

THEMO2, an open ocean station at a depth of ~1500 m (~50 Km from the coast, 32.820 N, 34.380 E), and THEMO1 which is positioned at the edge of the continental shelf at ~125m depth (~10 Km from the coast, 33.040 N, 34.950 E). THEMO2 was sampled from 12:00-22:00 (local time), while THEMO1 was sampled during the night, typically 00:00-02:00 (local time). Here, we will present information from data collected at the offshore THEMO2 station.

Start and end data of the cruises and sampling research vessel (no specific cruise IDs):

07/02/2018 08/02/2018: R/V Bat-Galim
05/03/2018 06/03/2018: R/V Mediterranean Explorer
09/04/2018 10/04/2018: R/V Mediterranean Explorer
14/05/2018 15/05/2018: R/V Bat-Galim
18/06/2018 19/06/2018: R/V Mediterranean Explorer
09/07/2018 10/07/2018: R/V Mediterranean Explorer
06/08/2018 07/08/2018: R/V Bat-Galim
05/09/2018 06/09/2018: R/V Mediterranean Explorer
08/10/2018 09/10/2018: R/V Mediterranean Explorer
05/11/2018 06/11/2018: R/V Bat-Galim
03/12/2018 04/12/2018: R/V Mediterranean Explorer
21/01/2019 22/01/2019: R/V Mediterranean Explorer

Samples were collected using a 12-bottle rosette with 8 L Niskin bottles. Samples were collected at 20-24 depths across the entire water column (11-12 bottles between the surface and 200 m, which we define here as the photic zone). Sampling depths were selected based on real-time data of Conductivity, Temperature, Depth (CTD) profiler (Seabird 19 Plus) from the down-cast before each sample collection in the up-cast, an oxygen optode (on some cruises) and a fluorescence meter (Turner designs, Cyclops-7). The continuous data was processed using the Sea-Bird data conversion software, and minimized using bin averaging. One bin of data lines was defined as a change of 1 decibar (db) between each bin. The first two meters of measurements were compiled together to account for sensors and CTD pump adjustment time and rosette depth while at sea surface.

Nutrients

Nutrient samples were collected in acid-washed 500 ml plastic containers and immediately filtered through 0.22 µm Nalgene rapid-flow filter units. The first two filtrates were discarded, and the final sub- samples collected in new 50 ml falcon tubes and stored in the dark at 4 ◦C in racks. The samples were transported to the analytical lab at the marine station at Sdot-Yam within 12–15 h of sampling and dissolved nutrients determined using a SEAL AA-3 autoanalyzer system (SEAL, 2011). To minimize crosscontamination in the laboratory, ammonium was analyzed first alone using an automated ophthalaldehyde (OPA) fluorescence method. Samples were placed in the sample trays and only opened immediately before the sample probe took the sample. The baseline water used for ammonium determination was freshly prepared Milli-Q (MQ) water. The next parameters to be determined were dissolved nitrate and silicate. The methods used were Cd reduction and diazo dye for nitrate & nitrite (hereafter referred to as Nox), and molybdate blue in the presence of oxalic acid for Silicate. The baseline water used for these determinations was also MQ water. For the August cruise nitrite was also determined by carrying out a run also using coloured diazo dye but without Cd reduction. Finally, a 3rd run was carried out using an ultra-low level phosphate (DIP) method involving using a 100 cm long flow cell (LWCC) and molybdate blue determination derived from Murphy and Riley (1962). The blank used for phosphate determination was surface seawater, whose DIP value was determined in a previous experiment in which we determined a refractive index correction by removing the ascorbic acid reagent. It was not possible to use MQ as the baseline, as has been used elsewhere because the MQ water in our lab (derived from desalinated water) contains ~20 nM DIP.

