Compound-specific nitrogen stable isotope ratios of amino acids in size-fractionated particles from Monterey Bay, CA, 2017

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Data Type: Cruise Results
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Project
» Collaborative research: The effects of predator traits on the structure of oceanic food webs (SiphWeb)

Contributors	Affiliation	Role
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Abstract
In this dataset we present compound-specific nitrogen stable isotope ratios of amino acids in size-fractionated particles from Monterey Bay, CA. Particles were collected near Monterey Bay Aquarium Research Institute's Midwater 1 time series site via in situ filtration in July and August 2017. Particles were collected at 10 depths from the surface to approximately 500 m and size-fractionated into three size-classes: 0.7-20 µm, 20-100 µm, and >100 µm. Particle data were used for a midwater food web study as well as a study on microbial and metazoan contributions to particulate organic matter. The collection of this data was supported by NSF OCE and the David and Lucille Packard Foundation through the Monterey Bay Aquarium Research Institute, as well as the L'Oreal For Women in Science Fellowship, which funded ship time and work aboard the R/V Paragon.

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Coverage

Location: Monterey Bay, California, 36.78 N 122.058 W, 1600 m depth, time-series site Midwater 1 (MW1)
Spatial Extent: **N**:36.69938 **E**:-122.03142 **S**:36.69855 **W**:-122.04203
Temporal Extent: 2017-07-31 - 2017-08-03

Methods & Sampling

Particles were collected off the coast of Monterey Bay, California using in situ filtration (WTS-LV, McLane Research Laboratories) on four consecutive days (July 31-August 3, 2017) at three discrete depths per day aboard Monterey Bay Aquarium Research Institute's R/V *Paragon*. Pumping duration was between 90 and 165 minutes, longer at deeper sampling depths and pumps filtered approximately 400-600 L of seawater. The

vessel drifted freely during collection; start and end locations are recorded in the dataset. One pump failed to initiate pumping, and filters recovered from this pump were used as full process blanks. The three size classes were collected using three filters mounted on mini-MULVFS 3-tiered filter holders (Bishop, Lam, and Wood, 2012: 100 µm nylon (Nitex) mesh with 150 µm nylon (Nitex) mesh backing, 20 µm nylon (Nitex) mesh with 150 µm nylon (Nitex) mesh backing, and two, stacked 0.7 µm pre-combusted glass microfiber filters (GF/F). Nitex was pre-cleaned using 10% hydrochloric acid and methanol. After collection, filter holders were stored in a cooler with ice packs frozen at -80°C for two hours until processing in the lab, where filters were photographed, folded, and stored in combusted foil at -80°C until analysis.

Before analysis, particles collected on the 100 µm nylon (Nitex) and 20 µm nylon (Nitex) filters were resuspended in 0.2 µm filtered seawater in an acid-cleaned plastic bottle with gentle shaking and sonication, then re-filtered onto combusted 47-mm GF/Fs; this process was repeated three times. All filters were lyophilized and inspected under a dissecting microscope (10-40x magnification) to remove Nitex, plastic fibers, or swimmers. Filters were quantitatively split; approximately 1/8 to 1/4 of the filter was used for compound-specific isotope analysis.

Filter splits for Compound-Specific Stable Isotope Analysis of Amino Acids (CSIA-AA) were hydrolyzed to extract amino acids (20 hours at 110° C, 6N hydrochloric acid), purified on cation exchange resin columns (50W-X8, 100-200 mesh) and derivatized to trifluoroacetyl/isopropyl esters for gas chromatography following the methods of Hannides et al. (2013) and identical to Doherty et al. (2021). The derivatized amino acids were analyzed for nitrogen isotopic composition on a Thermo Trace 1310 gas chromatograph with a BPX5 column (50 m x 0.32 mm, 1.0 µm film thickness) through a combined combustion/reduction interface (Thermo Isolink II, 1000° C) and liquid nitrogen cold trap, interfaced to a Thermo Conflo IV and MAT 253 isotope ratio mass spectrometer. Three injections were made for each sample where possible, with norleucine and aminoadipic acid with known $\delta^{15}N$ values as co-injection standards. Analytical uncertainty for each amino acid $\delta^{15}N$ value was derived from the standard deviation of replicate injections. For some samples, only one injection was obtained due to low particle concentration. For these samples a conservative uncertainty estimate of 1‰ was assumed. A standard solution of 14 amino acids with known $\delta^{15}N$ values was also analyzed with each set of three injections to track instrument performance, and to correct for instrument drift, including that due to oxidation state of the reactor (Hannides et al., 2013). Data from standards injected over the lifetime of the instrument were used to correct for relationships between measured $\delta^{15}N$ values and peak area on the instrument.

