Nitrogen compound-specific isotope values of amino acids for each gelatinous zooplankton sample and the sample's estimated trophic position from R/V Sally Ride and R/V Roger Revelle cruises in the southern California Current Ecosystem from 2020-2023

Website: https://www.bco-dmo.org/dataset/982454
Data Type: Cruise Results
Version: 1
Version Date: 2025-08-13

Project
» Resolving vertical trophic linkages between surface and deep pelagic food webs (DeepSeaWebs)

Contributors	Affiliation	Role
Choy, C. Anela	University of California-San Diego Scripps (UCSD-SIO)	Principal Investigator
Chavarry, Julia	University of California-San Diego Scripps (UCSD-SIO)	Student
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
We estimated the trophic positions of abundant gelatinous zooplankton (chaetognaths, cnidarians, ctenophores, molluscs, and pelagic tunicates) in the southern California Current Ecosystem using stable carbon and nitrogen isotope analysis. Gelatinous zooplankton were collected on four research cruises on the R/V Sally Ride and R/V Roger Revelle between 2020 and 2023 and from 0 to 3,000 meters depth using a 10-square-meter Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS). 561 samples of gelatinous zooplankton from thirteen taxonomic groups were chosen for bulk tissue stable isotope analysis. An additional twenty samples from seven gelatinous genera were chosen for nitrogen compound-specific isotope analysis of amino acids because they were abundant across our region and represented a range of hypothesized feeding guilds and depth habitats (0 – 1,025 meters). Gelatinous zooplankton were briefly thawed to remove visible gut contents using forceps and a scalpel. Samples were then lyophilized and homogenized. To ensure sufficient sample mass for stable isotope analysis, samples often contained multiple individuals from the same net, taxonomic group, and size class. The number of individuals per sample was typically fewer than 100, with a larger number of individuals pooled for some samples of Pantachogon spp. and Hormiphora spp. Samples were processed for nitrogen compound-specific isotope analysis at the Laboratory for Marine Organic Isotope Geochemistry at the University of Miami. This dataset includes the nitrogen compound-specific isotope values of amino acids for each gelatinous zooplankton sample and the sample's estimated trophic position.

Table of Contents

Coverage

Location: Southern California Current Ecosystem
Spatial Extent: **N**:32.56 **E**:-120.21 **S**:32.4 **W**:-120.33
Temporal Extent: 2021-06-24 - 2021-06-25

Methods & Sampling

Gelatinous zooplankton were collected on four research cruises between 2020 and 2023 at seven stations representing four nearshore and escarpment, and two offshore regions within the Southern California Bight. We conducted depth-discrete sampling of gelatinous zooplankton using a 10-square-meter (m^2) Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) equipped with five depth-discrete nets (mesh sizes 5-millimeter (mm), Wiebe et al., 1985). The 10 m^2 MOCNESS was towed obliquely as the ship traveled at a speed between 1 to 2 knots, with depth-discrete collections occurring on the upcast. Sampling stations and depth intervals varied across stations and cruises, but there were typically two depth intervals sampled within the upper 500 meters (m) and larger depth intervals below 500 m. The maximum depth of sampling increased from 1,250 m nearshore to 3,000 m offshore, corresponding with the deepening of the water column.

Upon recovery, samples were stored in chilled seawater and kept at 5 degrees Celsius (°C) until processing. All sample processing was performed on ice to preserve body condition. Gelatinous zooplankton were identified to the most specific taxonomic level using published keys. The concentration of carbon and/or nitrogen can be low in gelatinous individuals (Lüskow et al., 2021), so we pooled multiple gelatinous individuals from the same taxonomic groups into a single sample, while standardizing size ranges. 561 samples of gelatinous zooplankton representing 13 taxonomic groups were chosen for bulk tissue stable carbon and nitrogen isotope analysis. A subset of twenty samples from seven gelatinous genera were chosen for nitrogen compound-specific isotope analysis of amino acids (CSIA-AA): *Pyrosoma atlanticum*, *Beroe cucumis*, *Hormiphora* spp., *Periphylla periphylla*, *Atolla vanhoeffeni*, *Aegina* spp., and *Pantachogon* spp. Taxa were selected for CSIA-AA because they represented a range in hypothesized feeding guilds, were found across a range of depth habitats (0 to 1,025 m), and were abundant in our sampling region. To constrain possible spatiotemporal variability in baseline δ15N values, all the samples selected for CSIA-AA were limited to a daytime collection event at the escarpment in August 2021.