40 ml subsamples for Total Dissolved Phosphorus (TDP) were taken from the filtered samples on-board, acidified with 0.2 ml of 2M sulfuric acid and frozen immediately in racks. The samples were transported to the laboratory at the Sdot Yam marine station and stored at −4 ◦C until later analysis. After thawing the samples, 4 ml of acidified potassium persulphate was added to each sample in a glass autoclavable bottle. The closed bottles were autoclaved for at least 30 min and allowed to cool overnight. The samples were then transferred to 50 ml Falcon tubes and analyzed using the same procedure as described for DIP. In order to determine the

reagent blank, a similar procedure was used substituting MQ (and 50 nM and 100 nM phosphate) for the sample, adding 4 ml of acidified potassium persulphate into glass autoclave bottles. The reagent blank was treated the same way as the seawater samples.

Bacterial and primary productivity

Heterotrophic prokaryotic productivity (hereafter referred to as bacterial productivity, BP) was estimated using the 3H-leucine incorporation method (Simon and Azam, 1989; Smith and Azam, 1992). Triplicate 1.7 ml of ocean water were taken from each sampled depth and incubated with a 7:1 mixture of 'cold' leucine and 'hot' 3H-leucine, respectively (final concentration 100 nmol leucine L-1) for 4 h at room temperature in the dark immediately after sampling. Preliminary experiments show that this was the saturating level of leucine in the offshore water of the SE Mediterranean Sea. After incubation, incorporation was terminated by adding 100 µl trichloroacetic acid (TCA). As a negative control for non-specific binding, another set of triplicates were sampled from a surface layer and treated with TCA immediately after the addition of the radioactive tracer. At the end of each cruise, the samples were processes using the micro-centrifugation protocol and 1ml scintillation cocktail (ULTIMA-GOLD) was added to all samples before counted using TRI-CARB 2100 TR (PACKARD) scintillation counter. A conversion factor of 3 kg C per mole of leucine incorporated and an isotopic dilution of 2.0 were used to calculate the C incorporated (Simon and Azam, 1989).

Net daily photosynthetic carbon fixation rates were estimated using the 14C incorporation method (Nielsen, 1952), with several modifications (Hazan et al., 2018). Triplicate 50 ml samples were taken from each depth within the photic zone and from one aphotic depth using sterile vials and kept at surface light and temperature conditions. The 'dark' sample served as blank and was kept under the same temperature as the 'light' samples. Radioactive spiking was done at ~08:00 AM the day following of the cruise in order to start a 24h incubation for all samples (including those collected at THEMO-1 station, not shown) at the same time. Early work by Letelier and colleagues (1996) at station HOT showed that prolonged on-deck incubations, similarly to the protocol used in this study, may result in underestimated PP rates as it cannot precisely mimic the temperature and illumination levels in-situ. Our preliminary tests concur with this conclusion and found that ashore incubations underestimate PP rates by up to ~20% compared to incubations onto a mooring rope tied to the ship (Figure S2). Samples were spiked with 50µl (5 µCi) of $NaH^{14}CO_3$ tracer and were incubated for 24 h under 3 light regimes: surface illumination (samples from the upper mixing depths), 50% illumination (samples from below the mixing depth to the DCM) and ~1% illumination (samples from the DCM and below). Shading was performed using neutral density nets, thus changing light intensity but not spectral properties. Water samples were then filtered through GF/F filters (0.7 µm nominal pore size, 25 mm diameter) using low vacuum pressure (< 50 mmHg) and rinsed 3 times with filtered sea water. Filters from each sample were then put in scintillation vials where 50 µl of 32%HCl solution was immediately added in order to remove excess 14C-bicarbonate and kept overnight for incubation. After incubation 5 mL scintillation cocktail (ULTIMA-GOLD) was added to the samples and counted using TRI-CARB 2100 TR (PACKARD) scintillation counter. Three random aliquots were counted immediately after the addition of the radiotracer (without incubation) with ethanolamine to serve as added activity measurements.

