

Amino acid compound specific isotope analyses of abyssal deposit feeders, gut contents, and surrounding surface sediments collected on R/V Atlantis cruise AT42-10 and R/V Western Flyer Pulse 72 in the eastern North Pacific in 2019

Website: <https://www.bco-dmo.org/dataset/840749>

Data Type: Cruise Results

Version: 1

Version Date: 2021-03-30

Project

» [Collaborative Research: Assessing the relative importance of small vs large particles as sources of nutrition to abyssal communities](#) (Abyssal food web)

| Contributors | Affiliation | Role |
|--------------------------------------|---|---------------------------|
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Abstract

Abyssal ecosystems depend on the quantity and quality of organic material reaching the deep-sea floor. During R/V Atlantis cruise (AT42-10) in May 2019 and R/V Western Flyer cruise (Pulse 72) in October 2019, samples from deep-sea benthic communities were collected in the eastern North Pacific Ocean. Station M was visited to investigate how surface ocean processes are coupled to food-webs at the deep ocean seafloor and to understand the sources of nutrition to the deep-sea benthos. This dataset presents compound specific stable isotope analyses of amino acids (AA-CSIA) of abyssal deposit feeders, their gut contents, and the surrounding sediments.

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Coverage

Spatial Extent: Lat:34.5 Lon:-123.06

Temporal Extent: 2019-05-01 - 2019-10-24

Acquisition Description

Sediment cores and megafauna were collected in May and October 2019 using the HOV Alvin and the ROV Doc Ricketts, respectively. Upon retrieval to the surface, samples were placed in a cool room (5° C) for further processing. Sediment cores of 7 centimeters diameter were sliced and the surface sediments (0–0.5 cm) were placed in petri dishes and stored frozen at -80° C. Specimens of megafauna were weighed and measured, then dissected using a scalpel. We made a longitudinal cut along the digestive tract and took a sample of the foregut and hindgut contents, avoiding gut tissue. Then we removed the remaining guts and took a sample from cleaned body tissue, or in the case of echinoids, from the test. All samples were placed in cryovials and frozen in liquid nitrogen, and subsequently stored at -80° C. In the laboratory, samples of sediments, gut contents and body tissue were freeze dried and ground to a homogenous powder using mortar and pestle.

For analysis of bulk nitrogen and carbon isotopic composition, samples were placed in silver capsules in the following amounts: ~ 0.7 milligrams of body tissue from holothurians, 3 milligrams of body tissue from echinoids, ~ 5 milligrams of gut content, and ~ 20 milligrams of sediment. Samples were acidified to remove carbonates with 1M HCl, which was added dropwise until bubbling ceased, then dried at 60°C and packed.

For $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ analysis of individual amino acids, samples were analyzed following the methods of Hannides et al. (2013). For the analysis of carbon isotope composition, we also derivatized and analyzed under the same conditions a sample containing a set of 13 pure amino acids. $\delta^{13}\text{C}$ values were corrected based on the analysis of that set of pure amino acids (Silfer et al. 1991; Arthur et al. 2014).

Processing Description

BCO-DMO processing description:

- Converted dates to ISO date format (yyyy-mm-dd)
- Adjusted field/parameter names to comply with database requirements
- Missing data identifier 'NA' replaced with 'nd' (BCO-DMO's default missing data identifier)
- Converted latitudes and longitudes to decimal degrees
- Added a conventional header with dataset name, PI names, version date

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Related Publications

Arthur, K. E., Kelez, S., Larsen, T., Choy, C. A., & Popp, B. N. (2014). Tracing the biosynthetic source of essential amino acids in marine turtles using $\delta^{13}\text{C}$ fingerprints. *Ecology*, 95(5), 1285–1293.

doi:[10.1890/13-0263.1](https://doi.org/10.1890/13-0263.1)

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](https://doi.org/10.4319/lo.2013.58.6.1931)

