Biological oceanographic measurements, 16S rRNA gene amplicons and metagenomes from surface seawater taken from August 2017 to June 2021 at sites within and adjacent to Kāneʻohe Bay, Oʻahu, Hawaiʻi

Website: https://www.bco-dmo.org/dataset/930163
Data Type: Other Field Results
Version: 1
Version Date: 2024-08-30

Project
» Population genomics and ecotypic divergence in the most dominant lineage of marine bacteria (Pelagibacteromics)

Contributors	Affiliation	Role
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Abstract
These data include temperature, pH, salinity, chlorophyll a concentrations, cellular abundances of Prochlorococcus, Synechococcus, photosynthetic picoeukaryotes, and heterotrophic bacteria,16S ribosomal RNA gene amplicon libraries, metagenomes, inorganic nutrient concentrations, and photosynthetic pigment measurements via high performance liquid chromatography from surface seawater samples collected as part of the Kāneʻohe Bay Time-series (KByT). This dataset reflects near-monthly sampling of surface seawater that was conducted between between August 2017 and June 2021 at 10-12 sites within and adjacent to Kāneʻohe Bay, Oʻahu, Hawaiʻi. Instruments used were a YSI 6,600 sonde, a ProDSS multi-parameter sonde, a Turner 10AU fluorometer, a Beckman Coulter CytoFLEX S flow cytometer, a Seal Analytical AA3 HR Nutrient Autoanalyzer, an Illumina MiSeq v2 platform, and the Illumina NovaSeq 6000. These data reveal a remarkably persistent transition in surface ocean biogeochemistry, phytoplankton biomass, and phytoplankton community structure, despite high water exchange and define surface ocean biogeochemical and phytoplankton regimes over space and time across nearshore to offshore waters in the tropical Pacific. These results provide insight into drivers of seasonal and spatial variability of phytoplankton communities. Data were collected and analyzed by Sarah J. Tucker, Yoshimi M. Rii, Kelle C. Freel, Keli'iahonui Kotubetey, A. Hi'ilei Kawelo, and Kawika B. Winter, Michael S. Rappé.

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Coverage

Spatial Extent: **N**:21.526 **E**:-157.7663 **S**:21.43582 **W**:-157.83585
Temporal Extent: 2017-08-23 - 2021-06-21

Dataset Description

The current dataset includes and expands upon the data collected from samples that were previously published in the PeerJ paper (Tucker at al., 2021). We would like to note that in this current dataset flow cytometry for all samples collected between 2017-2021 were measured using the Beckman Coulter CytoFLEX S. In the PeerJ publication of the 2017-2019 KByT dataset (see related dataset), the flow cytometry measures were conducted with the EPICS ALTRA flow cytometer. Thus intercomparison between the 2017-2019 dataset and this 2017-2021 dataset will show differences in cellular abundances reported.

Other Grants:
* "National Science Foundation Graduate Research Fellowship Program" (Grant ID 1842402, National Science Foundation)
* "NOAA Margaret A. Davidson Fellowship" (Grant ID NA20NOS4200123, National Oceanic and Atmospheric Administration)

Methods & Sampling

The methods summarized below are part of the following publication, currently in review and available as a pre-print: Tucker, S. J. *et al.* Sharp transitions in phytoplankton communities across estuarine to open ocean waters of the tropical Pacific. (2024) doi:10.1101/2024.05.23.595464.

The methods employed in this study were collaboratively developed with He'eia Fishpond stewards and the He'eia National Estuarine Research Reserve (NERR; Winter et al. 2020). Sampling campaigns were conducted with permission from Paepae o He'eia, the stewards of He'eia Fishpond, and the private landowner, Kamehameha Schools.

At all stations, seawater samples for biogeochemical analyses and nucleic acids were collected, as were in situ measurements of seawater temperature, pH, and salinity with a YSI 6600 or ProDSS multi-parameter sonde (YSI Incorporated, Yellow Springs, OH, USA). Approximately one liter of seawater was prefiltered with 85-µm Nitex mesh and subsequently filtered through a 25-mm diameter, 0.1-µm pore-sized polyethersulfone (PES) filter membrane (Supor-100, Pall Gelman Inc., Ann Arbor, MI, USA) to collect microbial cells for DNA isolation. The filters were subsequently submerged in DNA lysis buffer (Suzuki et al. 2001; Yeo et al. 2013) and stored in −80°C until further processing.