Data Processing Description

A standard solution of 14 amino acids with known $\delta^{15}N$ values was analyzed with each set of three injections to track instrument performance, and to correct for instrument drift, including that due to oxidation state of the reactor (Hannides et al., 2013). Data from standards injected over the lifetime of the instrument were used to correct for relationships between measured $\delta^{15}N$ values and peak area on the instrument. Analytical uncertainty for each amino acid $\delta^{15}N$ value was derived from the standard deviation of replicate injections. Analytical uncertainty <0.2 ‰ was adjusted to 0.2 ‰ to account for instrument performance in most amino acids, for glycine uncertainty <0.5‰ was adjusted to 0.5‰ . For some samples, only one injection was obtained due to low particle concentration, and for these samples a conservative uncertainty estimate of 1‰ was assumed.

BCO-DMO Processing Description

- Imported "Monterey_particle_BCO-DMO_v2.csv" into the BCO-DMO data system
- Converted date and times to create new fields for ISO formatted UTC start datetimes and end datetimes
- Renamed original time fields to indicate local PST timezones
- Exported file as "958460_v1_particle_csia-aa.csv"

Problem Description

One pump failed to initiate pumping, and filters recovered from this pump were used as full process blanks. Samples estimated to fall below nitrogen amino acid detection limits, based on bulk nitrogen measurements, did

not undergo CSIA-AA. Contamination from an aborted Gas chromatography (GC) injection created overlapping peaks in the first half of a chromatogram of one sample; the isotope ratios from amino acids subject to overlapping peaks are omitted from the dataset.

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Data Files

File
958460_v1_particle_csia-aa.csv (Comma Separated Values (.csv), 4.16 KB) MD5:cffe9c793794764dd3d795ad04e61410 Primary data file for dataset ID 958460, version 1

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Related Publications

Bishop, J. K. B., Lam, P. J., & Wood, T. J. (2012). Getting good particles: Accurate sampling of particles by large volume in-situ filtration. Limnology and Oceanography: Methods, 10(9), 681–710. doi:10.4319/lom.2012.10.681
Methods

Doherty, S. C., Maas, A. E., Steinberg, D. K., Popp, B. N., & Close, H. G. (2021). Distinguishing zooplankton fecal pellets as a component of the biological pump using compound-specific isotope analysis of amino acids. Limnology and Oceanography, 66(7), 2827–2841. Portico. https://doi.org/10.1002/lno.11793
Methods

Hannides, C. C. S., Popp, B. N., Choy, C. A., & Drazen, J. C. (2013). Midwater zooplankton and suspended particle dynamics in the North Pacific Subtropical Gyre: A stable isotope perspective. Limnology and Oceanography, 58(6), 1931–1946. doi:10.4319/lo.2013.58.6.1931
Methods

Hetherington, E. D., Close, H. G., Haddock, S. H. D., Damian-Serrano, A., Dunn, C. W., Wallsgrove, N. J., Doherty, S. C., & Choy, C. A. (2024). Vertical trophic structure and niche partitioning of gelatinous predators in a pelagic food web: Insights from stable isotopes of siphonophores. Limnology and Oceanography, 69(4), 902–919. Portico. https://doi.org/10.1002/lno.12536
Results

