High-throughput sequencing of the 16S rRNA gene, microscopy, and flow cytometry of pyrosome-associated microorganisms compared to seawater sampled during a Pyrosoma atlanticum bloom in the Northern California Current System in July 2018.

Website: https://www.bco-dmo.org/dataset/926093
Data Type: Other Field Results
Version: 1
Version Date: 2024-04-26

Project
» Collaborative Research: Comparative feeding by gelatinous grazers on microbial prey (Gelatinous Grazer Feeding)

Contributors	Affiliation	Role
Thompson, Anne W.	Portland State University (PSU)	Co-Principal Investigator, Contact
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Abstract
Pyrosomes are widely distributed pelagic tunicates that have the potential to reshape marine food webs when they bloom. However, their grazing preferences and interactions with the background microbial community are poorly understood. The diversity, relative abundance, and taxonomy of pyrosome-associated microorganisms were compared to seawater during a Pyrosoma atlanticum bloom in the Northern California Current System using high-throughput sequencing of the 16S rRNA gene, microscopy, and flow cytometry.

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Coverage

Location: Northern California Current System
Spatial Extent: **N**:44.652141 **E**:-124.589313 **S**:44.651756 **W**:-125.117573
Temporal Extent: 2018-07-09 - 2018-07-11

Methods & Sampling

Pyrosomes and seawater were collected from the NCC, off the Oregon Coast, in July 2018, near the peak of a multiyear bloom of *P. atlanticum.* Samples were collected from the R/V Sally Ride (SR1810) along the Newport Hydrographic Line. Station D5 (Cast 20, 44.652141N; 125.117573W) was sampled on July 9, 2018 in the presence of a strong temperature gradient in the top 20 meters and a chlorophyll peak at 17 meters. Station D3 (Cast 26, 44.651756N; 124.589313W) was sampled on July 11, 2018 in the presence of a mixed layer depth of 15 meters and a chlorophyll peak at the base of the mixed layer.

Data Processing Description

DNA extraction was done using the DNeasy Plant Tissue Mini Kit (Qiagen) with the following modifications. Pyrosome tissue was ground with a sterile pestle (Axygen, Tewksbury, USA) for 3 minutes prior to extraction. Seawater and pyrosome samples were lysed by bead beating with 0.55 mm and 0.25 mm sterile glass beads at 30 Hz for 2 minutes after addition of lysis buffer, freeze-fractured 3 times, incubated with Proteinase K (VWR Chemicals, Solon, OH, USA) at 20 mg/mL for 1 hour at 55 ˚C, and incubated with RNase A at 100 mg/mL for 10 minutes at 65 ˚C. To minimize amplification of eukaryotic host DNA, the primer pair 515F-Y/806R was chosen to amplify the 16S rRNA V4 hypervariable region with conditions as published. Reactions were performed with 0.5-2 ng of DNA using the QuantaBio 5Prime HotMasterMix (Qiagen Beverly, MA, USA). The Agilent High Sensitivity Kit in the Bioanalyzer (Agilent Technologies, Waldbronn, Germany) confirmed amplicon size. Triplicate reactions from each sample were pooled and paired-end sequenced with Illumina MiSeq v.3 (Illumina, San Diego, USA).

BCO-DMO Processing Description

* Converted NCBI biosample file to flat file format
* Merged biosample and SRA run file
* Removed no data columns from files
* Adjusted parameters to comply with databaser requirements (spaces, characters, etc)
* Converted date to ISO format
* Split lat/lon column into their own columns

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Related Publications

Thompson, A. W., Ward, A. C., Sweeney, C. P., & Sutherland, K. R. (2021). Host-specific symbioses and the microbial prey of a pelagic tunicate (Pyrosoma atlanticum). ISME Communications, 1(1). https://doi.org/10.1038/s43705-021-00007-1
Results

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Related Datasets

Results

Portland State University. Pyrosome microbiome Raw sequence reads. 2020/08. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA659246. NCBI:BioProject: PRJNA659246.

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Parameters

Parameter	Description	Units
bioproject_accession	NCBI Bioproject accession ID	unitless
biosample_accession	NCBI Biosample accession ID	unitless
sample_name	Submitter sample name	unitless