Seawater subsamples for fluorometric chlorophyll a concentrations (125 mL) and photosynthetic pigments via high-performance liquid chromatography (HPLC; 2 L) were collected on 25-mm diameter GF/F glass microfiber filters (Whatman, GE Healthcare Life Sciences, Chicago, IL, USA) and stored in aluminum foil at −80°C until extraction. The collection of phytoplankton pigments on the GF/F glass microfiber filters allow for comparisons with the Hawaii Ocean Time-series data. However, because the filters have a pore size of 0.7µm, we acknowledge that most small cyanobacteria were likely missed. Chlorophyll a was extracted with 100% acetone and measured with a Turner 10-AU fluorometer (Turner Designs, Sunnyvale, CA, USA) following standard techniques (Welschmeyer 1994). Photosynthetic pigments measured via high performance liquid chromatography were extracted in 100% acetone and analyzed on a Waters 2690 separations module equipped with a C18 column and full spectrum photodiode array detector, following (Mantoura and Llewellyn 1983) and modified according to (Bidigare et al. 1989).

For cellular enumeration, seawater was preserved in 2 mL aliquots in a final concentration of 0.95% (v:v) paraformaldehyde (Electron Microscopy Services, Hatfield, PA, USA) at −80 °C until analyzed via flow cytometry. Cellular enumeration of cyanobacterial picophytoplankton (Synechococcus and Prochlorococcus), eukaryotic picophytoplankton, and non-cyanobacterial (presumably heterotrophic) bacteria and archaea (hereafter referred to as heterotrophic bacteria) was performed on a Beckman Coulter CytoFLEX S, following the method of (Monger and Landry 1993). Inorganic nutrients were measured using a Seal Analytical AA3 HR Nutrient Autoanalyzer (detection limits: $NO_2^- + NO_3^-$, 0.009 µM; SiO_4, 0.09 µM; PO_4^{3-}, 0.009 µM; NH_4, 0.03 µM).

DNA extraction and 16S rRNA gene sequencing followed previously published methods (Tucker et al. 2021). Briefly, amplicon libraries were made from polymerase chain reactions of the 16S rRNA gene using barcoded 515F and 926R universal primers (Parada et al. 2016) and paired-end sequenced with MiSeq v2 2x250 technology (Illumina, San Diego, CA, USA). Genomic DNA from a subset of 32 of the 368 total samples collected between 2017-2021 were used for metagenomic sequencing. This included samples from four sampling events between 2017 and 2019 at 6-10 stations. Libraries were constructed from approximately 100 ng of genomic DNA using the Kappa HyperPrep Kit (Roche, Pleasanton, CA, USA) with mechanical shearing (Covaris, Woburn, MA, USA) and paired-end sequenced on a single lane of the NovaSeq 6000 SP 150 (Illumina, San Diego, CA, USA).

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Data Files

File
930163_v1_phytoplankton.csv (Comma Separated Values (.csv), 213.88 KB) MD5:cac01492a69a53dfddc171cfc7c95d32 Primary data file for dataset ID 930163, version 1

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Related Publications

Bidigare, R., Schofield, O., & Prezelin, B. (1989). Influence of zeaxanthin on quantum yield of photosynthesis of Synechococcus clone WH7803 (DC2). Marine Ecology Progress Series, 56, 177–188. https://doi.org/10.3354/meps056177
Methods

Mantoura, R. F. C., & Llewellyn, C. A. (1983). The rapid determination of algal chlorophyll and carotenoid pigments and their breakdown products in natural waters by reverse-phase high-performance liquid chromatography. Analytica Chimica Acta, 151, 297–314. https://doi.org/10.1016/S0003-2670(00)80092-6
Methods

