Salp and pteropod associated microorganisms from the Western Edge of the Gulf Stream sampled in September 2019.

Website: https://www.bco-dmo.org/dataset/926841
Data Type: experimental
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
Microbial mortality impacts the structure of food webs, carbon flow, and the interactions that create dynamic patterns of abundance across gradients in space and time in diverse ecosystems. In the oceans, estimates of microbial mortality by viruses, protists, and small zooplankton do not account fully for observations of loss, suggesting the existence of underappreciated mortality sources. We examined how ubiquitous mucous mesh feeders (i.e. gelatinous zooplankton) could contribute to microbial mortality in the open ocean. We coupled capture of live animals by blue-water diving to sequence-based approaches to measure the enrichment and selectivity of feeding by two coexisting mucous grazer taxa (pteropods and salps) on numerically dominant marine prokaryotes. We show that mucous mesh grazers consume a variety of marine prokaryotes and select between coexisting lineages and similar cell sizes. We show that Prochlorococcus may evade filtration more than other cells and that planktonic archaea are consumed by macrozooplanktonic grazers. Discovery of these feeding relationships identifies a new source of mortality for Earth's dominant marine microbes and alters our understanding of how top-down processes shape microbial community and function.

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Coverage

Location: Western edge of the Gulf Stream
Spatial Extent: **Lat**:26.7425 **Lon**:-79.9875
Temporal Extent: 2019-09-15

Methods & Sampling

Collected from the western edge of the Gulf Stream (26°43′93″ N, 79° 59′15″ W) in September 2019, 5–8 km east of West Palm Beach, Florida. All samples were collected during daylight in the upper 15 m. Sampling was done by hand.

Jars with animals and jars with seawater were brought on the deck of a 10 m dive vessel for processing. Within 30 min of divers surfacing, samples were archived or processed as follows. Salps and pteropods were gently poured onto a metal sieve then rinsed with 0.2 µm filtered seawater. Each gut was then removed with dissecting scissors, avoiding as much of the gelatinous tissue as possible. Guts were placed into sterile bead-beating tubes with 0.55 and 0.25 mm sterile glass beads and stored on dry ice until archiving at −80°C in a shore-based laboratory. Salp faecal pellets were sampled from different salp specimens incubated in jars for approximately 1-h after collection. Faecal pellets were collected on a mesh sieve (500 µm), rinsed with 0.2 µm filtered seawater, then stored as above. Jars containing seawater collected near sampled animals were transported on blue ice to the shore-based laboratory. For flow cytometry samples, 2 ml of seawater was fixed at a final concentration of 0.125% TEM grade glutaraldehyde (Tousimis), incubated at room temperature for 10 min, then flash frozen in ethanol cooled with dry ice. Seawater DNA samples were taken by peristaltic pumping onto 0.2 µm membrane filters and were stored on dry ice until archiving at −80°C.

Data Processing Description

DNA was extracted with the DNeasy Plant Tissue Mini Kit (Qiagen) with the following modifications. Salp guts, salp fecal pellets, and pteropod tissues were ground with a sterile disposable pestle (Axygen, Tewksbury, USA) for 3 minutes prior to extraction. All samples, including seawater, 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 a final concentration of 2 mg/mL Proteinase K (VWR Chemicals, Solon, OH, USA) for 1 hour at 55 ˚C, and then incubated with a final concentration of 0.9 mg/mL RNase A 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. Reactions were performed with 0.5-2 ng of DNA using the QuantaBio 5Prime HotMasterMix (Qiagen Beverly, MA, USA). To overcome PCR inhibition in salp samples, bovine serum albumin (BSA) was added to the salp PCRs, see details below. The Agilent Bioanalyzer High Sensitivity Kit (Agilent Technologies, Waldbronn, Germany) confirmed amplicon size. Triplicate PCRs from each sample were pooled, cleaned with magnetic beads, and paired-end sequenced (2 x 300 bp) with Illumina MiSeq v.3 (Illumina, San Diego, USA). Sequences were deposited in the Sequence Read Archive (SRA).

BCO-DMO Processing Description

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

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Data Files

File
926841_v1_salps.csv (Comma Separated Values (.csv), 9.66 KB) MD5:5b3ff815e2cf5aafbbb9de6d0242b8c5 Primary data file for dataset ID 926841, version 1

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Related Publications

Thompson, A. W., Sweeney, C. P., & Sutherland, K. R. (2023). Selective and differential feeding on marine prokaryotes by mucous mesh feeders. Environmental Microbiology, 25(4), 880–893. Portico. https://doi.org/10.1111/1462-2920.16334
Results

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Related Datasets

Results

Portland State University. Salps_Pteropod_microbes. 2022/08. 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/PRJNA867417. NCBI:BioProject: PRJNA867417.

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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
sample_title	Sample accession title	unitless
organism	Organism name by submitter	unitless
collection_date	Collection date of organism	unitless
depth	Sampling depth	feet
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
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
filename	Forward reads file name	unitless
filename2	Reverse reads file name	unitless

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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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