KByT 2017-2021 with samples from He'eia Fishpond, biological oceanographic measures and 16S rRNA gene amplicons and metagenomes from surface seawater

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

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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 to 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, Keliʻiahonui Kotubetey, A. Hiʻilei 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

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 Heʻeia Fishpond stewards and the Heʻeia National Estuarine Research Reserve (NERR; Winter et al. 2020). Sampling campaigns were conducted with permission from Paepae o Heʻeia, the stewards of Heʻeia 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: NO2− + NO3− , 0.009 µM; SiO4, 0.09 µM; PO43 –, 0.009 µM; NH4, 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).

The current dataset includes and expands upon the data collected from samples that were previously published in the PeerJ paper. 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 (10.7717/peerj.12274), 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.

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Related Publications

Tucker, S. J., Rii, Y. M., Freel, K. C., Kotubetey, K., Kawelo, A. H., Winter, K. B., & Rappe, M. S. (2024). Sharp transitions in phytoplankton communities across estuarine to open ocean waters of the tropical Pacific. https://doi.org/10.1101/2024.05.23.595464
Results

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Parameters

Parameters for this dataset have not yet been identified

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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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