Monger, B. C., & Landry, M. R. (1993). Flow Cytometric Analysis of Marine Bacteria with Hoechst 33342 †. Applied and Environmental Microbiology, 59(3), 905–911. doi:10.1128/aem.59.3.905-911.1993
Methods

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2016). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. Environmental Microbiology, 18(5), 1403–1414. doi:10.1111/1462-2920.13023
Methods

Suzuki, M. T., Béjà, O., Taylor, L. T., & DeLong, E. F. (2001). Phylogenetic analysis of ribosomal RNA operons from uncultivated coastal marine bacterioplankton. Environmental Microbiology, 3(5), 323–331. Portico. https://doi.org/10.1046/j.1462-2920.2001.00198.x
Methods

Tucker, S. J., Freel, K. C., Monaghan, E. A., Sullivan, C. E. S., Ramfelt, O., Rii, Y. M., & Rappé, M. S. (2021). Spatial and temporal dynamics of SAR11 marine bacteria across a nearshore to offshore transect in the tropical Pacific Ocean. PeerJ, 9, e12274. Portico. https://doi.org/10.7717/peerj.12274
Results

Tucker, S. J., Rii, Y. M., Freel, K. C., Kotubetey, K., Kawelo, A. H., Winter, K. B., & Rappé, M. S. (2025). Seasonal and spatial transitions in phytoplankton assemblages spanning estuarine to open ocean waters of the tropical Pacific. Limnology and Oceanography. Portico. https://doi.org/10.1002/lno.70075
Results

Welschmeyer, N. A. (1994). Fluorometric analysis of chlorophyll a in the presence of chlorophyll b and pheopigments. Limnology and Oceanography, 39(8), 1985–1992. doi:10.4319/lo.1994.39.8.1985
Methods

Winter, K. B., Rii, Y. M., Reppun, F. A. W. L., Hintzen, K. D., Alegado, R. A., Bowen, B. W., Bremer, L. L., Coffman, M., Deenik, J. L., Donahue, M. J., Falinski, K. A., Frank, K., Franklin, E. C., Kurashima, N., Lincoln, N. K.,

Madin, E. M. P., McManus, M. A., Nelson, C. E., Okano, R., … Toonen, R. J. (2020). Collaborative research to inform adaptive comanagement: a framework for the Heʻeia National Estuarine Research Reserve. Ecology and Society, 25(4). https://doi.org/10.5751/es-11895-250415 https://doi.org/10.5751/ES-11895-250415
Methods

Yeo, S. K., Huggett, M. J., Eiler, A., & Rappé, M. S. (2013). Coastal Bacterioplankton Community Dynamics in Response to a Natural Disturbance. PLoS ONE, 8(2), e56207. https://doi.org/10.1371/journal.pone.0056207
Methods

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Parameters

Parameter	Description	Units
SampleID	Sample ID. Sample ID is composed of the station ID abbreviation and a uniqe sample ID #. In most cases a month abbreviation is also included.	unitless
Universal_Sample_ID	Universal Sample ID. Universal Sample ID is used to connect multiple sample types within the Kāneʻohe Bay Time-series. It is composed of the Project ID "KBT", the date (mm.dd.yyyy), and Station ID.	unitless
Metagenome	Metagenome associated	unitless
Metagenome_ID	Metagenome ID	unitless
Year	Year of sampling.	unitless
Sampling_Order	Order of sampling events from 1 to 36.	unitless
Season	Season as defined by analyses included in associated paper.	unitless
Month	Month of sampling.	unitless
Month_abb	Abbreviation of month of sampling.	unitless
Time	Local time (Hawaiʻi Standard Time) of sampling surface seawater.	hh:mm
Date	Collection date.	unitless
ISO_DateTime_UTC	Date Time of surface seawater sampling in ISO format. UTC timezone	unitless

