Compound specific isotopic analysis (15N) of the amino acids of size-fractionated zooplankton collected near the Chatham Rise on the R/V Tangaroa SalpPOOP (TAN1810) cruise in Oct. and Nov. of 2018

Website: https://www.bco-dmo.org/dataset/908476
Version: 1
Version Date: 2023-09-15

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

Contributors	Affiliation	Role
Stukel, Michael R.	Florida State University (FSU)	Principal Investigator
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Abstract
This dataset presents compound specific isotopic analysis (15N) of the amino acids of size-fractionated zooplankton collected near the Chatham Rise on the SalpPOOP (TAN1810) cruise. The cruise focus was on studying the impact of salp blooms and marine biogeochemistry and food webs. Stable isotopes were measured to investigate trophic positions of zooplankton. Samples were collected by bongo tows and size-fractionated through nested sieves (4-mm, 2-mm, 1-mm, 0.5-mm, and 0.2-mm). Samples were then analyzed for bulk stable isotopes at the UC Davis stable isotope facility.

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Coverage

Spatial Extent: **N**:-42.6597 **E**:-179.843 **S**:-45.5498 **W**:173.7833
Temporal Extent: 2018-10-24 - 2018-11-18

Methods & Sampling

We conducted double oblique zooplankton net tows from 200 m water depth to the sea-surface using a 0.7 m-diameter Bongo frame with paired 200-µm mesh nets, equipped with two General Oceanics flow meters to measure the filtered volume and a temperature-depth recorder. A fraction of each tow was size-fractionated through nested sieves (4-mm, 2-mm, 1-mm, 0.5-mm, 0.2-mm), rinsed with isotonic ammonium formate, and stored for isotopic analyses. Samples were then dried, fumed with HCl (to remove calcium carbonate), packed in pre-combusted tins and shipped to the U.C. Davis Stable Isotope Facility.

Per the U.C. Davis Stable Isotope Facility analytical methods are as follows:

Amino acids are made suitable for gas chromatography by derivatization as N-acetyl methyl esters

(NACME[1]). Prior to derivatization, amino acids are liberated from sample material proteins by acid hydrolysis (6 M HCl, 70 min, 150 ºC under N2 headspace). Additional purification steps, such as strong cation-exchange chromatography (SCX; Dowex 50WX8 resin), may be required for sample materials with significant fractions of carbohydrates, lipids, salts, or other potential matrix interferences. NACME amino acid derivatives are injected at 260 ºC (splitless, 1 min) and separated on an Agilent DB-35 column (60 m x 0.32 mm ID x 1.5 µm film thickness) at a constant flow rate of 2 mL/min under the following temperature program: 70 °C (hold 2 min); 140 °C (15 °C/min, hold 4 min); 240 °C (12 °C/min, hold 5 min); and 255 °C (8 °C/min, hold 35 min).

GC-C-IRMS is performed on a Thermo Trace GC 1310 gas chromatograph coupled to a Thermo Scientific Delta V Advantage isotope-ratio mass spectrometer via a GC IsoLink II combustion interface. The combustion reactor is a NiO tube containing CuO and NiO wires maintained at 1000 °C. Water is subsequently removed through a Nafion dryer before the analyte gases are transferred to the IRMS.

During 15N analysis, CO2 is removed from the post-combustion carrier stream through the use of a liquid nitrogen trap to prevent isobaric interferences within the ion source.

All samples are analyzed in duplicate; further replicates may be analyzed if initial measurements fall outside expected measurement error. Replicates of the quality control and assurance reference materials are measured every five samples.

Instruments:
Thermo Trace GC 1310 gas chromatograph coupled to a Thermo Scientific Delta V Advantage isotope-ratio mass spectrometer via a GC IsoLink II combustion interface.