Gelatinous zooplankton were briefly thawed to remove visible gut contents using forceps and a scalpel, which were cleaned with ethanol between samples. Both gelatinous zooplankton and mesozooplankton samples were then lyophilized and homogenized in Whirl-Paks. To ensure sufficient sample mass for stable isotope analysis, samples often contained multiple individuals from the same net, taxonomic group, and size class. The number of individuals per sample was typically fewer than 100, with a larger number of individuals pooled for some samples of *Pantachogon* spp. and *Hormiphora* spp.

Dried, homogenized tissues were packaged into tin capsules (1.5 to 4 milligrams (mg) per sample) for bulk tissue stable isotope analyses, which were conducted at the University of Hawaii at Manoa and the University of California Merced. Briefly, samples were run on a Costech 4010 Elemental Combustion System coupled to either a ThermoScientific DELTA V Advantage, ThermoScientific DELTA V+, or a ThermoFinnigan DeltaPlus XP isotope ratio mass spectrometer through a ThermoScientific Conflo IV interface. Stable isotope values are reported in the standard per mille notation (‰), compared to the standards atmospheric N_2 and Vienna Pee Dee Belemnite for nitrogen and carbon, respectively. To ensure accuracy and instrument precision, both labs used a combination of international reference materials (from the United States Geological Survey or the National Institute of Standards and Technology) and in-house reference materials (squid or tuna) with known δ15N and δ13C values. Based on analyzed reference materials, sample reproducibility was ± 0.2‰ for samples run at the University of Hawaii at Manoa, and sample reproducibility was ± 0.4‰ for samples run at the University of California Merced.

Samples were processed for CSIA-AA at the Laboratory for Marine Organic and Isotope Geochemistry at the University of Miami following the methods of Popp et al. (2007), Hannides et al. (2013), and Wojtal et al. (2023). Briefly, ~50 mg of each dried sample was hydrolyzed, purified, and derivatized. Derivatives were then injected into a Thermo Trace 1310 gas chromatograph with a BPX5 column (50 m x 0.32 mm, 1.0 micrometer (µm) film thickness), fed into a combined oxidation/reduction reactor (Thermo Isolink II, 1000°C), and passed through a liquid nitrogen cold trap and into a Thermo Conflo IV and MAT 253 isotope ratio mass spectrometer. Three separate laboratory mixtures with known isotope ratios were used to correct δ15N values of gelatinous zooplankton samples and to ensure instrument accuracy and precision. Reliable data for each sample in comparison to standards were obtained from triplicate injections where possible but replicate injections for eight samples.

We used five approaches to estimate the trophic position of samples run for CSIA-AA. The first approach, TP_{diet}, was based on published diet studies, including *in situ* observations and gut content analyses. The second approach used δ15N values of bulk tissues to estimate the consumer trophic position (TP_{bulk}) following

the methods outlined in Post (2002). This estimate is based on the $\delta 15N_{bulk}$ values of gelatinous zooplankton, the trophic discrimination factor (TDF), and the δ15N value and trophic position of the isotopic baseline. Limited studies suggest that the TDF of gelatinous zooplankton may be lower than 3.4‰ (e.g., Schaub et al., 2021; Stukel et al., 2024; Tilves et al., 2018). We thus used a range in TDF (2.4 – 4.4‰; $TP_{bulk\text{-}TDF\text{-}2.4}$ and $TP_{bulk\text{-}TDF\text{-}4.4}$) based on the reported standard deviation in TDF of 1‰ (Post, 2002). The third approach utilized published diet data along with δ15N values of bulk tissues to estimate trophic position ($TP_{diet\text{-}bulk}$). We used known information about animal diet to designate a more accurate TDF. The fourth and fifth approaches for estimating trophic position relied on CSIA-AA following methods outlined in Chikaraishi et al. (2009) (TP_{AA}). Briefly, phenylalanine was designated as a 'source' amino acid (after Chikaraishi et al., 2009; McMahon & McCarthy 2016; Nielsen et al., 2015). We estimated TP_{AA} two different ways by considering two 'trophic' amino acids, glutamic acid (TP_{Glu}) and alanine (TP_{Ala}). Glutamic acid is commonly used as the 'trophic' amino acid in food web studies (e.g., Nielsen et al., 2015; McMahon & McCarthy 2016). However, we expected microbial cycling to be prominent within southern California Current Ecosystem food webs and subsequently designated alanine as another 'trophic' amino acid to capture these microbial contributions (after Décima et al., 2017).