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Parameters

Parameter	Description	Units
collection_date	Date of sample collection	unitless
start_collection_local_PST	Pump start time, local time (PST)	unitless
start_collection_ISO_UTC	Pump start ISO datetime (UTC)	unitless
end_collection_local_PST	pump end time, local time (PST)	unitless
end_collection_ISO_UTC	Pump end ISO datetime (UTC)	unitless

start_lat	Latitude at the start of sample collection, North is positive	decimal degrees
end_lat	Latitude at the end of sample collection, North is positive	decimal degrees
start_lon	Longitude at the start of sample collection, West is negative	decimal degrees
end_lon	Longitude at the end of sample collection, West is negative	decimal degrees
Pore_size	Pore size of particle filter	micron (µm)
Depth	Depth at which pump filtered	meters (m)
Ala	Nitrogen stable isotope ratio of alanine	permil (‰)
Gly	Nitrogen stable isotope ratio of glycine	permil (‰)
Thr	Nitrogen stable isotope ratio of threonine	permil (‰)
Ser	Nitrogen stable isotope ratio of serine	permil (‰)
Val	Nitrogen stable isotope ratio of valine	permil (‰)
Leu	Nitrogen stable isotope ratio of leucine	permil (‰)
Ile	Nitrogen stable isotope ratio of isoleucine	permil (‰)
Pro	Nitrogen stable isotope ratio of proline	permil (‰)
Asp	Nitrogen stable isotope ratio of aspartic acid/asparagine	permil (‰)
Glu	Nitrogen stable isotope ratio of glutamic acid/glutamine	permil (‰)
Phe	Nitrogen stable isotope ratio of phenylalanine	permil (‰)
Lys	Nitrogen stable isotope ratio of lysine	permil (‰)
Ala_au	Analytical uncertainty for nitrogen stable isotope ratio of alanine	permil (‰)

Gly_au	Analytical uncertainty for nitrogen stable isotope ratio of glycine	permil (‰)
Thr_au	Analytical uncertainty for nitrogen stable isotope ratio of threonine	permil (‰)
Ser_au	Analytical uncertainty for nitrogen stable isotope ratio of serine	permil (‰)
Val_au	Analytical uncertainty for nitrogen stable isotope ratio of valine	permil (‰)
Leu_au	Analytical uncertainty for nitrogen stable isotope ratio of leucine	permil (‰)
Ile_au	Analytical uncertainty for nitrogen stable isotope ratio of isoleucine	permil (‰)
Pro_au	Analytical uncertainty for nitrogen stable isotope ratio of proline	permil (‰)
Asp_au	Analytical uncertainty for nitrogen stable isotope ratio of aspartic acid/asparagine	permil (‰)
Glu_au	Analytical uncertainty for nitrogen stable isotope ratio of glutamic acid/glutamine	permil (‰)
Phe_au	Analytical uncertainty for nitrogen stable isotope ratio of phenylalanine	permil (‰)
Lys_au	Analytical uncertainty for nitrogen stable isotope ratio of lysine	permil (‰)

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Instruments

Dataset-specific Instrument Name	Thermo Trace 1310 gas chromatograph
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	Amino acid isotope ratios were measured on a Thermo Trace 1310 gas chromatograph with a BPX5 column (50 m x 0.32 mm, 1.0 µm film thickness) through a combined combustion/reduction interface (Thermo Isolink II, 1000° C) and liquid nitrogen cold trap, interfaced to a Thermo Conflo IV and MAT 253 isotope ratio mass spectrometer
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 Conflo IV and MAT 253 isotope ratio mass spectrometer
Generic Instrument Name	Mass Spectrometer
Dataset-specific Description	Amino acid isotope ratios were measured on a Thermo Trace 1310 gas chromatograph with a BPX5 column (50 m x 0.32 mm, 1.0 µm film thickness) through a combined combustion/reduction interface (Thermo Isolink II, 1000° C) and liquid nitrogen cold trap, interfaced to a Thermo Conflo IV and MAT 253 isotope ratio mass spectrometer
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.