decimal_date	Decimal date of sampling collection day.	unitless
Day_of_year	Day of the year of sample collection.	unitless
Community_Type	Environment description, local. Defined by analyses included in associated publication.	unitless
latitude	Latitiude of sample collection site.	Decimal Degrees
longitude	Longitude of sample collection site.	Decimal Degrees
Site	Site ID for collection.	unitless
SW_Temperature_at_site_degC	Temperature of surface seawater in situ.	degrees Celsius
Salinity_ppt	Salinity of surface seawater in situ.	ppt
Depth_m	Depth of sample collection.	meters
pH	pH of surface seawater in situ.	no unit
Prochlorococcus_cells_per_mL	Surface seawater cellular abundances of Prochlorococococcus cells counted on CytoFLEX S flow cytometer.	cells per mL
Synechococcus_cells_per_mL	Surface seawater cellular abundances of Synechococcus cells counted on CytoFLEX S flow cytometer.	cells per mL
Eukaryotic_picophytoplankton_cells_per_mL	Surface seawater cellular abundances of photosynthetic picoeukaryotes counted on CytoFLEX S flow cytometer.	cells per mL
Heterotrophic_bacteria_cells_per_mL	Surface seawater cellular abundances of non-cyanobacterial (presumably heterotrophic) bacteria and archaea (referred to as heterotrophic bacteria) counted on CytoFLEX S flow cytometer.	cells per mL
chlorophyll_a_ug_per_L	Extracted chlorophyll a concentrations from surface seawater.	micrograms per Liter

Phosphate_uM	Inorganic nutrients. Concentrations of phosphate in surface sewater sample (PO43 –).	µM
Silicate_uM	Inorganic nutrients. Concentrations of silicate in surface sewater sample (SiO4).	µM
NitrateNitrite_uM	Inorganic nutrients. Concentrations of nitrate+nitrite in surface sewater sample (NO2− + NO3−).	µM
Ammonia_uM	Inorganic nutrients. Concentrations of ammonia in surface sewater sample (NH4).	µM
X19_butanoyloxyfucoxanthin_ng_per_L	Photosynthetic pigment 19'-But-Fucoxanthin measured via high performance liquid chromatography	ng per L
X19_hexanoyloxyfucoxanthin_ng_per_L	Photosynthetic pigment 19'-Hex-Fucoxanthin measured via high performance liquid chromatography	ng per L
Alloxanthin_ng_per_L	Photosynthetic pigment Alloxanthin measured via high performance liquid chromatography	ng per L
Beta_Carotene_ng_per_L	Photosynthetic pigment Beta Carotene measured via high performance liquid chromatography	ng per L
Alpha_Carotene_ng_per_L	Photosynthetic pigment Alpha Carotene measured via high performance liquid chromatography	ng per L
Chlorophyll_a_ng_per_L	Photosynthetic pigment Chlorophyll a measured via high performance liquid chromatography	ng per L
Chlorophyll_b_ng_per_L	Photosynthetic pigment Chlorophyll b measured via high performance liquid chromatography	ng per L
Chlorophyll_c_1_and_2_ng_per_L	Photosynthetic pigment Chlorophyll c 1&2 measured via high performance liquid chromatography	ng per L
Chlorophyll_c_3_ng_per_L	Photosynthetic pigment Chlorophyll c 3 measured via high performance liquid chromatography	ng per L

Chlorophyllide_ng_per_L	Photosynthetic pigment Chlorophyllide measured via high performance liquid chromatography	ng per L
Diadinoxanthin_ng_per_L	Photosynthetic pigment Diadinoxanthin measured via high performance liquid chromatography	ng per L
Diatoxanthin_ng_per_L	Photosynthetic pigment Diatoxanthin measured via high performance liquid chromatography	ng per L
Fucoxanthin_ng_per_L	Photosynthetic pigment Fucoxanthin measured via high performance liquid chromatography	ng per L
Lutein_ng_per_L	Photosynthetic pigment Lutein measured via high performance liquid chromatography	ng per L
Neoxanthin_ng_per_L	Photosynthetic pigment Neoxanthin measured via high performance liquid chromatography	ng per L
Peridinin_ng_per_L	Photosynthetic pigment Peridinin measured via high performance liquid chromatography	ng per L
Prasinoxanthin_ng_per_L	Photosynthetic pigment Prasinoxanthin measured via high performance liquid chromatography	ng per L
Violaxanthin_ng_per_L	Photosynthetic pigment Violaxanthin measured via high performance liquid chromatography	ng per L
Zeaxanthin_ng_per_L	Photosynthetic pigment Zeaxanthin measured via high performance liquid chromatography	ng per L
divinyl_chlorophyll_a_ng_per_L	Photosynthetic pigment divinyl chlorophyll a measured via high performance liquid chromatography	ng per L
monovinyl_chlorophyll_a_ng_per_L	Photosynthetic pigment monovinyl chlorophyll a measured via high performance liquid chromatography	ng per L
total_chlorophyll_a_ng_per_L	Photosynthetic pigments measured via high performance liquid chromatography (sum of monovinyl and divininyl chlorophyll a).	ng per L
biosample_accession	NCBI Bioproject Accession for amplicon data.	unitless