Methods

Silfer, J. A., Engel, M. H., Macko, S. A., & Jumeau, E. J. (1991). Stable carbon isotope analysis of amino acid enantiomers by conventional isotope ratio mass spectrometry and combined gas chromatography/isotope ratio mass spectrometry. *Analytical Chemistry*, 63(4), 370–374.

doi:[10.1021/ac00004a014](https://doi.org/10.1021/ac00004a014)

Methods

Parameters

| Parameter | Description | Units |
|------------------|---|------------------------|
| Sample | Sample identification code | unitless |
| Cruise | Cruise designation | unitless |
| Site | Site designation | unitless |
| ISO_Date_initial | Initial sampling date UTC (yyyy-mm-dd) | unitless |
| ISO_Date_final | Final sampling date UTC (yyyy-mm-dd) | unitless |
| Latitude | Latitude | decimal degrees |
| Longitude | Longitude (West is negative) | decimal degrees |
| Type | Type of sample: Sediment= surface sediment (0-5 mm); Body= deposit feeder body tissue; Gut= gut content | unitless |
| Species | Species of deposit feeder: Scotoplanes= <i>S. globosa</i> ; Echinocrepis= <i>E. rostrata</i> ; Onerophanta= <i>O. mutabilis</i> | unitless |
| Type_gut | Gut section: Hgut= hindgut; Fgut= foregut | unitless |
| delta15N | Bulk nitrogen isotopic composition | per mil (‰) vs AIR |
| delta13C | Bulk carbon isotopic composition | per mil (‰) vs VPDB |
| ALA_N | Mean delta15N value of all injections for Alanine | per mil (‰) vs AIR |
| GLY_N | Mean delta15N value of all injections for Glycine | per mil (‰) vs AIR |
| THR_N | Mean delta15N value of all injections for Threonine | per mil (‰) vs AIR |
| SER_N | Mean delta15N value of all injections for Serine | per mil (‰) vs AIR |
| VAL_N | Mean delta15N value of all injections for Valine | per mil (‰) vs AIR |
| LEU_N | Mean delta15N value of all injections for Leucine | per mil (‰) vs AIR |
| ILE_N | Mean delta15N value of all injections for Isoleucine | per mil (‰) vs AIR |
| PRO_N | Mean delta15N value of all injections for Proline | per mil (‰) vs AIR |
| ASX_N | Mean delta15N value of all injections for Aspartic Acid and Asparagine | per mil (‰) vs AIR |
| GLX_N | Mean delta15N value of all injections for Glutamic Acid and Glutamine | per mil (‰) vs AIR |

| | | |
|----------|---|------------------------|
| PHE_N | Mean delta15N value of all injections for Phenylalanine | per mil (‰) vs AIR |
| TYR_N | Mean delta15N value of all injections for Tyrosine | per mil (‰) vs AIR |
| LYS_N | Mean delta15N value of all injections for Lysine | per mil (‰) vs AIR |
| ALA_N_sd | Standard deviation of delta15N values from all injections for Alanine | per mil (‰) vs AIR |
| GLY_N_sd | Standard deviation of delta15N values from all injections for Glycine | per mil (‰) vs AIR |
| THR_N_sd | Standard deviation of delta15N values from all injections for Theronine | per mil (‰) vs AIR |
| SER_N_sd | Standard deviation of delta15N values from all injections for Serine | per mil (‰) vs AIR |
| VAL_N_sd | Standard deviation of delta15N values from all injections for Valine | per mil (‰) vs AIR |
| LEU_N_sd | Standard deviation of delta15N values from all injections for Leucine | per mil (‰) vs AIR |
| ILE_N_sd | Standard deviation of delta15N values from all injections for Isoleucine | per mil (‰) vs AIR |
| PRO_N_sd | Standard deviation of delta15N values from all injections for Proline | per mil (‰) vs AIR |
| ASX_N_sd | Standard deviation of delta15N values from all injections for Aspartic Acid and Asparagine | per mil (‰) vs AIR |
| GLX_N_sd | Standard deviation of delta15N values from all injections for Glutamic Acid and Glutamine | per mil (‰) vs AIR |
| PHE_N_sd | Standard deviation of delta15N values from all injections for Phenylalanine | per mil (‰) vs AIR |
| TYR_N_sd | Standard deviation of delta15N values from all injections for Tyrosine | per mil (‰) vs AIR |
| LYS_N_sd | Standard deviation of delta15N values from all injections for Lysine | per mil (‰) vs AIR |
| ALA_C | Mean delta13C value of all injections for Alanine | per mil (‰) vs VPDB |
| GLY_C | Mean delta13C value of all injections for Glycine | per mil (‰) vs VPDB |
| THR_C | Mean delta13C value of all injections for Theronine | per mil (‰) vs VPDB |
| SER_C | Mean delta13C value of all injections for Serine | per mil (‰) vs VPDB |
| VAL_C | Mean delta13C value of all injections for Valine | per mil (‰) vs VPDB |
| LEU_C | Mean delta13C value of all injections for Leucine | per mil (‰) vs VPDB |
| ILE_C | Mean delta13C value of all injections for Isoleucine | per mil (‰) vs VPDB |