BCO-DMO Processing Description

BCO-DMO Data Manager Processing Notes:
* Sheet 1 of file "SalpPOOP Size-fractionated Zooplankton CSIA-AA.xlsx" was imported into the BCO-DMO data system.
* Column names adjusted to conform to BCO-DMO naming conventions designed to support broad re-use by a variety of research tools and scripting languages. [Only numbers, letters, and underscores. Can not start with a number]
* ISO_DateTime_UTC column added to the data from date and time columns provided as "NZST" which is UTC+12
* lat lons rounded to 5 decimal places.
* isotope d125 N columns rounded from 14 to 4 decimal places

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Related Publications

Décima, M., Stukel, M. R., Nodder, S. D., Gutiérrez-Rodríguez, A., Selph, K. E., dos Santos, A. L., Safi, K., Kelly, T. B., Deans, F., Morales, S. E., Baltar, F., Latasa, M., Gorbunov, M. Y., & Pinkerton, M. (2023). Salp blooms drive strong increases in passive carbon export in the Southern Ocean. Nature Communications, 14(1). https://doi.org/10.1038/s41467-022-35204-6
Methods

Fender, C. K., Décima, M., Gutiérrez-Rodríguez, A., Selph, K. E., Yingling, N., & Stukel, M. R. (2023). Prey size spectra and predator to prey size ratios of southern ocean salps. Marine Biology, 170(4). https://doi.org/10.1007/s00227-023-04187-3
Results

Stukel, M. R., Décima, M., & Landry, M. R. (2022). Quantifying biological carbon pump pathways with a data-constrained mechanistic model ensemble approach. Biogeosciences, 19(15), 3595–3624. https://doi.org/10.5194/bg-19-3595-2022
Results

Stukel, M.R., Décima, M., Selph, K.E. and Gutiérrez-Rodríguez, A. (2021), Size-specific grazing and competitive

interactions between large salps and protistan grazers. Limnol Oceanogr, 66: 2521-2534. https://doi.org/10.1002/lno.11770
Results

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Related Datasets

IsRelatedTo

Stukel, M. R., Decima, M. (2023) **Bulk stable isotopes (d13C, d15N) of size-fractionated zooplankton collected near the Chatham Rise on the R/V Tangaroa SalpPOOP (TAN1810) cruise in Oct. and Nov. of 2018.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-09-15 http://lod.bco-dmo.org/id/dataset/908460 [view at BCO-DMO]
Relationship Description: Data from analyses performed on the same bongo tow samples.

Stukel, M. R., Decima, M. (2023) **Salp & Hyperiid Amphipod bulk isotopes.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-09-15 http://lod.bco-dmo.org/id/dataset/908486 [view at BCO-DMO]
Relationship Description: Data from analyses performed on the same bongo tow samples.

Stukel, M. R., Decima, M. (2023) **Salps & Hyperiid Amphipods CSIA-AA.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-09-15 http://lod.bco-dmo.org/id/dataset/908493 [view at BCO-DMO]
Relationship Description: Data from analyses performed on the same bongo tow samples.

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Bongo Net
Generic Instrument Description	A Bongo Net consists of paired plankton nets, typically with a 60 cm diameter mouth opening and varying mesh sizes, 10 to 1000 micron. The Bongo Frame was designed by the National Marine Fisheries Service for use in the MARMAP program. It consists of two cylindrical collars connected with a yoke so that replicate samples are collected at the same time. Variations in models are designed for either vertical hauls (OI-2500 = NMFS Pairovet-Style, MARMAP Bongo, CalVET) or both oblique and vertical hauls (Aquatic Research). The OI-1200 has an opening and closing mechanism that allows discrete "known-depth" sampling. This model is large enough to filter water at the rate of 47.5 m3/minute when towing at a speed of two knots. More information: Ocean Instruments, Aquatic Research, Sea-Gear

Dataset-specific Instrument Name	Thermo Trace GC 1310 gas chromatograph
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	Thermo Trace GC 1310 gas chromatograph coupled to a Thermo Scientific Delta V Advantage isotope-ratio mass spectrometer via a GC IsoLink II combustion interface.
Generic Instrument Description	Instrument separating gases, volatile substances, or substances dissolved in a volatile solvent by transporting an inert gas through a column packed with a sorbent to a detector for assay. (from SeaDataNet, BODC)

Dataset-specific Instrument Name	Thermo Scientific Delta V Advantage isotope-ratio mass spectrometer
Generic Instrument Name	Mass Spectrometer
Dataset-specific Description	Thermo Trace GC 1310 gas chromatograph coupled to a Thermo Scientific Delta V Advantage isotope-ratio mass spectrometer via a GC IsoLink II combustion interface.
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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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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