Microbial abundance of phytoplankton and bacteria from RV/Tangaroa cruise TAN1810SALP to Chatham Rise vicinity, east of New Zealand, Oct - Nov. 2018

Website: https://www.bco-dmo.org/dataset/809670
Data Type: Cruise Results
Version: 1
Version Date: 2020-04-20

Project
» Collaborative Research: Quantifying trophic roles and food web ecology of salp blooms of the Chatham Rise (Salp Food Web Ecology)

Contributors	Affiliation	Role
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Abstract
Microbial abundance of phytoplankton and bacteria from RV/Tangaroa cruise TAN1810SALP to Chatham Rise vicinity, east of New Zealand, Oct - Nov. 2018.

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Coverage

Spatial Extent: **N**:-42.6622 **E**:179.9428 **S**:-45.5557 **W**:174.1138
Temporal Extent: 2018-10-25 - 2018-11-18

Methods & Sampling

Sampling and analytical procedures: Samples (15 mL) were collected from hydrographic casts with Niskin bottles on a CTD-rosette for live ship-board and preserved shore-based flow cytometry analyses for profiles of phytoplankton and heterotrophic (non-pigmented) bacteria abundance. Live samples (~800 uL) were analyzed within 2 hours of collection (and usually sooner), kept in the dark at room temperature prior to analysis. Samples (2 mL) for shore-based analyses were aliquoted into cryovials, preserved with a final concentration of 0.5% paraformaldehyde (Electron Microscopy Sciences, methanol-free), then flash frozen in liquid nitrogen. After freezing, samples were transferred to a -80°C freezer. Upon completion of the cruise, samples were transferred to a charged dry shipper for transport to the University of Hawaii. Samples were thawed in batches, stained with the DNA stain Hoechst 34580 for 1 hour (1 ug/ml, final concentration), then quantitatively analyzed (100 uL).

Offline analysis software: FlowJo Software (Mac) Version 10.6.1. Ashland, OR: Becton Dickinson and Company; 2019.Offline analysis software: FlowJo Software (Mac) Version 10.6.1. Ashland, OR: Becton Dickinson and Company; 2019.

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- reformatted date from m/d/yy to yyyy-mm-dd
- converted latitude and longitude to decimal degrees

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Data Files

File
microbe_abund.csv (Comma Separated Values (.csv), 11.69 KB) MD5:a3db7a792c224957a25a16c19c02ebae Primary data file for dataset ID 809670

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Parameters

Parameter	Description	Units
DATE	Date collected; formatted as yyyy-mm-dd	unitless
LAT	Latitude; north is positive	decimal degrees
LONG	Longitude; east is positive	decimal degrees
CAST	Cruise-based cast number	unitless
STATION	Station number as recorded by the bridge	unitless
DEPTH	Depth of water collection	meters (m)
PRO	Prochlorococcus abundance determined via preserved shore-based flow cytometry	cells/milliliter
SYN	Synechococcus abundance determined via preserved shore-based flow cytometry	cells/milliliter
PEUK	Photosynthetic eukaryotes determined via live ship-board flow cytometry	cells/milliliter
HBACT	Heterotrophic (non-pigmented) bacteria determined via preserved shore-based flow cytometry	cells/milliliter

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Instruments

Dataset-specific Instrument Name	Becton Dickinson Accuri C6 Plus with CSampler Plus
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Used for cell counts on board ship.
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

Dataset-specific Instrument Name	Beckman Coulter CytoFLEX S, with Near UV (375 nm), Violet (405 nm), Blue (488 nm), and Yellow-Green (561 nm) lasers, with 96-well plate loader
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Used for shore-based cell counts
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

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Deployments

TAN1810

Website	https://www.bco-dmo.org/deployment/757070
Platform	R/V Tangaroa
Start Date	2018-10-23
End Date	2018-11-21

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Project Information

Collaborative Research: Quantifying trophic roles and food web ecology of salp blooms of the Chatham Rise (Salp Food Web Ecology)

Coverage: East of New Zealand, Chatham Rise area

NSF Award Abstract:
Salps are unique open-ocean animals that range in size from a few millimeters to greater than twenty centimeters, have a gelatinous (jelly-like) body, and can form long chains of many connected individuals. These oceanic organisms act as oceanic vacuum cleaners, having incredibly high feeding rates on phytoplankton and, unusual for consumers of their size, smaller bacteria-sized prey. This rapid feeding and the salps' tendency to form dense blooms, allows them move substantial amounts of prey carbon from the surface into the deep ocean, leading to carbon dioxide removal from the atmosphere. However, salps are often considered a trophic dead-end, rather than a link, in the food web due to the assumption that they themselves are not consumed, since their gelatinous bodies are less nutritious than co-occurring crustacean prey. Along with this, salp populations are hypothesized to be increasing due to climate change. This proposal addresses these questions: 1) Do salps compete primarily with crustaceans (as in the prevailing paradigm) or are they competitors of single-celled protists, which are the dominant grazers of small phytoplankton? 2) Do salp blooms increase the efficiency of food-web pathways from tiny phytoplankton to fisheries production in nutrient-poor ocean regions?

This project will support the interdisciplinary education of a graduate student who will learn modeling and laboratory techniques in the fields of biological and chemical oceanography and stimulate international collaborations between scientists in the United States and New Zealand. Additionally, several Education and Outreach initiatives are planned, including development of a week-long immersive high school class in biological oceanography, and education modules that will serve the "scientists-in-the schools" program in Tallahassee, FL.

It is commonly assumed that salps are a trophic sink. However, this idea was developed before the discovery that protists (rather than crustaceans) are the dominant grazers in the open ocean and was biased by the difficulty of recognizing gelatinous salps in fish guts. More recent studies show that salps are found in guts of a diverse group of fish and seabirds and are a readily available prey source when crustacean abundance is low. This proposal seeks to quantify food web flows through contrasting salp-dominated and salp-absent water parcels near the Chatham Rise off western New Zealand where salp blooms are a predictable phenomenon. The proposal will leverage previously obtained data on salp abundance, bulk grazing impact, and biogeochemical significance during Lagrangian experiments conducted by New Zealand-based collaborators. The proposal will determine 1) taxon- and size-specific phytoplankton growth rate measurements, 2) taxon- and size-specific protozoan and salp grazing rate measurements, 3) compound specific isotopic analysis of the amino acids of mesozooplankton to quantify the trophic position of salps, hyperiid amphipods, and other crustaceans, 4) sediment traps to quantify zooplankton carcass sinking rates, and 5) linear inverse ecosystem modeling syntheses. Secondary production and trophic flows from this well-constrained ecosystem model will be compared to crustacean-dominated and microbial loop-dominated ecosystems in similarly characterized regions (California Current, Costa Rica Dome, and Gulf of Mexico).

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756465
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756610

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