

Putative taxonomic information for ARISA bins as generated from clone libraries, 2014 (Bacterial, Archaeal, and Protistan Biodiversity project, Marine Viral Dynamics project)

Website: <https://www.bco-dmo.org/dataset/535507>

Version: 2014-11-05

Version Date: 2014-11-03

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)

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Dataset Description

This dataset contains putative taxonomic information for the ARISA bins, as generated from clone libraries. The protocol for assigning these IDs is described in Cram et al. (in press).

This file also contains statistics (eg. mean, standard deviation, etc.) of every variable measured.

Related Dataset:

[SPOT environmental data](#)

[ARISA Relative Abundances](#)

[SPOT cruises](#)

Methods & Sampling

Detailed information on the [Methodology](#) (pdf), including:

Satellite measurements

Assigning Taxonomic Identities to ARISA peaks

Environmental parameter variability

Seasonal variability of microbial community structure

Mantel test approach

Interannual variability of microbial community structure

Alpha diversity:

Variability between depths
Relation to season
Relation to community similarity between depths
Relation to community change
Environmental parameters and community structure: Mantel tests
Temporal dynamics of microbial taxa over time
Transformations
Taxonomic Groups
OTUs

Relevant References:

Beman JM, Steele JA, Fuhrman JA. (2011). Co-occurrence patterns for abundant marine archaeal and bacterial lineages in the deep chlorophyll maximum of coastal California. *ISME J* 5: 1077-1085.

Cram JA, Chow C-ET, Sachdeva R, et al. (2014) Seasonal and interannual variability of the marine bacterioplankton community throughout the water column over ten years. *The ISME Journal*. doi: 10.1038/ismej.2014.153.

Frouin R, Franz BA, Werdell PJ (2003) The SeaWiFS PAR product. Algorithm updates for the fourth SeaWiFS data reprocessing 46-50.

Fuhrman J, Azam F (1982) Thymidine incorporation as a measure of heterotrophic bacterioplankton production in marine surface waters - evaluation and field results. *marine biology* 66:109-120.

Kirchman D, K'nees E, Hodson R (1985) Leucine incorporation and its potential as a measure of protein synthesis by bacteria in natural aquatic systems. *Appl Environ Microbiol* 49:599-607.

Morel A, Gentili B (2009) A simple band ratio technique to quantify the colored dissolved and detrital organic material from ocean color remotely sensed data. *Remote Sensing of Environment* 113:998-1011. doi: 10.1016/j.rse.2009.01.008

Noble RT, Fuhrman JA. (1998). Use of SYBR Green I for rapid epifluorescence counts of marine viruses and bacteria. *Aquat. Microb. Ecol* 14: 113-118.

Parsons TR (1984) A manual of chemical and biological methods for seawater analysis, 1st ed. Pergamon Press, Oxford [Oxfordshire]; New York

Patel A, Noble RT, Steele JA, Schwalbach MS, Hewson I, Fuhrman JA. (2007). Virus and prokaryote enumeration from planktonic aquatic environments by epifluorescence microscopy with SYBR Green I. *Nat Protoc* 2: 269-276.

Stramski D, Reynolds RA, Babin M, et al. (2008) Relationships between the surface concentration of particulate organic carbon and optical properties in the eastern South Pacific and eastern Atlantic Oceans. *Biogeosciences* 5:171-201.

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- moved columns amoA through bcsim89 before the ARISA_# columns
- transformed ARISA_#.# columns to rows with new column of arisa_frag for the arisa name and rel_abund for the values
- replaced NA with nd
- reformatted date from m/d/yyyy to yyyy-mm-dd

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Data Files

File
bins_taxonomy.csv (Comma Separated Values (.csv), 468.83 KB) MD5:02c5186272a709b178e107c73ebfbab7
Primary data file for dataset ID 535507

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Parameters

Parameter	Description	Units
nodeIDs	Full name of variable; if arisa fragment the format is depth_ARISA_ITS-length; if environmental variable depth_variable-name	unitless
nodeType	ARISA=arisa fragment bin; Env= other measurement	unitless
nodeDepths	depth to which the measurment corresponds	meters
mean	mean value of parameter at a given depth - ARISA node or environmental parameter as described in nodeIDs	various
sd	standard deviation of parameter - ARISA node or environmental parameter as described in nodeIDs	various
median	median value of parameter - ARISA node or environmental parameter as described in nodeIDs	various
mad	median adjusted deviation - ARISA node or environmental parameter as described in nodeIDs	various
count1000	count1000 is the number of occurrences in the data set in which the organism shows up with greater than 0.1% relative abundance.	unitless
countALL	the number of occurrences in the data set in which the organism shows up with greater than 0.01% relative abundance	unitless
LB	lower bound of ARISA fragment bin	unitless
UB	upper bound of ARISA fragment bin	unitless
Project	Identity of project from which clone (used to identify the bin) was isolated	unitless
Location	Location from which the clone (used to identify the bin) was isolated	unitless
DepthCat	Category of depth from which that clone was isolated: surf =500m; nd = unknown	unitless
Clone1Hits	Number of occurrences in library of most frequently found clone of this ARISA fragment size	unitless
Clone2Hits	Number of occurrences in library of second most frequently found clone of this ARISA fragment size	unitless
OtherHits	Number of occurences in library of other clones of this ARISA fragment size	unitless
Clone1ID	Internal ID number for Clone 1	unitless
Clone2ID	Internal ID number for Clone 2	unitless
Accession	NCBI accession number of clone1	unitless
SecAccession	NCBI accession of clone2	unitless
Domain	Clone 1 Greengenes Domain ID	unitless
Phylum	Clone 1 Greengenes Phylum	unitless
Class	Clone 1 Greengenes Class	unitless
Order	Clone 1 Greengenes Order	unitless
Family	Clone 1 Greengenes Family	unitless
Genus	Clone 1 Greengenes Genus	unitless

Species	Clone 1 Greengenes Species	unitless
SilvaTag	Clone 1 Silva Taxonomy finest level identifier	unitless
RDP_Clade	Clone 1 RDP Taxonomy clade level identifier	unitless
Ecotype	Ecotype as assigned by Chow et al 2013	unitless
SecDomain	Clone 2 Greengenes Domain ID	unitless
SecPhylum	Clone 2 Greengenes Phylum	unitless
SecClass	Clone 2 Greengenes Class	unitless
SecOrder	Clone 2 Greengenes Order	unitless
SecFamily	Clone 2 Greengenes Family	unitless
SecGenus	Clone 2 Greengenes Genus	unitless
SecSpecies	Clone 2 Greengenes Species	unitless
SecSilvaTag	Clone 2 Silva Taxonomy finest level identifier	unitless
SecRDP_Clade	Clone 2 RDP Taxonomy clade level identifier	unitless
SecEcotype	Clone 2 Ecotype as assigned by Chow et al 2013	unitless
Letter6	6 letters or fewer long identifier plus ARISA fragment size	unitless
amean	mean value of ARISA fragment	various
asd	standard deviation of ARISA fragment	various
amedian	median value of ARISA fragment	various
amad	median adjusted deviation of ARISA fragment	various
acount1000	the number of times the ARISA fragment is seen with greater than 0.1% relative abundance	unitless
acountall	the number of times the ARISA fragment is seen with greater than 0.01% relative abundance	unitless

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Deployments

lab_Fuhrman_2014

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

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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

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
NSF Division of Ocean Sciences (NSF OCE)	OCE-1136818
NSF Division of Molecular and Cellular Biosciences (NSF MCB)	MCB-0703159

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