16S rRNA gene of microorganisms sampled along the Newport Hydrographic (NH) and Trinidad Head (TR) lines, in OR and CA in 2018 and 2019

Website: https://www.bco-dmo.org/dataset/926850
Data Type: Other Field Results
Version: 1
Version Date: 2024-05-06

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

Contributors	Affiliation	Role
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Abstract
The Northern California Current ecosystem is a productive system which supports major fisheries. To determine how the microbial community responds to variable upwelling, we examined the 16S rRNA gene of microorganisms from two size fractions, 0.2-1.6µm and greater than 1.6µm along the Newport Hydrographic (NH) and Trinidad Head (TR) lines, in OR and CA.

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Coverage

Location: Northern California Current, off the coast of Oregon and Northern California.
Spatial Extent: **N**:44.6607 **E**:-124.00338333 **S**:41.05433333 **W**:-125.18113333
Temporal Extent: 2018-02-16 - 2019-07-25

Methods & Sampling

Transects ranged from 24 to 86 km in length were sampled along the Newport Hydrographic (NH) line as well as the Trinidad Head (TR) line during the winters (February-March) and summers (July-August) of 2018 and 2019 (winter 2018 transect sample size was n=2 per location due to weather days while summer 2018 – summer 2019, n=4-5). Located off Newport, Oregon, the NH Line has been sampled since 1961 (Peterson and Miller, 1975), while the TR line off northern California has been sampled since 2007.

DNA sampling for microbes was carried out from surface (5-10 meters depth) seawater samples (500-1000 mL, n=2 per station, 6 stations per transect), collected by CTD, that were size fractionated on 47 mm 1.6 µm GF/A filters (Whatman) followed by 47 mm 0.2 µm Supor polyethersulfone filters (Pall Corporation) using a peristaltic pump. Filter membranes were moved to bead-beater tubes and frozen immediately at -20 ˚C and stored at -80 ˚C. DNA extraction was done using the DNeasy Plant Tissue Mini Kit (Qiagen) with the following modifications. 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. PCR was performed in triplicate on 1 ng of DNA with the primer pair 515F-Y/806R amplified the 16S rRNA V4 hypervariable region with conditions as published (Parada et al. 2016) using golay barcodes on the forward primers as in the EMP protocols. Reactions were performed with the QuantaBio 5Prime HotMasterMix (Qiagen Beverly, MA, USA). The Agilent High Sensitivity Kit in the Bioanalyzer (Agilent Technologies, Waldbronn, Germany) confirmed amplicon size. Triplicate PCR reactions from each sample were pooled then purified by magnetic beads. Each final pooled sample was paired-end sequenced with Illumina MiSeq v.3 (Illumina, San Diego, USA).

Data Processing Description

Amplicon sequence variants (ASVs) of seawater samples were identified based on 16S rRNA gene sequence reads that were processed using *dada2* and *phyloseq*. Sequences were quality controlled using *filterAndTrim()* with truncLen set to 190 (forward reads) and 160 (reverse reads), maxEE was set to 3, and maxN set to 0 to eliminate low quality base calls. Forward and reverse primers were trimmed from all reads. Error learning, sample inference, and merging of paired-end reads were done with *dada2* default settings to yield unique amplicon sequence variants (ASVs). Chimeric ASVs were removed with the "consensus" method. The reference database "RefSeq-RDP16S_v2_May2018" was used to assign taxonomy to the ASVs. *phyloseq* was used to connect ASV sequence counts per sample to taxonomic data and metadata. Sequence abundances were standardized to the median sequencing depth of all samples (“standardized relative abundance”) without rarefying. Raw sequence data can be accessed from the NCBI Sequence Read Archive at https://www.ncbi.nlm.nih.gov/bioproject/PRJNA999694/.

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Related Publications

Schmid, M. S., Sponaugle, S., Thompson, A. W., Sutherland, K. R., & Cowen, R. K. (2023). Drivers of plankton community structure in intermittent and continuous coastal upwelling systems–from microbes and microscale in-situ imaging to large scale patterns. Frontiers in Marine Science, 10. https://doi.org/10.3389/fmars.2023.1166629
Results

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Related Datasets

Results

Portland State University. Northern California Current Microorganisms. 2023/07. 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/PRJNA999694. NCBI:BioProject: PRJNA999694.
https://www.ncbi.nlm.nih.gov/bioproject/PRJNA999694

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Parameters

Parameter	Description	Units
bioproject_accession	NCBI Bioproject accession ID	unitless
biosample_accession	NCBI Biosample accession ID	unitless
message	NCBI message	unitless
sample_name	Submitter sample name	unitless
organism	Organism name by submitter	unitless
collection_date	Collection date of organism	unitless
depth	Sampling depth	meter (m)
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
sampling_lat	Latitude of sampling location, south is negative	decimal degrees
sampling_lon	Longitude of sampling location, west is negative	decimal degrees
size_frac	Selected size fraction	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_filename	Forward reads file name	unitless
fasta_filename2	Reverse reads file name	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	
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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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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