

Nutrient concentrations and cell/virus-like particles counts

Website: <https://www.bco-dmo.org/dataset/866781>

Data Type: Other Field Results

Version: 1

Version Date: 2022-09-21

Project

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

Contributors	Affiliation	Role
Fuhrman, Jed A.	University of Southern California (USC)	Principal Investigator, Contact
Sieradzki, Ella	University of Southern California (USC)	Co-Principal Investigator
Soenen, Karen	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

Nutrient concentrations and cell/virus-like particles counts.

Table of Contents

- [Coverage](#)
 - [Dataset Description](#)
 - [Methods & Sampling](#)
 - [Data Processing Description](#)
 - [Data Files](#)
 - [Related Publications](#)
 - [Parameters](#)
 - [Project Information](#)
 - [Funding](#)
-

Coverage

Temporal Extent: 2012-07 - 2013-04

Dataset Description

Related sequence data for the sampling locations can be found here:

* The project accession number for raw data on NCBI is PRJEB12234

* The project accession number for partial genomes of viruses is PRJNA472807

Methods & Sampling

Whole surface seawater for nutrients measurement were collected in triplicates in 50 mL conical tubes and kept in -20° C until flow-injection analysis at the Marine Sciences Institute Analytical Lab at University of California, Santa Barbara (<http://www.msi.ucsb.edu/services/analytical-lab>). Water collected by bucket.

Data Processing Description

Bacteria and viruses per ml seawater were counted on duplicate slides using SYBR green epifluorescence microscopy.

Data Files

File
nutrients.csv (Comma Separated Values (.csv), 1.27 KB) MD5:d5a68f482ba06c0609084a0336551f4a
Primary data file for dataset ID 866781

Related Publications

Sieradzki, E. T., Fuhrman, J. A., Rivero-Calle, S., & Gómez-Consarnau, L. (2018). Proteorhodopsins dominate the expression of phototrophic mechanisms in seasonal and dynamic marine picoplankton communities. *PeerJ*, 6, e5798. doi:[10.7717/peerj.5798](https://doi.org/10.7717/peerj.5798)

Results

Sieradzki, E. T., Ignacio-Espinoza, J. C., Needham, D. M., Fichot, E. B., & Fuhrman, J. A. (2019). Dynamic marine viral infections and major contribution to photosynthetic processes shown by spatiotemporal picoplankton metatranscriptomes. *Nature Communications*, 10(1). doi:[10.1038/s41467-019-09106-z](https://doi.org/10.1038/s41467-019-09106-z)

Related Research

Parameters

Parameter	Description	Units
Date	Sample collection date	unitless
Sample_ID	Sample identifier	unitless
Latitude	Sample collection longitude	decimal degrees
Longitude	Sample collection latitude	decimal degrees
Phosphate	concentration of phosphate	micromolar (μM)
Phosphate_flag	below detection	unitless
Silicate	concentration of silicate	micromolar (μM)
Silicate_flag	below detection	unitless
Nitrite_Nitrate	concentration of nitrite/nitrate	micromolar (μM)
Nitrite_Nitrate_flag	below detection	unitless
Chl_a	concentration of chlorophyll A	migrograms per liter ($\mu\text{g/L}$)
Bacteria_archaea	number of cells per ml seawater measured by epifluorescent microscopy using SYBR gold	cells per ml
Bacteria_archaea_stdev	number of cells per ml seawater measured by epifluorescent microscopy using SYBR gold	cells per ml
Viruses	number of virus like particles per ml seawater measured by epifluorescent microscopy using SYBR gold	viruses per ml
Viruses_stdev	number of virus like particles per ml seawater measured by epifluorescent microscopy using SYBR gold	viruses per ml

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.

[[table of contents](#) | [back to top](#)]

Funding

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

[[table of contents](#) | [back to top](#)]