BCO-DMO Processing Description

- Imported original file "gelatinous_zooplankton_csia_aa.csv" into the BCO-DMO system.
- Created Date_UTC column in YYYY-MM-DD format.
- Renamed fields to comply with BCO-DMO naming conventions.
- Saved final file as "982454_v1_csia_gelatinous_zooplankton.csv".

[table of contents | back to top]

Data Files

File	
982454_v1_csia_gelatinous_zooplankton.csv	(Comma Separated Values (.csv), 4.49 KB) MD5:33eb47e2806edb8b86d587de694588d8
Primary data file for dataset ID 982454, version 1	

[table of contents | back to top]

Related Publications

Chavarry, J., Hetherington, H., Close, H., Choy, C. A. (under review) Using stable isotopes to describe the trophic structure of gelatinous zooplankton across the deep pelagic. Limnology and Oceanography.
Results

Chikaraishi, Y., Ogawa, N. O., Kashiyama, Y., Takano, Y., Suga, H., Tomitani, A., Miyashita, H., Kitazato, H., & Ohkouchi, N. (2009). Determination of aquatic food-web structure based on compound-specific nitrogen isotopic composition of amino acids. Limnology and Oceanography: Methods, 7(11), 740–750. Portico. https://doi.org/10.4319/lom.2009.7.740
Methods

Décima, M., Landry, M. R., Bradley, C. J., & Fogel, M. L. (2017). Alanine δ15N trophic fractionation in heterotrophic protists. Limnology and Oceanography, 62(5), 2308–2322. Portico. https://doi.org/10.1002/lno.10567
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

Lüskow, F., Galbraith, M., Hunt, B., Perry, R., & Pakhomov, E. (2021). Gelatinous and soft-bodied zooplankton in the Northeast Pacific Ocean: organic, elemental, and energy contents. Marine Ecology Progress Series, 665,

19–35. https://doi.org/10.3354/meps13663
Methods

McMahon, K. W., & McCarthy, M. D. (2016). Embracing variability in amino acid δ15N fractionation: mechanisms, implications, and applications for trophic ecology. Ecosphere, 7(12). Portico. https://doi.org/10.1002/ecs2.1511
Methods

Nielsen, J. M., Popp, B. N., & Winder, M. (2015). Meta-analysis of amino acid stable nitrogen isotope ratios for estimating trophic position in marine organisms. Oecologia, 178(3), 631–642. https://doi.org/10.1007/s00442-015-3305-7
Methods

Popp, B. N., Graham, B. S., Olson, R. J., Hannides, C. C. S., Lott, M. J., López-Ibarra, G. A., … Fry, B. (2007). Insight into the Trophic Ecology of Yellowfin Tuna, Thunnus albacares, from Compound-Specific Nitrogen Isotope Analysis of Proteinaceous Amino Acids. Terrestrial Ecology, 173–190. doi:10.1016/s1936-7961(07)01012-3
Methods

Post, D. M. (2002). Using stable isotopes to estimate trophic position: Models, methods, and assumptions. Ecology, 83(3), 703–718. https://doi.org/10.1890/0012-9658(2002)083[0703:USITET]2.0.CO;2
Methods

Schaub, J., McLaskey, A. K., Forster, I., & Hunt, B. P. V. (2021). Experimentally derived estimates of turnover and modification for stable isotopes and fatty acids in scyphozoan jellyfish. Journal of Experimental Marine Biology and Ecology, 545, 151631. https://doi.org/10.1016/j.jembe.2021.151631
Methods

