

# Listing of monthly cruises to San Pedro Channel sampling station from 2010-2014 (Bacterial, Archaeal, and Protistan Biodiversity project, Marine Viral Dynamics project)

**Website:** <https://www.bco-dmo.org/dataset/536264>

**Version:** 2

**Version Date:** 2014-11-04

## Project

» [Pattern and Process in Marine Bacterial, Archaeal, and Protistan Biodiversity, and Effects of Human Impacts](#)

(Bacterial, Archaeal, and Protistan Biodiversity)

» [Marine viral dynamics and incorporation into microbial association networks](#) (Marine Viral Dynamics)

## Program

» [Dimensions of Biodiversity](#) (Dimensions of Biodiversity)

Contributors	Affiliation	Role
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## Dataset Description

This dataset is a listing of the cruises to stations off the coast of California near Los Angeles for the ARISA data.

The purpose of these cruises was to collect microbial specimens in water samples for genetic, taxonomic, and functional diversity. Cruise and/or CTD logs are available at: <http://dornsife.usc.edu/spot/document-access/>

### Monthly station:

Deployments with MO\_SPOT and Wrigley\_SPOT in the cruise\_id went to a single monthly station, a coastal temperate system, oligotrophic to mesotrophic, in San Pedro Basin (sill depth ~740 m, maximum depth ~890 m) off of Los Angeles, California. lat/lon: +33°33.00'N, -118°24.00'W

### Quarterly stations:

2012-2014: Deployments with DOBD\_POLA\_SPOT\_CAT in the cruise\_id visited three quarterly stations. Coastal temperate system, three sites off of Los Angeles, California:

- 1) the Port of Los Angeles (POLA), lat/lon: 33°42.76'N, 118°15.57'W,
- 2) San Pedro Time Series station (SPOT), lat/lon: 33°33.00'N, 118°24.00'W, and
- 3) off of Santa Catalina Island (CAT), lat/lon: 33°27.18'N, 118°28.51'W

### Related Dataset:

[SPOT environmental data](#)

[ARISA Relative Abundances](#)

[ARISA Bin Taxonomy](#)

## Data Processing Description

### BCO-DMO processing:

added conventional header with dataset name, PI name, version date

renamed parameters to BCO-DMO standard

reformated date from d-Mon-yy to yyyy-mm-dd

replaced blank cells with nd

replaced blanks and / with underscores

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## Data Files

File
<b>spot_cruises_v2.csv</b> (Comma Separated Values (.csv), 35.16 KB) MD5:7e5f521b99a4f05ebc7db1444425ec17
Primary data file for dataset ID 536264

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## Parameters

<b>Parameter</b>	<b>Description</b>	<b>Units</b>
year	year of cruise	yyyy-mm-dd
cruise_id	cruise identification	unitless
cruise_id_alt	alternate cruise identification	unitless
platform	vessel name	unitless
operator	operator of vessell	unitless
sampling_timing	whether cruise was part of monthly or quarterly sampling	unitless
date_start	cruise date	yyyy-mm-dd
time_start	approximate start time of cruise	HH:MM
time_end	approximate end time of cruise	HH:MM
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
site	general location of sampling	unitless
brief_cruise_description	brief description of cruise purpose	unitless
chief_scientist	chief scientist name	unitless
co_chief_scientist	co-chief scientist name	unitless
funding	award number of funding support	unitless

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## **Instruments**

<b>Dataset-specific Instrument Name</b>	CTD Sea-Bird
<b>Generic Instrument Name</b>	CTD Sea-Bird
<b>Generic Instrument Description</b>	A Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics. This instrument designation is used when specific make and model are not known or when a more specific term is not available in the BCO-DMO vocabulary. Refer to the dataset-specific metadata for more information about the specific CTD used. More information from: <a href="http://www.seabird.com/">http://www.seabird.com/</a>

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## Deployments

### lab\_Fuhrman\_2014

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/535519">https://www.bco-dmo.org/deployment/535519</a>
<b>Platform</b>	USC
<b>Start Date</b>	2014-10-17
<b>End Date</b>	2014-10-17
<b>Description</b>	Microbial diversity laboratory studies. Monthly cruises to collect water samples in Los Angeles, California area.

### MO\_SPOT\_Oct\_2010

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536289">https://www.bco-dmo.org/deployment/536289</a>
<b>Platform</b>	R/V Yellowfin
<b>Start Date</b>	2010-10-21
<b>End Date</b>	2010-10-21
<b>Description</b>	To collect water samples for microbial diversity study.

