

Nutrients (phosphate and nitrite+nitrate) from daily sampling at the Santa Monica Pier (SMP), Santa Monica Bay, CA from 2018 to 2019

Website: <https://www.bco-dmo.org/dataset/883916>

Data Type: Other Field Results

Version: 1

Version Date: 2022-11-17

Project

» [Protistan, prokaryotic, and viral processes at the San Pedro Ocean Time-series](#) (SPOT)

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Abstract

This dataset contains nutrients (phosphate and nitrite+nitrate) from daily sampling at the Santa Monica Pier (SMP) from 2018 to 2019. These data were published in Ollison et al (2022). These data were collected as part of a study of high frequency (daily) changes in relative abundance dynamics of the metabolically active protistan community were followed via expressed 18S V4 rRNA genes (RNA) throughout two algal blooms during the spring of 2018 and 2019 in Santa Monica Bay (central Southern California Bight) to examine the environmental factors that influence protistan community dynamics during algal blooms.

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Coverage

Spatial Extent: Lat:34.009 Lon:-118.497

Temporal Extent: 2018-03-26 - 2019-05-05

Methods & Sampling

Blooms were targeted in Santa Monica Bay during spring 2018 and 2019 using local meteorological information to anticipate coastal upwelling events (Figure S1, Ollison et al., 2022). Sampling from the Santa Monica Pier (SMP) was conducted daily at 0900 (PST/PDT) from the same location and orientation on the SMP from the 16th through the 30th in April 2018 (15 days), and in 2019 from the 13th April through 6th May (22 days; no sample was collected on the 14th April 2019). Sampling periods are henceforth referred to as 2018 and 2019, respectively.

An RBR Concerto (<https://rbr-global.com>) was deployed in surface water for 15 minutes at the time of each

sample collection to obtain temperature, conductivity, chlorophyll *a* fluorescence, and dissolved oxygen concentrations (See "Related Dataset" section for CTD data). A 20 µm mesh plankton net was drift towed from the pier (15 min), and samples were examined via light microscopy to identify the dominant planktonic taxa and their relative abundances.

Surface water for 18S rRNA sequencing (see Related Datasets section), nutrient analyses, cell counts, extracted chlorophyll concentrations, and domoic acid concentrations was collected via bucket toss from the pier; an extended funnel was used to gently fill a single acid-washed-3x-rinsed 20 L carboy per established lab protocol (<https://www.protocols.io/view/sample-collection-from-the-field-for-downstream-mo-hisb4ee>). The carboy was protected from the light and immediately transported approximately 300 meters to the Heal the Bay Aquarium located at the SMP for sample processing.

Samples for nitrite + nitrate and phosphate were measured from 0.02 µm filtered seawater via flow injection analysis on a Quickchem 8500 at the Marine Science Institute Analytical Lab, UCSB (See supplemental files for metadata about these analyses).

Data Processing Description

BCO-DMO Data Manager Processing Notes:

- * Data from source files nutrients_2018_metadata.txt, nutrients_2019_metadata.txt were imported into the BCO-DMO data system and concatenated into one data table.
- * blank column heading named "location" to be consistent with related datasets.
- * date format converted to ISO8601 format

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Supplemental Files

File
Nutrient Analysis Metadata 2018 filename: nutrients_2018_metadata.txt (Plain Text, 364 bytes) MD5:6d3291fcb7bc12098f84c14e68eb2b7a Analysis metadata from the "FIA Nutrient Analysis Results" conducted by the Marine Science Institute Analytical Lab, UCSB in 2018.
Nutrient Analysis Metadata 2019 filename: nutrients_2019_metadata.txt (Plain Text, 351 bytes) MD5:2c7b29bdde6b8d579d69991350a8e32d Analysis metadata from the "FIA Nutrient Analysis Results" conducted by the Marine Science Institute Analytical Lab, UCSB in 2019.

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Related Publications

Hu, S. (2017). Sample collection from the field for downstream molecular analysis - microbial eukaryote-focused v1. Protocols.io. doi:[10.17504/protocols.io.hisb4ee](https://doi.org/10.17504/protocols.io.hisb4ee)

Methods

Kim, H.-J., Miller, A. J., McGowan, J., & Carter, M. L. (2009). Coastal phytoplankton blooms in the Southern California Bight. Progress in Oceanography, 82(2), 137–147. <https://doi.org/10.1016/j.pocean.2009.05.002>

Methods

Ollison, G. A., Hu, S. K., Hopper, J. V., Stewart, B. P., Smith, J., Beatty, J. L., Rink, L. K., & Caron, D. A. (2022). Daily dynamics of contrasting spring algal blooms in Santa Monica Bay (central Southern California Bight). Environmental Microbiology. Portico. <https://doi.org/10.1111/1462-2920.16137>