Stukel, M. R., Décima, M., Fender, C. K., Gutierrez-Rodriguez, A., & Selph, K. E. (2024). Gelatinous filter feeders increase ecosystem efficiency. Communications Biology, 7(1). https://doi.org/10.1038/s42003-024-06717-1
Methods

Tilves, U., Fuentes, V., Milisenda, G., Parrish, C., Vizzini, S., & Sabatés, A. (2018). Trophic interactions of the jellyfish Pelagia noctiluca in the NW Mediterranean: evidence from stable isotope signatures and fatty acid composition. Marine Ecology Progress Series, 591, 101–116. https://doi.org/10.3354/meps12332
Methods

Wiebe, P. H., Morton, A. W., Bradley, A. M., Backus, R. H., Craddock, J. E., Barber, V., … Flierl, G. R. (1985). New development in the MOCNESS, an apparatus for sampling zooplankton and micronekton. Marine Biology, 87(3), 313–323. doi:10.1007/bf00397811 https://doi.org/10.1007/BF00397811
Methods

Wojtal, P. K., Doherty, S. C., Shea, C. H., Popp, B. N., Benitez-Nelson, C. R., Buesseler, K. O., Estapa, M. L., Roca-Martí, M., & Close, H. G. (2023). Deconvolving mechanisms of particle flux attenuation using nitrogen isotope analyses of amino acids. Limnology and Oceanography. Portico. https://doi.org/10.1002/lno.12398
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
specimen_number	sample identifier that can be used to link to sample metadata in the related bulk tissue stable isotope dataset	unitless
best_taxonomic_ID	the finest taxonomic level the gelatinous zooplankton were identified to	unitless
tow	the tow number when the sample was collected	unitless

net	the net number when the sample was collected	unitless
Date_UTC	date the sample was collected (UTC)	unitless
year	the year the sample was collected (UTC)	unitless
month	the month the sample was collected (UTC)	unitless
day	the day the sample was collected (UTC)	unitless
latitude	the latitude of where the sample was collected	decimal degrees
longitude	the longitude of where the sample was collected	decimal degrees
hypothesized_diet	the hypothesized primary diet of the gelatinous zooplankton taxonomic group, based on published diet data	unitless
TP_glu	The estimated trophic position of the sample, based on nitrogen compound-specific isotope analysis of amino acids and the 'trophic' amino acid glutamic acid	unitless
TP_glu_SD	The trophic position uncertainty of TP_glu based on propagation of errors	unitless
TP_ala	The estimated trophic position of the sample, based on nitrogen compound-specific isotope analysis of amino acids and the 'trophic' amino acid alanine	unitless
TP_ala_SD	The trophic position uncertainty of TP_ala based on propagation of errors	unitless
TP_bulk_TDF_2_4	The estimated trophic position of the sample based on bulk tissue stable nitrogen isotope analysis and a trophic discrimination factor of 2.4‰	unitless
TP_bulk_TDF_4_4	The estimated trophic position of the sample based on bulk tissue stable nitrogen isotope analysis and a trophic discrimination factor of 4.4‰	unitless
TP_diet_bulk	The estimated trophic position of the sample based on bulk tissue stable nitrogen isotope analysis and a trophic discrimination factor that is dependent on the taxonomic group's hypothesized diet	unitless
TP_diet	The estimated trophic position of the sample based on the taxonomic group's hypothesized diet	unitless