| | | |
|----------|--|------------------------|
| PRO_C | Mean delta13C value of all injections for Proline | per mil (‰) vs VPDB |
| ASX_C | Mean delta13C value of all injections for Aspartic Acid and Asparagine | per mil (‰) vs VPDB |
| GLX_C | Mean delta13C value of all injections for Glutamic Acid and Glutamine | per mil (‰) vs VPDB |
| PHE_C | Mean delta13C value of all injections for Phenylalanine | per mil (‰) vs VPDB |
| TYR_C | Mean delta13C value of all injections for Tyrosine | per mil (‰) vs VPDB |
| LYS_C | Mean delta13C value of all injections for Lysine | per mil (‰) vs VPDB |
| ALA_C_sd | Standard deviation of delta13C values from all injections for Alanine | per mil (‰) vs VPDB |
| GLY_C_sd | Standard deviation of delta13C values from all injections for Glycine | per mil (‰) vs VPDB |
| THR_C_sd | Standard deviation of delta13C values from all injections for Theronine | per mil (‰) vs VPDB |
| SER_C_sd | Standard deviation of delta13C values from all injections for Serine | per mil (‰) vs VPDB |
| VAL_C_sd | Standard deviation of delta13C values from all injections for Valine | per mil (‰) vs VPDB |
| LEU_C_sd | Standard deviation of delta13C values from all injections for Leucine | per mil (‰) vs VPDB |
| ILE_C_sd | Standard deviation of delta13C values from all injections for Isoleucine | per mil (‰) vs VPDB |
| PRO_C_sd | Standard deviation of delta13C values from all injections for Proline | per mil (‰) vs VPDB |
| ASX_C_sd | Standard deviation of delta13C values from all injections for Aspartic Acid and Asparagine | per mil (‰) vs VPDB |
| GLX_C_sd | Standard deviation of delta13C values from all injections for Glutamic Acid and Glutamine | per mil (‰) vs VPDB |
| PHE_C_sd | Standard deviation of delta13C values from all injections for Phenylalanine | per mil (‰) vs VPDB |
| TYR_C_sd | Standard deviation of delta13C values from all injections for Tyrosine | per mil (‰) vs VPDB |
| LYS_C_sd | Standard deviation of delta13C values from all injections for Lysine | per mil (‰) vs VPDB |

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Instruments

| | |
|---|--|
| Dataset-specific Instrument Name | ROV Doc Ricketts |
| Generic Instrument Name | Remotely Operated Vehicle |
| Dataset-specific Description | Sediment cores and megafauna were collected in October 2019 using the ROV Doc Ricketts |
| Generic Instrument Description | Remotely operated underwater vehicles (ROVs) are unoccupied, highly maneuverable underwater robots operated by a person aboard a surface vessel. They are linked to the ship by a group of cables that carry electrical signals back and forth between the operator and the vehicle. Most are equipped with at least a video camera and lights. Additional equipment is commonly added to expand the vehicle's capabilities. These may include a still camera, a manipulator or cutting arm, water samplers, and instruments that measure water clarity, light penetration, and temperature. |