Results

Seubert, E. L., Gellene, A. G., Howard, M. D. A., Connell, P., Ragan, M., Jones, B. H., Runyan, J., & Caron, D. A. (2013). Seasonal and annual dynamics of harmful algae and algal toxins revealed through weekly monitoring at two coastal ocean sites off southern California, USA. Environmental Science and Pollution Research, 20(10), 6878–6895. <https://doi.org/10.1007/s11356-012-1420-0> <https://doi.org/10.1007/S11356-012-1420-0>

Related Datasets

IsRelatedTo

Caron, D., Ollison, G. A., Hu, S. K. (2022) **CTD data from daily sampling at the Santa Monica Pier (SMP), Santa Monica Bay, CA from 2018 to 2019**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-11-17 <http://lod.bco-dmo.org/id/dataset/883908> [[view at BCO-DMO](#)]

Relationship Description: Data collected as part of targeted sampling of blooms in the Santa Monica Bay during spring 2018 and 2019.

Caron, D., Ollison, G. A., Hu, S. K. (2022) **Sampling information and sequence accessions for 18S-V4 sequences from surface water collected at the Santa Monica Pier (SMP) Santa Monica Bay, CA from 2018 to 2019**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-11-17 <http://lod.bco-dmo.org/id/dataset/883924> [[view at BCO-DMO](#)]

Relationship Description: Data from the same samples collected as part of targeted sampling of blooms in the Santa Monica Bay during spring 2018 and 2019.

Parameters

Parameter	Description	Units
Project	Associated project	unitless
Date	Date sampled	unitless
Location	Location of sampling (e.g. Surface, st.3, SPOT= San Pedro Ocean Time-series)	unitless
Sample_ID	Sample Identification number	unitless
Phosphate	Phosphate concentration	micromolar (uM)
Nitrite_plus_nitrate	Nitrite+nitrate concentration	micromolar (uM)

Instruments

Dataset-specific Instrument Name	Quickchem 8500
Generic Instrument Name	Flow Injection Analyzer
Generic Instrument Description	An instrument that performs flow injection analysis. Flow injection analysis (FIA) is an approach to chemical analysis that is accomplished by injecting a plug of sample into a flowing carrier stream. FIA is an automated method in which a sample is injected into a continuous flow of a carrier solution that mixes with other continuously flowing solutions before reaching a detector. Precision is dramatically increased when FIA is used instead of manual injections and as a result very specific FIA systems have been developed for a wide array of analytical techniques.

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Project Information

Protistan, prokaryotic, and viral processes at the San Pedro Ocean Time-series (SPOT)

Coverage: San Pedro Channel off the coast of Los Angeles

Planktonic marine microbial communities consist of a diverse collection of bacteria, archaea, viruses, protists (phytoplankton and protozoa) and small animals (metazoan). Collectively, these species are responsible for virtually all marine pelagic primary production where they form the basis of food webs and carry out a large fraction of respiratory processes. Microbial interactions include the traditional role of predation, but recent research recognizes the importance of parasitism, symbiosis and viral infection. Characterizing the response of pelagic microbial communities and processes to environmental influences is fundamental to understanding and modeling carbon flow and energy utilization in the ocean, but very few studies have attempted to study all of these assemblages in the same study. This project is comprised of long-term (monthly) and short-term (daily) sampling at the San Pedro Ocean Time-series (SPOT) site. Analysis of the resulting datasets investigates co-occurrence patterns of microbial taxa (e.g. protist-virus and protist-prokaryote interactions, both positive and negative) indicating which species consistently co-occur and potentially interact, followed by examination gene expression to help define the underlying mechanisms. This study augments 20 years of baseline studies of microbial abundance, diversity, rates at the site, and will enable detection of low-frequency changes in composition and potential ecological interactions among microbes, and their responses to changing environmental forcing factors. These responses have important consequences for higher trophic levels and ocean-atmosphere feedbacks. The broader impacts of this project include training graduate and undergraduate students, providing local high school student with summer lab experiences, and PI presentations at local K-12 schools, museums, aquaria and informal learning centers in the region. Additionally, the PIs advise at the local, county and state level regarding coastal marine water quality.

This research project is unique in that it is a holistic study (including all microbes from viruses to small metazoan) of microbial species diversity and ecological activities, carried out at the SPOT site off the coast of southern California. In studying all microbes simultaneously, this work aims to identify important ecological interactions among microbial species, and identify the basis(es) for those interactions. This research involves (1) extensive analyses of prokaryote (archaeal and bacterial) and eukaryote (protistan and micro-metazoan) diversity via the sequencing of marker genes, (2) studies of whole-community gene expression by eukaryotes and prokaryotes in order to identify key functional characteristics of microorganismal groups and the detection of active viral infections, and (3) metagenomic analysis of viruses and bacteria to aid interpretation of transcriptomic analyses using genome-encoded information. The project includes exploratory metatranscriptomic analysis of poorly-understood aphotic and hypoxic-zone protists, to examine their stratification, functions and hypothesized prokaryotic symbioses.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1737409

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