Alanine	The mean nitrogen stable isotope value of alanine for samples run in replicate/triplicate	parts per thousand
Aspartic_Acid	The mean nitrogen stable isotope value of aspartic acid for samples run in replicate/triplicate	parts per thousand
Glutamic_Acid	The mean nitrogen stable isotope value of glutamic acid for samples run in replicate/triplicate	parts per thousand
Glycine	The mean nitrogen stable isotope value of glycine for samples run in replicate/triplicate	parts per thousand
Isoleucine	The mean nitrogen stable isotope value of isoleucine for samples run in replicate/triplicate	parts per thousand
Leucine	The mean nitrogen stable isotope value of leucine for samples run in replicate/triplicate	parts per thousand
Lysine	The mean nitrogen stable isotope value of lysine for samples run in replicate/triplicate	parts per thousand
Phenylalanine	The mean nitrogen stable isotope value of phenylalanine for samples run in replicate/triplicate	parts per thousand
Proline	The mean nitrogen stable isotope value of proline for samples run in replicate/triplicate	parts per thousand
Serine	The mean nitrogen stable isotope value of serine for samples run in replicate/triplicate	parts per thousand
Threonine	The mean nitrogen stable isotope value of threonine for samples run in replicate/triplicate	parts per thousand
Valine	The mean nitrogen stable isotope value of valine for samples run in replicate/triplicate	parts per thousand
Alanine_SD	The standard deviation of the nitrogen stable isotope value of alanine for samples run in replicate/triplicate	parts per thousand
Aspartic_Acid_SD	The standard deviation of the nitrogen stable isotope value of aspartic acid for samples run in replicate/triplicate	parts per thousand

Glutamic_Acid_SD	The standard deviation of the nitrogen stable isotope value of glutamic acid for samples run in replicate/triplicate	parts per thousand
Glycine_SD	The standard deviation of the nitrogen stable isotope value of glycine for samples run in replicate/triplicate	parts per thousand
Isoleucine_SD	The standard deviation of the nitrogen stable isotope value of isoleucine for samples run in replicate/triplicate	parts per thousand
Leucine_SD	The standard deviation of the nitrogen stable isotope value of leucine for samples run in replicate/triplicate	parts per thousand
Lysine_SD	The standard deviation of the nitrogen stable isotope value of lysine for samples run in replicate/triplicate	parts per thousand
Phenylalanine_SD	The standard deviation of the nitrogen stable isotope value of phenylalanine for samples run in replicate/triplicate	parts per thousand
Proline_SD	The standard deviation of the nitrogen stable isotope value of proline for samples run in replicate/triplicate	parts per thousand
Serine_SD	The standard deviation of the nitrogen stable isotope value of serine for samples run in replicate/triplicate	parts per thousand
Threonine_SD	The standard deviation of the nitrogen stable isotope value of threonine for samples run in replicate/triplicate	parts per thousand
Valine_SD	The standard deviation of the nitrogen stable isotope value of valine for samples run in replicate/triplicate	parts per thousand

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	ThermoScientific Conflo IV interface
Generic Instrument Name	Continuous Flow Interface for Mass Spectrometers
Dataset-specific Description	used for the determination of stable isotope ratios of carbon and nitrogen from bulk tissues
Generic Instrument Description	A Continuous Flow Interface connects solid and liquid sample preparation devices to instruments that measure isotopic composition. It allows the introduction of the sample and also reference and carrier gases. Examples: Finnigan MATConFlo II, ThermoScientific ConFlo IV, and Picarro Caddy. Note: This is NOT an analyzer

Dataset-specific Instrument Name	Thermo Isolink II
Generic Instrument Name	Continuous Flow Interface for Mass Spectrometers
Dataset-specific Description	used for the determination of nitrogen compound-specific stable isotope ratios from amino acids
Generic Instrument Description	A Continuous Flow Interface connects solid and liquid sample preparation devices to instruments that measure isotopic composition. It allows the introduction of the sample and also reference and carrier gases. Examples: Finnigan MATConFlo II, ThermoScientific ConFlo IV, and Picarro Caddy. Note: This is NOT an analyzer

Dataset-specific Instrument Name	Costech 4010 Elemental Combustion System
Generic Instrument Name	Costech International Elemental Combustion System (ECS) 4010
Dataset-specific Description	used for the determination of stable isotope ratios of carbon and nitrogen from bulk tissues
Generic Instrument Description	The ECS 4010 Nitrogen / Protein Analyzer is an elemental combustion analyser for CHNSO elemental analysis and Nitrogen / Protein determination. The GC oven and separation column have a temperature range of 30-110 degC, with control of +/- 0.1 degC.