| | |
|---|--|
| Dataset-specific Instrument Name | DeltaPlusXP or Delta-V-Advantage |
| Generic Instrument Name | Isotope-ratio Mass Spectrometer |
| Dataset-specific Description | Bulk nitrogen and carbon isotopic composition were determined using an isotope ratio mass spectrometer (DeltaPlusXP or Delta-V-Advantage) coupled to an elemental analyzer (Costech Model 4010). |
| 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 | Thermo Scientific Delta V Plus |
| Generic Instrument Name | Isotope-ratio Mass Spectrometer |
| Dataset-specific Description | Nitrogen isotope composition of amino acids was determined using an isotope ratio mass spectrometer (Thermo Scientific Delta V Plus) interfaced with a Thermo Finnigan GC-C III. |
| 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 | Thermo-Fisher Scientific MAT 253 |
| Generic Instrument Name | Isotope-ratio Mass Spectrometer |
| Dataset-specific Description | Carbon isotope composition of amino acids was measured using a Thermo-Fisher Scientific MAT 253 isotope ratio mass spectrometer interfaced with a Trace Ultra GC-III via ConFlo IV. |
| 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 | Costech Model 4010 |
| Generic Instrument Name | CHN Elemental Analyzer |
| Dataset-specific Description | Bulk nitrogen and carbon isotopic composition were determined using an isotope ratio mass spectrometer (DeltaPlusXP or Delta-V-Advantage) coupled to an elemental analyzer (Costech Model 4010). |
| Generic Instrument Description | A CHN Elemental Analyzer is used for the determination of carbon, hydrogen, and nitrogen content in organic and other types of materials, including solids, liquids, volatile, and viscous samples. |

| | |
|---|--|
| Dataset-specific Instrument Name | |
| Generic Instrument Name | Alvin tube core |
| Dataset-specific Description | Sediment cores and megafauna were collected in May 2019 using the HOV Alvin |
| Generic Instrument Description | A plastic tube, about 40 cm (16 inches) long, is pushed into the sediment by Alvin's manipulator arm to collect a sediment core. |

| | |
|---|--|
| Dataset-specific Instrument Name | Thermo Finnigan GC-C III |
| Generic Instrument Name | Gas Chromatograph |
| Dataset-specific Description | Nitrogen isotope composition of amino acids was determined using an isotope ratio mass spectrometer (Thermo Scientific Delta V Plus) interfaced with a Thermo Finnigan GC-C III. |
| 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 | ConFlo IV (input from IRMS, output to GC) |
| Generic Instrument Name | Continuous Flow Interface for Mass Spectrometers |
| Dataset-specific Description | Carbon isotope composition of amino acids was measured using a Thermo-Fisher Scientific MAT 253 isotope ratio mass spectrometer interfaced with a Trace Ultra GC-III via ConFlo IV. |
| Generic Instrument Description | Continuous Flow Interface connects solid and liquid sample preparation devices to instruments that measure isotopic composition. It allows 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 |

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Deployments

Pulse 72

| | |
|--------------------|--|
| Website | https://www.bco-dmo.org/deployment/840845 |
| Platform | R/V Western Flyer |
| Start Date | 2019-10-16 |
| End Date | 2019-10-24 |
| Description | Collaborative Research: Assessing the relative importance of small vs large particles as sources of nutrition to abyssal communities Dive numbers: D1196, D1197, D1201 |

AT42-10

| | |
|--------------------|---|
| Website | https://www.bco-dmo.org/deployment/840850 |
| Platform | R/V Atlantis |
| Start Date | 2019-04-28 |
| End Date | 2019-05-09 |
| Description | Collaborative Research: Assessing the relative importance of small vs large particles as sources of nutrition to abyssal communities AT42-10; Alvin Dive numbers: D5027-D5030 |

Pulse72_ROV_dives

| | |
|-------------------|---|
| Website | https://www.bco-dmo.org/deployment/847068 |
| Platform | Doc Ricketts |
| Start Date | 2019-10-17 |
| End Date | 2019-10-24 |