sra_sample_accession	NCBI SRA sample accession ID	unitless
sample_accession_title	Sample accession title	unitless
organism_name	Organism name by submitter	unitless
organism_taxonomy_id	NCBI Taxonomy ID	unitless
organism_taxonomy_name	NCBI organism name related to taxonomy id	unitless
keywords	NCBI biosample keywords	unitless
biosample_package	NCBI biosample attribute package and package version	unitless
collection_date	Collection date of organism	unitless
env_broad_scale	Broad-scale environmental context	unitless
env_local_scale	Local-scale environmental context	unitless
env_medium	Material displaced by the entity at time of sampling	unitless
geo_loc_name	Geographic location of the origin of the sample	unitless
host	Host name	unitless
sampling_lat	Latitude of sampling location, south is negative	decimal degrees
sampling_lon	Longitude of sampling location, west is negative	decimal degrees
depth	Sampling depth	meter (m)
host_length	Length of the subject	milimeter (mm)
source_material_id	Unique identifier assigned to a material sample used for extracting nucleic acids, and subsequent sequencing.	unitless
status	Sample NCBI status (live)	unitless
when	When status set	unitless
access	Accessibility: public	unitless
date_publication	Date of publication at NCBI	unitless
date_last_update	Data of last update at NCBI	unitless
date_submission_date	Date of submisison at NCBI	unitless
sra_run_accession	NCBI SRA run accession ID	unitless
sra_study_accession	NCBI study accession ID	unitless
object_status	Status of object	unitless
library_ID	Unique identifier for the sequencing library (can be the sample name repeated).	unitless
title	Library title	unitless
library_strategy	Sequencing library strategy	unitless
library_source	Source of sequencing library	unitless
library_selection	Selection used for sequencing library	unitless
library_layout	single or paired end sequencing reads	unitless
platform	Sequencing platform manufacturer	unitless
instrument_model	Sequencer model	unitless
design_description	Description explaining how this library was prepared and sequenced	unitless
filetype	File type	unitless
fasta_filename1	Forward reads file name	unitless

fasta_filename2	Reverse reads file name	unitless

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Instruments

Dataset-specific Instrument Name	Niskin CTD Rosette for seawater
Generic Instrument Name	CTD - profiler
Generic Instrument Description	The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934.

Dataset-specific Instrument Name	MOCNESS for animals
Generic Instrument Name	MOCNESS
Generic Instrument Description	The Multiple Opening/Closing Net and Environmental Sensing System or MOCNESS is a family of net systems based on the Tucker Trawl principle. There are currently 8 different sizes of MOCNESS in existence which are designed for capture of different size ranges of zooplankton and micro-nekton Each system is designated according to the size of the net mouth opening and in two cases, the number of nets it carries. The original MOCNESS (Wiebe et al, 1976) was a redesigned and improved version of a system described by Frost and McCrone (1974).(from MOCNESS manual) This designation is used when the specific type of MOCNESS (number and size of nets) was not specified by the contributing investigator.

Dataset-specific Instrument Name	Niskin CTD Rosette for seawater
Generic Instrument Name	Niskin bottle
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

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Deployments

SR1810

Website	https://www.bco-dmo.org/deployment/783078
Platform	R/V Sally Ride
Start Date	2018-07-06
End Date	2018-07-11

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Project Information

Collaborative Research: Comparative feeding by gelatinous grazers on microbial prey (Gelatinous Grazer Feeding)

Coverage: North Pacific Subtropical Gyre, at a field site 3 nautical miles offshore of Kona, Hawai'i (19.710746 N, 22.75 W) & Sars Centre for Marine Molecular Biology in Bergen, Norway

NSF Award Abstract:
The oceans are dominated by microscopic plants and animals (microorganisms) that are at the base of the food web and drive energy and carbon cycles on global scales. Soft jellylike animals called gelatinous grazers specialize in feeding on microorganisms using nets made out of mucus. Gelatinous grazers are abundant in the ocean and have high feeding rates on microorganisms so could have a very strong influence on the abundance and diversity of microorganisms and could change how oceanic food webs are currently understood. However, gelatinous grazers are very fragile and patchy in their distributions so it has been difficult to determine the magnitude and dynamics of these important predator-prey relationships on a meaningful scale using traditional approaches, thus they have typically been disregarded in food web studies. Learning more about the predator-prey relationship between gelatinous grazers and microorganisms will improve understanding of the structure, mechanics, and dynamics of the ocean's food web, which is a critical economic and ecosystem resource on Earth. This project is determining grazing rates by gelatinous animals on microbes to inform food web models. The project also trains students to communicate, disseminate, and interpret scientific findings. These broader impacts goals will be attained through partnerships at the University of Oregon (Applied Scientific Communication) and Portland State University (Advanced Technical Writing), training of 1 PhD student, 2 undergraduates, and 4 science communication interns, and development of a week-long workshop and establish student mentorship relationships towards production of communication products.

The project integrates laboratory and oceanographic approaches to address several specific aspects of the predator-prey relationship between gelatinous grazers and ocean microorganisms. Five distinct types of gelatinous grazers, each with different feeding morphologies and life history, will be studied in an oceanographic setting with an abundant and diverse natural microbial population. These target organisms include pelagic tunicates (salps, appendicularians, doliolods and pyrosomes) and thecosome pteropods. The approach quantifies: 1) grazing rates in the natural ocean environment, 2) particle selectivity with a focus on size and shape and, 3) the morphological and hydrodynamic properties of feeding that underlie the measured grazing rates and particle selection. The project uses a variety of techniques including sampling via SCUBA diving, laboratory experiments, high speed/high resolution videography, flow cytometry, and DNA sequencing techniques.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1851412

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