Dataset-specific Instrument Name	WTS-LV pumps (McLane Research Laboratories)
Generic Instrument Name	McLane Large Volume Pumping System WTS-LV
Dataset-specific Description	Particles were collected with WTS-LV pumps (McLane Research Laboratories)
Generic Instrument Description	The WTS-LV is a Water Transfer System (WTS) Large Volume (LV) pumping instrument designed and manufactured by McLane Research Labs (Falmouth, MA, USA). It is a large-volume, single-event sampler that collects suspended and dissolved particulate samples in situ. Ambient water is drawn through a modular filter holder onto a 142-millimeter (mm) membrane without passing through the pump. The standard two-tier filter holder provides prefiltering and size fractioning. Collection targets include chlorophyll maximum, particulate trace metals, and phytoplankton. It features different flow rates and filter porosity to support a range of specimen collection. Sampling can be programmed to start at a scheduled time or begin with a countdown delay. It also features a dynamic pump speed algorithm that adjusts flow to protect the sample as material accumulates on the filter. Several pump options range from 0.5 to 30 liters per minute, with a max volume of 2,500 to 36,000 liters depending on the pump and battery pack used. The standard model is depth rated to 5,500 meters, with a deeper 7,000-meter option available. The operating temperature is -4 to 35 degrees Celsius. The WTS-LV is available in four different configurations: Standard, Upright, Bore Hole, and Dual Filter Sampler. The high-capacity upright WTS-LV model provides three times the battery life of the standard model. The Bore-Hole WTS-LV is designed to fit through a narrow opening such as a 30-centimeter borehole. The dual filter WTS-LV features two vertical intake 142 mm filter holders to allow simultaneous filtering using two different porosities.

Dataset-specific Instrument Name	dissecting microscope
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	All filters were lyophilized and inspected under a dissecting microscope (10-40x magnification) to remove Nitex, plastic fibers, or swimmers.
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of reflection and absorption of visible light. Includes conventional and inverted instruments. Also called a "light microscope".

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Project Information

Collaborative research: The effects of predator traits on the structure of oceanic food webs (SiphWeb)

Coverage: North Pacific

Food webs describe who eats whom, tracing the flow of energy from plants up to large animals. While many connections in food webs on land are quite familiar (lions eat antelope and antelope eat grass, for example), there are large gaps in our understanding of ocean food webs. Closing these gaps is critical to understanding how nutrients and energy move through ocean ecosystems, how organisms interact in the ocean, and how best to manage ocean resources. This project will study ocean food web structure with a focus on siphonophores, an abundant group of predators in the open ocean that range in length from less than an inch to more than one hundred feet. Siphonophores are closely related to corals and many jellyfish. They are known to be important predators within ocean food webs, but they are difficult to study because they live across great ocean depths and are gelatinous and fragile. The details of what they eat, as well as many other features of their biology, remain poorly known. This project will combine direct observations of feeding, genetic analysis of siphonophore gut contents, and stable isotope analyses to identify what different species of siphonophores eat. The team will also examine why they eat what they do. This will provide a new understanding of how the structure of food webs arise, aiding in our ability to predict future changes to food webs as the global climate shifts. Siphonophores feed in a very unique manner--they have highly specialized tentacles that are used solely for capturing prey--thus, the prey captured is determined largely by the anatomy and function of these tentacles. The project will describe these tentacles, reconstruct their evolutionary history, and investigate how evolutionary shifts in tentacle structure have led to changes in diet. This project will train one PhD student, one Master's student, a postdoc, and undergraduate students, including individuals of underrepresented groups. This project will support the production of scientifically rigorous yet engaging videos, foster the expansion of a citizen-science program, and create K-12 teaching modules.

This project will advance three scientific aims: First, it will identify the diet of a diverse range of siphonophores using DNA metabarcoding of gut contents and prey field, remotely operated vehicle (ROV) video of prey encounters, and stable isotope analysis. These approaches are highly complementary and allow for extensive cross validation. Second, the project will characterize the selectivity of siphonophore diets by comparing them to the relative prey abundances in the habitats of each of these species. Third, the project will characterize the structure of the siphonophore prey capture apparatus across species through detailed morphological analysis of their tentacles and nematocysts. These data will be integrated in an ecological and evolutionary framework to identify predator features associated with prey specialization. In a larger context, addressing these questions will advance our understanding of oceanic predation by revealing how evolutionary changes in predator selectivity correspond to evolutionary changes in habitat and feeding apparatus and how these changes shape current food web structure in the open ocean. We will test and refine an integrated approach to describing the structure and origin of food web topology, and evaluate the potential for phylogenetic relationships to explain prey selectivity.

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-1830016

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