Picophytoplankton abundance using flow-cytometry

Triplicates water samples (1.5 ml) were collected from each sampling depth, put in cryo-vials (Nunc), and supplemented with 7.5 µl 25% glutaraldehyde (Sigma). Vials were incubated in the dark for 10 min, flash-frozen in liquid nitrogen, and stored in -80 oC freezer. Before analysis, samples were thawed in the dark at room temperature. Each sample was run twice on a BD Canto II flow-cytometer with 2 µm diameter fluorescent beads (Polysciences, Warminster, PA, USA) as a size and fluorescence standard. In the first run three types of phytoplankton cells were identified based on their natural auto-fluorescence: *Prochlorococcus*, *Synechococcus* and picoeukaryotes. Cells were differentiated based on cell chlorophyll (Ex482nm/Em676nm, PerCP channel) and phycoerythrin fluorescence (Ex564nm/Em574nm), and by the size of cell (forward scatter). Before the second FCM, run samples were stained with SYBR Green I (Molecular Probes/ ThermoFisher) to enable counting followed by detection at Ex494nm/Em520nm (FITC channel). This provided counts of the total bacterial population (phytoplankton + heterotrophic bacteria and archaea) as well as a distinction between cells with High or Low DNA content (not shown). Data were processed using FlowJo software. Flow rates were determined several times during each running session by weighing tubes with double-distilled water, and counts of the standard beads were used to verify a consistent flow rate.

Algal pigment markers

Eight litters of seawater were collected from all photic sample depths and one from a dark depth (depth varies between cruises). Water was filtered onto GF/F filters (0.7 µm nominal pore size, 47mm diameter, Waters) using a peristaltic pump until either all 8 L were filtered or the filter became blocked, in which case the volume filtered was recorded. Filters were placed in cryo-vials and flash frozen in liquid nitrogen until they could be

stored in a -80 oC freezer. Pigments were extracted in 1ml 100% methanol for 3 h at room temperature and clarified using syringe filters (Acrodisc CR, 13 mm, 0.2 µm PTFE membranes, Pall Life Sciences). Total chlorophyll was measured spectrophotometrically using a NanoDrop 2000c (Thermo Sciences) at 632, 652, 665 and 695 nm, and the concentration of chlorophyll a was calculated (Ritchie 2008). Ultra high-pressure Liquid Chromatography (UPLC) was performed on an ACQUITY UPLC system (Waters) equipped with a photodiode array detector. A C8 column (1.7 µm particle size, 2.1 mm internal diameter, 50 mm column length, ACQUITY UPLC BEH, 186002877) was used. The chromatography method was adapted for UPLC from the LOV method (Hooker et al., 2005). Samples were preheated to 30 °C and column to 50 °C before each run. Running buffers were a 70:30 mixture of methanol and 0.5M ammonium acetate (buffer A) and 100% methanol (buffer B). The program consisted of an isocratic run using a 80:20 mixture of buffers A:B for 2min, followed by a linear gradient to 50:50 for 7 minutes and an increase to 100% solvent B. The flow rate was 0.5ml/min. Pigment standards from DHI (Denmark) were used to identify the UPLC peaks (chlorophyll a, divinyl-chlorophyll a, chlorophyll b, zeaxanthin, diatoxanthin, fucoxanthin, peridinin, 19'- butanoyloxyfucoxanthin and 19'- hexanoyloxyfucoxanthin). Due to potential degradation of the pigment standards, we present the total chlorophyll measured spectrophotometrically and the pigment ratios within each UPLC run.

Data Processing Description

Data processing has been done with the following programs: Seabird processing programs, FlowJo, Excel ad Waters UPLC software.

BCO-DMO processing notes:

* Removed column time_ISO_Depth after discussion with submitter. This column was created to be used in other applications that can interpret both parameters from a single cell, but is redundant when publishing it for reuse.