### MO\_SPOT\_Nov\_2010

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536294">https://www.bco-dmo.org/deployment/536294</a>
<b>Platform</b>	R/V Yellowfin
<b>Start Date</b>	2010-11-23
<b>End Date</b>	2010-11-23
<b>Description</b>	To collect water samples for microbial diversity study.

### MO\_SPOT\_Dec\_2010

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536299">https://www.bco-dmo.org/deployment/536299</a>
<b>Platform</b>	R/V Yellowfin
<b>Start Date</b>	2010-12-16
<b>End Date</b>	2010-12-16
<b>Description</b>	To collect water samples for microbial diversity study.

#### MO\_SPOT\_Jan\_2011

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536303">https://www.bco-dmo.org/deployment/536303</a>
<b>Platform</b>	R/V Yellowfin
<b>Start Date</b>	2011-01-11
<b>End Date</b>	2011-01-11
<b>Description</b>	To collect water samples for microbial diversity study.

#### MO\_SPOT\_Feb\_2011

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536308">https://www.bco-dmo.org/deployment/536308</a>
<b>Platform</b>	R/V Yellowfin
<b>Report</b>	<a href="http://dornsife.usc.edu/assets/sites/463/docs/SPOT_DATA/DOCS/2012/February_16_2012.pdf">http://dornsife.usc.edu/assets/sites/463/docs/SPOT_DATA/DOCS/2012/February_16_2012.pdf</a>
<b>Start Date</b>	2011-02-23
<b>End Date</b>	2011-02-23
<b>Description</b>	To collect water samples for microbial diversity study.

#### MO\_SPOT\_Mar\_2011

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/536439">https://www.bco-dmo.org/deployment/536439</a>
<b>Platform</b>	R/V Yellowfin
<b>Start Date</b>	2011-03-15
<b>End Date</b>	2011-03-15
<b>Description</b>	Water sample collection for microbial diversity study.

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## Project Information

### Pattern and Process in Marine Bacterial, Archaeal, and Protistan Biodiversity, and Effects of Human Impacts (Bacterial, Archaeal, and Protistan Biodiversity)

**Website:** <http://dornsife.usc.edu/labs/usc-microbial-observatory/>

**Coverage:** San Pedro Ocean Time Series; approx. 33N, 118W

*Description from NSF award abstract:*

Bacteria, Archaea, and Protists dominate global elemental cycling and are immensely diverse genetically, taxonomically, and functionally. Yet the extent of marine microbial diversity, its patterns, and relationships

among genetic, taxonomic, and functional diversity are very poorly characterized, even though the ocean covers 70% of the planet's surface. Among the least well known variables is the effect of human impacts on native marine microbial systems, although it is recognized that impacted systems are more prone to events like harmful algal blooms. Knowledge of these relationships and impacts are necessary to anticipate the responses of biota to global changes and feedback mechanisms that may alter the extents, rates, and even pathways of such changes. This project will expand upon an existing NSF-funded 10+-year monthly ocean time series (Microbial Observatory) that has focused on a single site midway between Los Angeles and Santa Catalina Island, to also include quarterly sampling adjacent to the impacted LA Harbor region to the barely-impacted Catalina coast. USC already runs facilities in LA Harbor and Catalina, with daily boats between (no cost). Measurements include (1) Genetic diversity: high throughput DNA sequences of "housekeeping" and functional genes. (2) Taxonomic diversity: high throughput tag sequences of small subunit ribosomal RNA genes, flow cytometry, automated image analysis (3) Functional Diversity: (a) Functional measurements (carbon fixation and respiration rates, microbial growth and grazing rates, cell size, morphology, and biomass variations), (b) distribution and expression of particular target functional genes involved with processes central to the cycles of carbon, nitrogen, and sulfur, (c) exploratory metatranscriptomics to explore functionalities that were not anticipated. (4) Integrating these: Multivariate statistical and network approaches including newly developed techniques (e.g. Bayesian networks to examine cause-effect relationships), and high speed computational approaches to assess the relationships among the genetic, taxonomic, and functional aspects of biodiversity observed. The PIs will also examine the collected data for signatures and specific effects (on organism identity and functions) associated with human impacted harbor site vs. the relatively pristine one.