Amplicon_bioproject_accession	NCBI Biosample Accession.	unitless
Amplicon_SRA_accession	NCBI SRA Accession for amplicon data.	unitless
Amplicon_study	NCBI Study ID for amplicon data.	unitless
Amplicon_library_strategy	Sequencing library type for amplicon data.	unitless
Amplicon_library_source	Source of sequencing library for amplicon data.	unitless
Amplicon_library_layout	Single or paired end sequencing reads for amplicon data.	unitless
Amplicon_platform	Platform used for library creation for amplicon data.	unitless
Amplicon_instrument_model	Sequencer model for amplicon data.	unitless
Amplicon_design_description	Description of ampicon library.	unitless
Amplicon_filetype	File type for amplicon data.	unitless
Amplicon_filename	Forward reads file name for amplicon data.	unitless
Amplicon_filename2	Reverse reads file name for amplicon data.	unitless
Metagenome_bioproject_accession	NCBI Biosample Accession.	unitless
Metagenome_SRA_accession	NCBI SRA Accession for metagenomes.	unitless
Metagenome_study	NCBI Study ID for metagenomes.	unitless
Metagenome_library_strategy	Sequencing library type for metagenomes.	unitless
Metagenome_library_selection	Selection used for sequencing library for metagenomes.	unitless
Metagenome_library_layout	Single or paired end sequencing reads for metagenomes.	unitless

Metagenome_platform	Platform used for library creation for metagenomes.	unitless
Metagenome_instrument_model	Sequencer model for metagenomes.	unitless
Metagenome_design_description	Description of metagenome library.	unitless
Metagenome_filetype	File type for metagenomes.	unitless
Metagenome_filename	Forward reads file name for metagenomes.	unitless
Metagenome_filename2	Reverse reads file name for metagenomes.	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq v2
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Amplicon sequencing
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	NovaSeq 6000 SP 150
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Metagenome sequencing
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Beckman Coulter CytoFLEX S
Generic Instrument Name	Flow Cytometer
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	Turner 10AU fluorometer (Turner Designs, Sunnyvale, CA, USA)
Generic Instrument Name	Fluorometer
Dataset-specific Description	Chlorophyll a measurements
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	Waters 2690 separations module equipped with a C18 column and full spectrum photodiode array detector
Generic Instrument Name	High-Performance Liquid Chromatograph
Dataset-specific Description	Photosynthetic pigments measured via high performance liquid chromatography: Waters 2690 separations module equipped with a C18 column and full spectrum photodiode array detector,
Generic Instrument Description	A High-performance liquid chromatograph (HPLC) is a type of liquid chromatography used to separate compounds that are dissolved in solution. HPLC instruments consist of a reservoir of the mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by high pressure pumping of the sample mixture onto a column packed with microspheres coated with the stationary phase. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase.

Dataset-specific Instrument Name	
Generic Instrument Name	Multi Parameter Portable Meter
Dataset-specific Description	In situ measurements: YSI 6,600 sonde or ProDSS multi-parameter sonde (YSI Incorporated, Yellow Springs, OH, USA)
Generic Instrument Description	An analytical instrument that can measure multiple parameters, such as pH, EC, TDS, DO and temperature with one device and is portable or hand-held.