Dataset-specific Instrument Name	Thermo Trace 1310 gas chromatograph
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	used for the determination of nitrogen compound-specific stable isotope ratios from amino acids
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	ThermoFinnigan Deltaplus XP isotope ratio mass spectrometer
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	used for the determination of stable isotope ratios of carbon and nitrogen from bulk tissues
Generic Instrument Description	The Isotope-ratio Mass Spectrometer is a particular type of mass spectrometer used to measure the relative abundance of isotopes in a given sample (e.g. VG Prism II Isotope Ratio Mass-Spectrometer).

Dataset-specific Instrument Name	MAT 253 isotope ratio mass spectrometer
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	used for the determination of nitrogen compound-specific stable isotope ratios from amino acids
Generic Instrument Description	The Isotope-ratio Mass Spectrometer is a particular type of mass spectrometer used to measure the relative abundance of isotopes in a given sample (e.g. VG Prism II Isotope Ratio Mass-Spectrometer).

Dataset-specific Instrument Name	10 m2 Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS)
Generic Instrument Name	MOCNESS
Dataset-specific Description	used to collect gelatinous zooplankton at sea
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	Marel M2400 motion compensating scale
Generic Instrument Name	scale or balance
Dataset-specific Description	used to weigh gelatinous zooplankton at sea
Generic Instrument Description	Devices that determine the mass or weight of a sample.

Dataset-specific Instrument Name	ThermoScientific DELTA V Advantage isotope ratio mass spectrometer
Generic Instrument Name	Thermo Fisher Scientific DELTA V Advantage isotope ratio mass spectrometer
Dataset-specific Description	used for the determination of stable isotope ratios of carbon and nitrogen from bulk tissues
Generic Instrument Description	The Thermo Scientific DELTA V Advantage is an isotope ratio mass spectrometer designed to measure isotopic, elemental, and molecular ratios of organic and inorganic compounds. The DELTA V Advantage is the standard model of the DELTA V series of isotope ratio mass spectrometers, which can be upgraded to the DELTA V Plus. The DELTA V Advantage can be operated in Continuous Flow or Dual Inlet mode. The standard collector configuration is the Universal Triple Collector. H2 collectors with online hydrogen capability are optional. The DELTA V Advantage is controlled by an automated, integrated Isodat software suite. A magnet, whose pole faces determine the free flight space for the ions, eliminates the traditional flight tube. The magnet is designed for fast mass switching which is further supported by a fast jump control between consecutive measurements of multiple gases within one run. The sample gas is introduced at ground potential, eliminating the need for insulation of the flow path, ensuring 100 percent transfer into the ion source. The amplifiers register ion beams up to 50 V. The DELTA V Advantage has a sensitivity of 1200 molecules per ion (M/I) in Dual Inlet mode and 1500 M/I in Continuous Flow mode. It has a system stability of < 10 ppm and an effective magnetic detection radius of 191 nm. It has a mass range of 1 - 80 Dalton at 3 kV.

Dataset-specific Instrument Name	ThermoScientific DELTA V+ isotope ratio mass spectrometer
Generic Instrument Name	Thermo Fisher Scientific DELTA V Plus isotope ratio mass spectrometer
Dataset-specific Description	used for the determination of stable isotope ratios of carbon and nitrogen from bulk tissues
Generic Instrument Description	The Thermo Scientific DELTA V Plus is an isotope ratio mass spectrometer designed to measure isotopic, elemental and molecular ratios of organic and inorganic compounds. The DELTA V Plus is an enhanced model of the DELTA V series of isotope ratio mass spectrometers, which can be upgraded from the DELTA V Advantage. The DELTA V Plus can be operated in Continuous Flow or Dual Inlet mode and can accommodate up to 10 collectors, ensuring flexibility to cover many applications. The DELTA V Plus is controlled by an automated, integrated Isodat software suite. A magnet, whose pole faces determine the free flight space for the ions, eliminates the traditional flight tube. The magnet is designed for fast mass switching which is further supported by a fast jump control between consecutive measurements of multiple gases within one run. The sample gas is introduced at ground potential, eliminating the need for insulation of the flow path, ensuring 100 percent transfer into the ion source. The amplifiers register ion beams up to 50 V. The DELTA V Plus has refined optics, enabling greater ion transmission than the DELTA V Advantage. It has a sensitivity of 800 molecules per ion (M/I) in Dual Inlet mode and 1100 M/I in Continuous Flow mode. It has a system stability of < 10 ppm and an effective magnetic detection radius of 191 nm. It has a mass range of 1 - 96 Dalton at 3 kV.

