Roseobacter isolate Sulfitobacter sp. CB2047 and three of its infecting phage accessions at NCBI GenBank

Website: https://www.bco-dmo.org/dataset/654170
Data Type: Other Field Results
Version:
Version Date: 2016-09-06

Project
» Biogeochemical implications of marine phage: Roseophage as a relevant and tractable model (Roseophage as a Model)

Contributors	Affiliation	Role
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Table of Contents

Dataset Description

Related Reference: Ankrah, N. Y. D., A. L. May, J. L., Middleton, D. R. Jones, M. Hadden, J. R. Gooding, G. R. LeCleir, S. W. Wilhelm, S. R. Campagna and A. Buchan. (2014 Phage infection of an environmentally relevant marine bacterium alters host metabolism and lysate composition. International Society for Microbial Ecology Journal (2014) 8, 1089-1100; doi:10.1038/ismej.2013.216; published online 5 December 2013

See also, Supplemental Material (PDF)

Methods & Sampling

Phage DNA was submitted to the Broad Institute and sequenced under the Gordon and Betty Moore Foundation's Marine Phage, Virus, and Virome Sequencing Project. The Broad Institute sequencing data were assembled using the Lasergene SeqMan Pro. The assemblies resulted in the generation of single contigs for each phage genome.

The genome of Sulfitobacter sp. strain CB2047was sequenced using Illumina technology with an average sequencing coverage of approximately 600 x. The genome was assembled into 12 contigs, ranging in size from 18 kb to 2.3 Mb, using CLC Assembly Cell (CLC bio, Cambridge, MA, USA). The genome of CB2047 was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm .nih.gov/genome/annotation_prok/) and the KAAS genome annotation and pathway reconstruction server.

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- created a BCO-DMO servable table of accessions and associated metadata obtained from the GenBank source information.

[table of contents | back to top]

Data Files

File
Sulfitobacter_accessions.csv (Comma Separated Values (.csv), 758 bytes) MD5:eea79644e36cbf074abeb06249f75c60 Primary data file for dataset ID 654170

[table of contents | back to top]

Parameters

Parameter	Description	Units
taxon	taxonomic name of sequenced organism	unitless
strain	bacterial strain	unitless
description	type of genetic information	unitless
date	collection date	year-month-day
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
accession_NCBI	Linked NCBI GenBank accession number	unitless
comment	comments	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina HiSeq2000 at Center for Pediatric Genome Medicine Children's Mercy Hospitals and Clinics in Kansas City, MO.
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	DNA Engine Thermo cycler (PTC-200)
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

[table of contents | back to top]

Deployments

Buchan_lab

Website	https://www.bco-dmo.org/deployment/658256
Platform	UTenn
Start Date	2011-04-01
End Date	2015-12-31
Description	Microbial genomics work

[table of contents | back to top]

Project Information

Biogeochemical implications of marine phage: Roseophage as a relevant and tractable model (Roseophage as a Model)

Description from NSF award abstract:
Prokaryotic viruses (phage) have long been hypothesized to influence microbial community composition, nutrient biogeochemistry and both the flux and character of carbon in the world's oceans. Model estimates indicate that > 25% of the daily carbon production in marine surface waters is shunted to the dissolved organic matter (DOM) pool by viral activity. Through this process viruses redistribute nutrient elements from large biological particles (i.e., bacteria, algae) into biologically inactive (dead) particulate and dissolved pools of organic compounds. Many of these compounds contain macro- and micronutrients (e.g., P, N, Fe) that can be rapidly recycled back into the food web. While we now have a better (yet far from complete) appreciation of the role of viruses in the regeneration of nutrient elements, we remain almost completely ignorant to, and have almost no data for, the role of viruses in the regeneration of organic carbon, the subsequent partitioning of this carbon by size (e.g. dissolved vs particulate) and bioavailability (labile vs recalcitrant). Understanding the contribution of virus activity to the various carbon pools and the rates associated with this process is an absolute necessity if we are to develop accurate marine and global carbon models.

There is little doubt that the global-scale influence of viruses is determined by host-phage interactions, yet our

understanding of these interactions and their quantitative effects on system processes is in its infancy. To address these questions, it is imperative that we examine ecologically relevant model systems. To that end, this project focuses on phage that infect the Roseobacter clade, a numerically abundant and biogeochemically active group of heterotrophic marine bacteria. Despite the recognized importance of lineage members to the global cycling of elements (particularly carbon), we know little of the viruses ("roseophage") that infect them, the influence viruses have on host processes and the effects of this interaction on other members of the marine microbial community. As such this project is transformative in that it will exploit recently characterized virus-host models for biogeochemical and molecular studies of a major heterotrophic bacterioplankton lineage that is truly ecologically relevant.

The overall objectives of the project are to: (i) examine the distribution, diversity and production of roseophage, (ii) assess the composition and bioavailability of Roseobacter cell lysis-derived DOM and (iii) to track the subsequent uptake and metabolism of Roseobacter-derived carbon and nitrogen by marine surface water microbial communities. These objectives will be achieved through a combination of lab and field-based experiments: molecular tools will be developed to quantify specific rates of roseophage production and Roseobacter mortality under three different environmental regimes (a naturally productive open ocean regime, a near shore to off-shore gradient and induced phytoplankton blooms from mesocosms). The PIs will specifically determine the character and biological availability of carbon from lysates of Roseobacter in lab trials with model microbes. They will examine the rates of assimilation of radiolabeled Roseobacter lysate by natural communities which, when coupled with data on the composition, bioavailability and fate of the DOM released, will form the baseline for a model of Roseobacter-phage C-cycling through the microbial foodweb. Finally, complementary metabolomics studies of lysate consuming populations (in the lab and field) will provide unprecedented insight into how microbes perceive and process viral-lysed material. Collectively, these data will provide critical information on the interplay of phage with a major marine bacterial lineage and the ensuing influence these interactions have on microbial food webs.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1061352

[table of contents | back to top]