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Data Files

File
sommos.csv (Comma Separated Values (.csv), 5.67 MB) MD5:6160c38dd1a7dc8fdc7e5ca4b79c554d Primary data file for dataset ID 866995

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Parameters

Parameter	Description	Units
Cruise	THEMO: Texas-Haifa Eastern Mediterranean Observatory	unitless
Station	THEMO station 1 or 2	unitless
Type	Sampling type (Cast)	unitless
YYYY_MM_DD	Date of sampling in YYY_MM_DD format	unitless
hhmm	Time of sampling in hhmm format. The number is a timestamp unformatted. In excel it represents a time frame and other applications can interpret that (Like ODV). If the format of the column is changed to 'Time' it should show a hh:mm format.	unitless
Longitude	Longitude of sampling location, west is negative	decimal degrees

Latitude	Latitude of sampline location, south is negative	decimal degrees
Bot_Depth	Maxium depth at sampling station	m
Depth	Depth of sampling in each stration	m
time_ISO8601	Time of sampling in iso format. Time zone is UTC+2.	unitless
Cruise_nr	Cruise number (1 to 12)	unitless
Cast	Cast number	unitless
ID	Sample specific ID	unitless
Altimeter	height	m
Density	Water density as a function of temperature and pressure	kg/m^3
Fluorescence	Biological excitation, a proxy for chlorophyll content.	AU
Oxygen_Sat	Percentage of dissolved oxygen in the water	%
Oxygen	Concentration of dissolved oxygen in the water	umol/L
Pressure	Physical pressure on the water mass	db desibar
Salinity	Concentration of dissolved salt in the water	psu Practical Salinity Unit
Temperature	Water temperature	°C degrees celsius
Par	Photosynthetically active radiation designates the spectral range of solar radiation from 400 to 700 nanometers.	W/m2
Turbidity	An optical characteristic of water and is a measurement of the amount of light that is scattered by material in the water	ftu Formazin Turbidity Units
PicoEukaryotes	Cell count of PicoEukaryotes in the water sample. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
Prochloroccocus	Cell count of Prochloroccocus in the water sample. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
Synechococcus	Cell count of Synechococcus in the water sample. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
PicoEuk_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
Pro_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
Syn_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
HNA	A distinctive count of cells with high nucleic amino acids (HNA) content. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
LNA	A distinctive count of cells with low nucleic amino acids (LNA) content. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
HNA_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
LNA_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
Cell_Count	Count of total cells in the water sample. Count was done using flow cytometry.	Number of cells in a 1 ml of water cell/ml
Cell_Count_SD	The standard deviation between the triplicate samples analyzed.	Number of cells in a 1 ml of water cell/ml
Primary_production	The assimilation rate of carbon by autotrophic biological processes in the water samples.	ug C/L/d

Primary_production_SD	The standard deviation between the triplicate samples analyzed.	ug C/L/d
Bacterial_production	The assimilation rate of carbon by heterotrophic biological processes in the water samples.	ug C/L/d
Bacterial_production_SD	The standard deviation between the triplicate samples analyzed.	ug C/L/d
Tchla	The total concentration of the pigment chlorophyl-a. measurements was done using a NanoDrop.	ug/L
Total_Chlorophylla	The area under peak signal of the pigment chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
DVChlTa_TotalChla	The area under peak signal of the pigment Divinyl chlorophyl-a relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Total_19Hex_19But	The area under peak signal of the pigments 19-butanoyloxyfucoxanthin and 19-hexanoyloxyfucoxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Per_Total	The area under peak signal of the pigment Peridinin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Total_19But	The area under peak signal of the pigment 19-butanoyloxyfucoxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Fuco_Total	The area under peak signal of the pigment Fucoxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Total_19Hex	The area under peak signal of the pigment 19-hexanoyloxyfucoxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Diato_Total	The area under peak signal of the pigment Diatoxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Zea_Total	The area under peak signal of the pigment Zeaxanthin relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.