AT42-10_Alvin_dives

| | |
|-------------------|---|
| Website | https://www.bco-dmo.org/deployment/847070 |
| Platform | Alvin |
| Start Date | 2019-05-01 |
| End Date | 2019-05-04 |

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Project Information

Collaborative Research: Assessing the relative importance of small vs large particles as sources of nutrition to abyssal communities (Abyssal food web)

Coverage: California current, Station M (34° 50' N, 123° W) and North Pacific Subtropical Gyre, Station Aloha (22° 45' N, 158° W)

NSF Award Abstract:

The abyssal plains of the oceans cover roughly half of the earth's surface, host enormous reservoirs of biodiversity and mineral resources, and play important roles in nutrient recycling and carbon sequestration. The most important process controlling the structure and function of these ecosystems is the quantity and quality of food (mostly sinking organic particles) that reaches the deep-sea floor. However, we do not fully understand the processes provisioning this vast ecosystem. We propose to evaluate the relative importance of small and larger "marine snow" particles that sink to deep-sea benthic communities by using the stable isotope signature of amino acids within various food sources and trace their consumption by fauna on the seafloor. This project compares ecosystems from the productive waters off California with the nutrient poor central Pacific, north of Hawaii. This project provides novel insights into how surface ocean processes are coupled to food-webs at the deep ocean seafloor and how changes in food sources potentially impact deep-sea communities. This project also provides excellent training opportunities for graduate students, a postdoctoral researcher, and undergraduates at UH and USC, particularly underrepresented minorities who pursue majors in the geosciences. The project will sponsor an annual G6-12 teacher workshop to inform Hawaii educators about the deep sea and broadly disseminate knowledge to the community. All results are communicated broadly to inform the public as concerns regarding abyssal ecosystems are rising due to interests in deep-sea mining.

The most important process controlling the structure and function of abyssal ecosystems is the quantity and quality of organic material that ultimately reaches the deep-sea floor. Despite the strong relationship between euphotic zone export flux and benthic ecology, studies of abyssal ecosystems have observed a deficit between food supply and benthic community demand. Additional work is therefore needed, particularly with regards to understanding the sources of nutrition to the deep-sea benthos. Recent evidence suggests that small particles may be significant contributors to carbon export, increasing in relative importance with depth in the mesopelagic and reaching the abyssal seafloor. This project is to evaluate the relative importance of small and larger "marine snow" particles to deep-sea benthic communities using a combination of particle flux measurements and state of the art compound specific stable isotope analysis of amino acids (AA-CSIA) at two abyssal locations that contrast in overlying productivity, seasonality, and export magnitude. Time series measurements at these locations (Sta. M off California and Sta. Aloha off Hawaii) provide a rich context for the work. In the mesopelagic central North Pacific larger particles (>53 µm) can be resolved from microbially reworked, smaller (0.7-53 µm) particles using AA-CSIA. This project is characterizing the isotopic compositions of key individual compounds in a continuum of particle sizes (< 1.0 µm suspended particles to large sinking particles >53 µm) collected using in situ filtration near the seafloor and bottom-moored sediment traps, thereby defining source-specific isotopic signatures that can be traced into benthic fauna and sediments (that are collected by ROVs and epibenthic sleds). This research to understand pelagic-benthic coupling from particles to

megafauna using isotopic measurements at the compound-level will yield novel insights into the importance of small microbially reworked particles to deep-sea benthic food webs. This will more precisely couple surface ocean processes to food-webs at the deep ocean seafloor with implications for understanding climate change effects and the efficiency of energy transfer to higher trophic levels. Furthermore, isotopic measurements can also be used to further parameterize ecosystem models by quantifying trophic position across size classes and thus estimate predator-prey mass ratios in relation to variation in body size spectra, functional type, and ultimately to carbon flux and remineralization. Finally, the results will help refine interpretations of deep-sea paleorecords of past nitrogen dynamics by calibrating potential changes in organic matter isotope values between the surface and seafloor archives.

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-1829612 |

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