[table of contents | back to top]

Deployments

SR2007

Website	https://www.bco-dmo.org/deployment/971990
Platform	R/V Sally Ride
Start Date	2020-08-22
End Date	2020-09-04
Description	More information is available from R2R: https://www.rvdata.us/search/cruise/SR2007

SR2212

Website	https://www.bco-dmo.org/deployment/971993
Platform	R/V Sally Ride
Start Date	2022-11-25
End Date	2022-11-30
Description	More information is available from R2R: https://www.rvdata.us/search/cruise/SR2212

SR2323

Website	https://www.bco-dmo.org/deployment/971996
Platform	R/V Sally Ride
Start Date	2023-10-11
End Date	2023-10-25
Description	More information is available from R2R: https://www.rvdata.us/search/cruise/SR2323

RR2104

Website	https://www.bco-dmo.org/deployment/948513
Platform	R/V Roger Revelle
Start Date	2021-06-12
End Date	2021-07-01
Description	More information is available from R2R: https://www.rvdata.us/search/cruise/RR2104

[table of contents | back to top]

Project Information

Resolving vertical trophic linkages between surface and deep pelagic food webs (DeepSeaWebs)

Coverage: Southern California Current

NSF Award Abstract:
This CAREER award is advancing our understanding of connections between surface and deep water ocean food webs, which in turn has important implications for carbon cycling in the ocean. Although marine ecosystems deeper than 200 m encompass Earth's largest single habitat, the food web relationships of deep-sea organisms are poorly resolved. The investigator is evaluating active transport by fishes, squids, crustaceans, and gelatinous animals that move organic matter from the more productive surface into deeper waters through feeding and diel vertical migration. She is using a combination of data on abundance and distribution of species with measurements of stable isotope biomarkers to understand trophic relationships and connect community composition and migratory behavior with food-web processes in the southern California Current ecosystem. The investigator is from a group traditionally underrepresented in science, and she has designed a comprehensive educational plan to train a more diverse, inclusive generation of seagoing biological oceanographers through hands-on field and research experiences. In addition to providing support for graduate and undergraduate students to participate directly in this research, the investigator is creating a novel and cohesive undergraduate curriculum involving a seagoing laboratory course to teach interdisciplinary field methods to conduct research on pelagic ecosystems and a seminar course highlighting Native and Indigenous knowledge alongside more traditional oceanographic research. The overall goal is to broaden participation in science by combining hands-on interdisciplinary research, mentoring, and expanding networks of minority and majority scientists.

This study centers around Vinogradov's "ladder of migrations" as a conceptual framework, with the goal of understanding cumulative downward transport of organisms and organic matter to the deep ocean by overlapping vertical migrations and feeding. It is focusing on the role of micronekton, defined as ~2-20 cm fishes, cephalopods, crustaceans, and gelatinous animals, as active transporters of surface-derived organic matter across epipelagic, mesopelagic, and upper-bathypelagic layers in the southern California Current Ecosystem. One research cruise is sampling deep pelagic micronekton communities comprehensively and systematically and complements long-term data collected in the surface waters of this ecosystem. Depth-discrete MOCNESS tows are sampling organisms to assess micronekton abundance, biomass, and extent of diel vertical migrations to understand how relative compositions of taxa drive vertical connectivity. Analysis of bulk carbon and nitrogen stable isotopes and compound-specific isotopic analyses of amino acids (AA-CSIA) in organism tissue are providing quantitative assessments of deep-pelagic food webs and measuring the relative strength and composition of trophic linkages between surface and deeper water assemblages across distinct

environmental gradients.

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.

This award is funded in whole or in part under the American Rescue Plan Act of 2021 (Public Law 117-2).

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-2048210

[table of contents | back to top]