

16S rRNA and genomes of particle associated taxa

Website: <https://www.bco-dmo.org/dataset/849357>

Data Type: Other Field Results

Version: 1

Version Date: 2021-04-19

Project

» [Microbial interactions on particulate organic matter: from community structure to function](#) (MINTPOM)

| Contributors | Affiliation | Role |
|----------------------------------|---|------------------------|
| Cordero, Otto X. | Massachusetts Institute of Technology (MIT) | Principal Investigator |
| Rauch, Shannon | Woods Hole Oceanographic Institution (WHOI BCO-DMO) | BCO-DMO Data Manager |

Abstract

This dataset includes National Center for Biotechnology Information (NCBI) accession numbers and related information for 16S rRNA and genomes of particle associated taxa. Sequences can be found in NCBI under BioProject PRJNA478695.

Table of Contents

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

Coverage

Spatial Extent: Lat:42.4168 Lon:-70.9064

Methods & Sampling

Our study was based on laboratory enrichments with seawater as the sole inoculum and model marine particles as source of carbon and scaffolds for community assembly. Particles were incubated in 1L Nalgene bottles with overhead rotation and subsequently harvested for genomic analysis and isolation. The data here deposited corresponds to the 16S rRNA of the particle-associated community and the genomes of 7 isolates.

Data Processing Description

Data were processed using CLC Genomics Workbench 11, CheckM.

BCO-DMO Processing:

- renamed fields to comply with BCO-DMO naming conventions;
- created separate columns for latitude and longitude values;
- replaced 'NA' with 'nd' to indicate 'no data'.

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

Data Files

| File |
|---|
| accessions.csv (Comma Separated Values (.csv), 1.21 KB) MD5:b71bca368cf05b1d89b8f27e3754a0d2 Primary data file for dataset ID 849357 |

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

Related Publications

Enke, T. N., Datta, M. S., Schwartzman, J., Cermak, N., Schmitz, D., Barrere, J., ... Cordero, O. X. (2019). Modular Assembly of Polysaccharide-Degrading Marine Microbial Communities. *Current Biology*, 29(9), 1528-1535.e6. doi:[10.1016/j.cub.2019.03.047](https://doi.org/10.1016/j.cub.2019.03.047)

General

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

Related Datasets

IsRelatedTo

Massachusetts Institute of Technology. Marine Bacteria, Modular assembly of carbohydrate-degrading microbial communities in the ocean. 2018/06. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information. Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA478695>. NCBI:BioProject: PRJNA478695.

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

Parameters

| Parameter | Description | Units |
|------------------|-----------------------------------|-----------------|
| Accession_number | NCBI accession number | unitless |
| type | description of data type | unitless |
| taxon_name | taxon name | unitless |
| type_of_sample | description of sample | unitless |
| location | name of sampling location | unitless |
| latitude | latitude; positive values = North | decimal degrees |
| longitude | longitude; positive values = East | decimal degrees |

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

Project Information

Microbial interactions on particulate organic matter: from community structure to function (MINTPOM)

NSF Award Abstract:

For marine bacteria the ocean is a vast desert punctuated by hotspots of nutrients originating from fragments of animal and algal tissue rich in organic carbon. Marine bacteria colonize and consume these hotspots, turning them into dissolved nutrients and releasing CO₂ to the atmosphere. This process has tremendous implications for the global carbon cycle, but its dynamics and efficiency are fully determined by poorly understood ecological processes that unfold at the scale of those microscopic hotspots. The research aims to identify and quantify those micro-scale ecological processes, in particular with respect to how interactions between species of marine bacteria on nutrient hotspots impact the dynamics and efficiency of carbon turnover in the ocean. To this end, this project will use novel techniques to cultivate marine bacteria that live on nutrient hotspots and to measure their interspecies interactions as well as their effect on ecosystem function. This project will directly train two undergraduate students and one PhD. student. The findings of this project will be communicated to a broad audience via a series of podcasts focused on how the complex life of microbes at micro-scales impact biogeochemical cycles. These will be developed by undergraduate and graduate students at MIT.

The main hypothesis behind this research is that microbial interactions, frequently occurring on nutrient hotspots, have a significant impact on the rate of organic matter turnover, thereby affecting the global carbon cycle. To test this idea, model marine particles composed of biopolymers frequently found in marine environments will be used as scaffolds for natural microbial communities. This technique will allow the researchers to study community dynamics and function in a controlled and quantitative fashion. This work will identify the main ecological species active in the particle-attached communities as well as their functional roles during particle consumption. The research will also determine how interactions between bacteria in the community impact the degradation rate and the efficiency with which organic matter is turned into biomass, CO₂ and other forms of dissolved carbon that diffuse into the water column.

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

Funding

| Funding Source | Award |
|--|-----------------------------|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1658451 |

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