chlB_Total	The area under peak signal of the pigment chlorophyl-b relative to chlorophyl-a. measurements was done using UPLC.	Area under the peak of the signal derived from the questined pigment. A proxy of conncentration.
Phosphate	Concentration of Phosphate in the water.	uM
TOxN	Concentration of total Nitrogen in the water.	uM
Si	Concentration of Silica in the water.	uM
Ammonia	Concentration of Ammonia in the water.	uM
NO2	Concentration of Nitrit in the water.	uM
N_P_ratio	Ration of nitrogen to Phospate in the water.	AU
TDP	Concentration of total dissolved Phosphorus in the water.	nM
DOP	Concentration of dissolved organic Phosphate in the water.	nM

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Instruments

Dataset-specific Instrument Name	CTD profiler Seabird 19 Plus
Generic Instrument Name	CTD Sea-Bird SBE SEACAT 19plus
Dataset-specific Description	CTD profiler Seabird 19 Plus
Generic Instrument Description	Self contained self powered CTD profiler. Measures conductivity, temperature and pressure in both profiling (samples at 4 scans/sec) and moored (sample rates of once every 5 seconds to once every 9 hours) mode. Available in plastic or titanium housing with depth ranges of 600m and 7000m respectively. Minature submersible pump provides water to conductivity cell.

Dataset-specific Instrument Name	BD Canto II flow-cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	BD Canto II flow-cytometer with 2 µm diameter fluorescent beads (Polysciences, Warminster, PA, USA)
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

Dataset-specific Instrument Name	JASCO fluorometer
Generic Instrument Name	Fluorometer
Dataset-specific Description	JASCO fluorometer
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

Dataset-specific Instrument Name	TRI-CARB 2100 TR (PACKARD) scintillation counter
Generic Instrument Name	Liquid Scintillation Counter
Dataset-specific Description	TRI-CARB 2100 TR (PACKARD) scintillation counter
Generic Instrument Description	Liquid scintillation counting is an analytical technique which is defined by the incorporation of the radiolabeled analyte into uniform distribution with a liquid chemical medium capable of converting the kinetic energy of nuclear emissions into light energy. Although the liquid scintillation counter is a sophisticated laboratory counting system used the quantify the activity of particulate emitting (ß and a) radioactive samples, it can also detect the auger electrons emitted from 51Cr and 125I samples.

Dataset-specific Instrument Name	100 cm long flow cell (LWCC)
Generic Instrument Name	Liquid Waveguide Capillary Cells
Dataset-specific Description	100 cm long flow cell (LWCC)
Generic Instrument Description	Liquid Waveguide Capillary Cells (LWCC) are optical sample cells that combine an increased optical pathlength (2-500 cm) with small sample volumes. They can be connected via optical fibers to a spectrophotometer with fiber optic capabilities. Similar to optical fibers, light is confined within the (liquid) core of an LWCC by total internal reflection at the core/wall interface. Ultra-sensitive absorbance measurements can be performed in the ultraviolet (UV), visible (VIS) and near-infrared (NIR) to detect low sample concentrations in a laboratory or process control environment. According to Beer’s Law the absorbance signal is proportional to chemical concentration and light path length.

Dataset-specific Instrument Name	NanoDrop 2000c (Thermo Sciences)
Generic Instrument Name	Spectrophotometer
Dataset-specific Description	NanoDrop 2000c (Thermo Sciences)
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.

Dataset-specific Instrument Name	ACQUITY UPLC system (Waters)
Generic Instrument Name	Ultra high-performance liquid chromatography
Dataset-specific Description	ACQUITY UPLC system (Waters) equipped with a photodiode array detector and a C8 column (1.7 µm particle size, 2.1 mm internal diameter, 50 mm column length, ACQUITY UPLC BEH, 186002877)
Generic Instrument Description	Ultra high-performance liquid chromatography: Column chromatography where the mobile phase is a liquid, the stationary phase consists of very small (< 2 microm) particles and the inlet pressure is relatively high.

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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 *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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