Accession numbers for raw sequences associated with field collections & microcosms, 2015 and 2016

Website: https://www.bco-dmo.org/dataset/739077
Data Type: experimental
Version: 1
Version Date: 2018-06-19

Project
» Vibrio as a model microbe for opportunistic heterotrophic response to Saharan dust deposition events in marine waters (Vibrio-dust deposition)

Contributors	Affiliation	Role
Lipp, Erin K.	University of Georgia (UGA)	Principal Investigator
Ottesen, Elizabeth	University of Georgia (UGA)	Co-Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Accession numbers for raw sequences associated with field collections & microcosms, 2015 and 2016

Table of Contents

Coverage

Spatial Extent: **Lat**:24.634 **Lon**:-81.3547
Temporal Extent: 2015 - 2016

Dataset Description

This dataset includes NCBI GenBank accession from 2015 and 2016 field collections and experiments using Saharan source material and water from the lower Florida Keys to create microcosms for natural seawater communities. For full details, see (Westrich et al., 2016).

Methods & Sampling

Samples were collected as part of collections and experiments conducted at Looe Key reef microcosm experiments (2015 and 2016) and field collections (2016) in the Florida Keys National Marine Sanctuary (as described in other datasets with this project).

Samples (1 L) were prefiltered (2 um), concentrated on to 0.22 um filters, DNA extracted, and 16S rRNA in the V4 region amplified using 515F/806R primers with barcodes on both ends. Sequencing was conducted using Illumina MiSeq paired-end 250 chemistry.

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added links to NCBI BioProject pages

[table of contents | back to top]

Data Files

File
Vibrio_sequences.csv (Comma Separated Values (.csv), 394 bytes) MD5:0e6771cc88fa562c44a66e5638e2f90d Primary data file for dataset ID 739077

[table of contents | back to top]

Related Publications

Westrich, J. R., Ebling, A. M., Landing, W. M., Joyner, J. L., Kemp, K. M., Griffin, D. W., & Lipp, E. K. (2016). Saharan dust nutrients promoteVibriobloom formation in marine surface waters. Proceedings of the National Academy of Sciences, 113(21), 5964–5969. doi:10.1073/pnas.1518080113
Results

[table of contents | back to top]

Parameters

Parameter	Description	Units
BioProject	NCBI GenBank BioProject accession number	unitless
study	type of study	unitless
sample_description	description of samples	unitless
year	year of sample collection	unitless
num_sequences	number of sequences	unitless
NCBI_link	link to BioProject page at NCBI GenBank	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
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
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

Lipp_2014-16

Website	https://www.bco-dmo.org/deployment/663738
Platform	Florida Keys National Marine Sanctuary
Start Date	2014-07-22
End Date	2015-05-09
Description	Microbial studies

[table of contents | back to top]

Project Information

Vibrio as a model microbe for opportunistic heterotrophic response to Saharan dust deposition events in marine waters (Vibrio-dust deposition)

Coverage: Florida Keys, FL, USA

Description from NSF award abstract:
Dust and mineral aerosols are a significant source of micro and macronutrients to oligotrophic ocean surface waters. Evidence is growing that heterotrophic microbes may play key roles in processing deposited minerals and nutrients. Yet it is not known which components of dust stimulate the heterotrophic bacteria, which cellular mechanisms are responsible for the utilization of those components and how the activity of these bacteria affect the availability and utilization of dust-derived minerals and nutrients by marine autotrophs. Knowledge of these factors is key to understanding how dust deposition impacts carbon cycles and for predicting the response of tropical oceans to future changes in the frequency and intensity of dust deposition events. The objective of this project is to examine the specific effects of aeolian dust on heterotrophic microbes in a tropical marine system under controlled conditions. The central hypothesis is that in oligotrophic tropical systems numerically minor opportunistic bacteria are the first responders to influx of dust constituents and respond primarily by rapidly accessing soluble trace metals and limiting nutrients that are deposited with Saharan dust. The project will focus on two specific aims: 1) Quantify changes in community structure, composition and transcriptional activity among marine microbial populations upon exposure to dust, and 2) Identify key components in Saharan dust aerosols that stimulate or repress growth and/or activity in Vibrio, a model opportunistic marine heterotrophic group. The study will use a series of controlled experiments designed to identify and quantify heterotrophic microbial response to dust deposition events using both natural communities and model bacteria (Vibrio) through metagenomics, transcriptomics and atmospheric and marine biogeochemical techniques. This innovative approach will identify the most critical (reactive) components leached from dust aerosols on the microbial community as well as elucidate potential mechanisms of response.

There is great interest in the biological response to dust aerosols given its potentially large influence on biogeochemical cycling, but there has been relatively little work that has addressed the mechanisms of response (especially among the heterotrophic microbial fraction) or identified the relative importance of specific constituents of dust aerosols. A detailed framework for microbial response (focusing on opportunistic heterotrophs) will facilitate efforts to link autotrophic and heterotrophic processing. This contribution is significant because it will provide one of the first end-to-end (chemistry to physiology to ecology) mechanistic pathways for marine biological response to desert dust aerosols.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1357423

[table of contents | back to top]