Eukaryotic and prokaryotic microbial taxa retained by wild-caught doliolids collected during bloom events at three different shelf locations in the northern California Current system in June 2019.

Website: https://www.bco-dmo.org/dataset/926299
Data Type: Other Field Results
Version: 1
Version Date: 2024-04-29

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

Contributors	Affiliation	Role
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Abstract
Doliolids have a unique ability to impact the marine microbial community through bloom events and high filtration rates. Their predation on large eukaryotic microorganisms is established and evidence of predation on smaller prokaryotic microorganisms is beginning to emerge. We studied the retention of both eukaryotic and prokaryotic microbial taxa by wild-caught doliolids in the northern California Current system. Doliolids were collected during bloom events identified at three different shelf locations with variable upwelling intensity.

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Coverage

Location: Northern California Current
Spatial Extent: **N**:44.652883 **E**:-124.269333 **S**:41.057333 **W**:-125.129167
Temporal Extent: 2019-07-17 - 2019-07-22

Methods & Sampling

Samples were collected during daylight from the R/V *Atlantis* (AGOR-25) along the Newport Hydrographic (NH) Line at station “NH5” (N 44° 39.084’, W 125° 7.151’) on July 22nd as well as along the Trinidad Head (TR) Line at stations “TR1” (N 41° 3.467, W 124° 16.016) and “TR3” (N 41° 3.448, W 124° 26.7) on July 17th and 19th, respectively.

Doliolids were sampled using a modified coupled Multiple Opening and Closing Net and Environmental Sensing

System (MOCNESS). Doliolids were rinsed three times with 0.2 µm filtered seawater to remove unattached microbes, collected in a 1-mL sterile bead-beater tube containing 0.55- and 0.25-mm beads, and then frozen at -80 °C.

Data Processing Description

Seawater and doliolid samples were lysed by beadbeating with 0.55 mm and 0.25 mm sterile glass beads at 30 Hz for 2 min after addition of lysis buffer, freeze-fractured three times, incubated with Proteinase K (VWR Chemicals, Solon, OH) at 20 mg/mL for 1 h at 55 ˚C, and incubated with RNase A at 100 mg/mL for 10 min at 65˚C. 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). 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, CA). Raw sequence data are available in the Sequence Read Archive Project # PRJNA1055560.

BCO-DMO Processing Description

* Converted file to flat file format for improved interoperability
* Adjusted parameter names to comply with database requirements
* Split lat/lon column into their own columns
* Converted dates to ISO format

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Data Files

File
926299_v1_doliolids.csv (Comma Separated Values (.csv), 17.31 KB) MD5:41db357fe5280e7145b6c72ac50f5cea Primary data file for dataset ID 926299, version 1

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Related Datasets

Results

Portland State University. 16s rRNA from Doliolids from the Northern California Current. 2023/12. 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/PRJNA1055560. NCBI:BioProject: PRJNA1055560.

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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
keyword	NCBI biosample keywords	unitless
biosample_package	NCBI biosample attribute package and package version	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
host	Host name	unitless

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
publication_date	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

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Instruments

Dataset-specific Instrument Name	Niskin CTD Rosette for seawater collection
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 animal collection
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)

Dataset-specific Instrument Name	Niskin CTD Rosette for seawater collection
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

AT42-13

Website	https://www.bco-dmo.org/deployment/837042
Platform	R/V Atlantis
Start Date	2019-07-15
End Date	2019-07-26

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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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