Dataset-specific Instrument Name	Seal Analytical AA3 HR Nutrient Autoanalyzer
Generic Instrument Name	Nutrient Autoanalyzer
Dataset-specific Description	Inorganic nutrients: Seal Analytical AA3 HR Nutrient Autoanalyzer (detection limits: NO2− + NO3− , 0.009 µM; SiO4, 0.09 µM; PO43 –, 0.009 µM; NH4, 0.03 µM)
Generic Instrument Description	Nutrient Autoanalyzer is a generic term used when specific type, make and model were not specified. In general, a Nutrient Autoanalyzer is an automated flow-thru system for doing nutrient analysis (nitrate, ammonium, orthophosphate, and silicate) on seawater samples.

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Project Information

Population genomics and ecotypic divergence in the most dominant lineage of marine bacteria (Pelagibacteromics)

Website: https://rappelab.wordpress.com/marine-bacterioplankton/population-genomics-of-sar11-marine-bacteria/

Coverage: Moorea, Oahu, and Gulf of Alaska

In the upper water column of Earth's coastal and open oceans, roughly one million microscopic, single-celled bacteria inhabit each milliliter of seawater, where they play important roles in driving nutrient cycles and other processes that are vital to the habitability of these systems to other marine life. While some marine bacteria are similar to plants in that they use energy from the sun to transform the greenhouse gas carbon dioxide into living material and produce oxygen as a byproduct, other marine bacteria known as chemoheterotrophs are similar to humans and other animals in that they consume organic matter and oxygen, producing carbon dioxide as a consequence of their growth. Although they are limited in size and shape when observed under a microscope, genetic techniques such as DNA sequencing have revealed tremendous functional (i.e. what they are doing) and phylogenetic (i.e. how they are related) biodiversity in natural communities of marine bacteria. Despite this high genetic diversity, a single group of phylogenetically related chemoheterotrophic bacteria known as SAR11 can sometimes make up over 50% of the microscopic cells inhabiting seawater systems around the globe; it is considered one of the most abundant organisms on Earth and thus an important aspect of ocean ecology. While it is known that the SAR11 group consists of many distinct "types" that differ in abundance with location, depth and time, we know little about what genetically encoded features distinguish the different types, or how genetic characteristics are gained and lost within the group. The goal of this study is to use a genomics approach to understand the evolutionary processes that shape one of the most abundant groups of organisms on our planet, and to improve our theoretical understanding of the evolutionary processes that shape natural microbial biodiversity in general. This project will provide advanced, cross-disciplinary professional training for a postdoctoral scientist and a graduate student, and will increase the participation of underrepresented groups in scientific research by mentoring undergraduate students of native Hawaiian or Pacific Island ancestry in hands-on research and training. Results will be incorporated into a new university course offering on comparative genomics and microbial evolution. A culture collection of marine microorganisms will also be expanded and maintained, providing a valuable resource for other marine scientists.

This project will take advantage of recent advances in DNA sequencing technology and a high throughput extinction culturing approach in order to investigate the evolutionary characteristics of genomes from sympatric populations of the globally important SAR11 marine bacterial lineage. The major objectives of this project are to understand the forces that shape genomic diversity in large bacterial populations such as SAR11, and to determine the nature by which this diversity is reflected in functional differences between populations, as inferred from genomics. SAR11 cells will be isolated from similar ecosystems in the tropical

North and South Pacific, as well as the coastal ocean of the subpolar North Pacific, in order to investigate the effect of geographic distance versus habitat similarity on the population genetics of free-living, planktonic marine bacteria. By opening a unique genomic window that encompasses SAR11 lineages of varying degrees of genetic divergence simultaneously, this study will facilitate the investigation of evolutionary dynamics that spans a continuum between macro- and microevolutionary processes. Quantitative information regarding the mechanisms by which genetic diversity is generated, propagated, and removed from native SAR11 populations will also help efforts to model the fate of SAR11 and other large marine bacterioplankton populations in the face of predicted climate-induced changes to the global ocean.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1538628

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