The PIs will use network and time series analysis, along with other statistical tools to integrate "classical" microbial and oceanographic rate process measurements, flow cytometric and microscopic characterizations of communities, along with targeted as well as untargeted metagenomics and metatranscriptomics to relate genetic and taxonomic diversity with specific functions (at organismal, food web, and system levels). For example, they should be able to determine how different variants of particular taxa (e.g. at resolution levels ranging from what might be considered near the subspecies to genus levels) would differ in their association with particular measured functions, functional genes, or particular other taxa - or they might see how particular clusters of related organisms behave similarly or differently in their associations. This project offers an unprecedented and potentially transformative opportunity to combine and integrate measurements of genetic, taxonomic, and functional diversity along with direct measurements of system function in a well studied marine system that includes a gradient from one of the world's busiest harbors to a largely pristine ocean habitat. Far beyond just describing the distributions of organisms and functions (itself a necessary first step), they will specifically link spatial and temporal variations in a variety of functions with variations in genetic and taxonomic community composition.

### **Marine viral dynamics and incorporation into microbial association networks (Marine Viral Dynamics)**

**Website:** <http://dornsife.usc.edu/labs/fuhrmanlab/research/>

**Coverage:** Southern California between Los Angeles and Santa Catalina Island; Approx. 33.5N, 118.5 W

#### *Description from NSF award abstract:*

Marine microbes are tremendously abundant and are major players and driving forces in global biogeochemical cycles of carbon, nitrogen, phosphorus, and iron. We learned over the past two decades that viruses are pervasive elements in marine systems, with significant ecological, biogeochemical, genetic, and evolutionary effects on cellular marine organisms, but we have remarkably little information about the dynamics of marine viral community structure and how it relates to the community structure of their hosts (largely bacteria and phytoplankton). Such information is critical for developing proper conceptual and practical models of the roles of viruses and how these change over time and space. The goals of this project are:

- (1) primarily, to characterize a significant subset of the natural virus community and its dynamics, along with bacterial host communities, as they change over daily to monthly time scales at the USC well-studied marine Microbial Observatory site (midway between Los Angeles and Santa Catalina Island), testing hypotheses regarding repeating patterns, host range effects, and taxa-time relationships, and
- (2) secondarily, to incorporate these viruses into microbial association networks by statistically connecting particular types of viruses to specific potential hosts.

Approaches for this study include:

- (a) nested daily, weekly, and monthly collection of bacteria and viruses for nucleic acid samples,
- (b) amplification of conserved genes, as proxy phylogenetic markers, from a few moderately-well-characterized broad viral groups previously readily found in seawater (i.e. the T4-like myoviruses, T7-like podoviruses), as well as bacterial rRNA genes,
- (c) extensive sequencing, after screening by community fingerprinting, from the mixed amplified products,
- (d) binning of the sequences or fingerprint fragments into operational taxonomic units (OTUs) at different levels of resolution,
- (e) evaluation of the results with statistical approaches to examine temporal patterns, relationships (including time-lagged ones) with other viral OTUs, bacteria, protists (monthly only), and environmental parameters,
- (f) incorporating the viral OTUs mathematically into microbial association networks.

Data on environmental parameters, bacteria, and protists are already being collected monthly for an existing Microbial Observatory, so the viral work is complementary to this project, providing a major value-added component. Similarly, this project will add selected daily and weekly microbial data to the Microbial Observatory. Data from the literature and from the PI's preliminary results show they have the technology and capability to meet the first goal, and to our knowledge this would be the first such data set of its scope and kind. The investigators have already published in 2006 that the bacterial communities at the 5m depth of this site show a predictable repeating annual cycle in bacterial community composition, so the expectation of a predictable repeating viral community is not unreasonable. They also have some preliminary data showing some repeated viral occurrences. The second goal requires that there are indeed significant statistical relationships between the viruses and other measured parameters, which the PI anticipates to be the case, but of course cannot predict; if they cannot be demonstrated, this result itself would be informative and would constrain the possible modes of microbial/viral interactions.

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## Program Information

### Dimensions of Biodiversity (Dimensions of Biodiversity)

**Website:** [http://www.nsf.gov/funding/pgm\\_summ.jsp?pims\\_id=503446](http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446)

**Coverage:** global

(adapted from the NSF Synopsis of Program)

Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [\[MORE from NSF\]](#)

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1136818</a>
<a href="#">NSF Division of Molecular and Cellular Biosciences (NSF MCB)</a>	<a href="#">MCB-0703159</a>

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