Compound-specific nitrogen stable isotopes of amino acids in planktic foraminifera from Santa Barbara Basin sediment traps from 2018 to 2021

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Data Type: Other Field Results
Version: 1
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Project
» Collaborative Research: Constraining Planktic Foraminiferal Ecology Using Compound Specific Isotope Analysis of Amino Acids (Planktic Foraminiferal Ecology Using CSIA-AA)

Contributors	Affiliation	Role
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Abstract
We measured carbon and nitrogen compound-specific stable isotopes of amino acids (CSI-AA) in the shells the three most abundant species of planktic foraminifera from Santa Barbara Basin sediment traps from 2018 to 2021: Globigerina bulloides (d'Orbigny, 1826), Neogloboquadrina incompta (Cifelli, 1961), and Turborotalita quinqueloba (Natland, 1938). Multiple sediment trap collections were combined to constitute representative samples. The N. incompta sample included individuals from sediment trap collections from May 2019 to October 2021 (n=4082). The T. quinqueloba sample included individuals from December 2018 to October 2021 (n=4964). G. bulloides was sufficiently abundant to split into seasonal samples: spring/summer from February 2019 to July 2019 (n=5081) and fall/winter from October to January in years 2018-2019, 2019-2020, 2020-2021 (n=3132). The collection of these data were supported by NSF OCE. This dataset includes only the nitrogen CSI-AA data. Carbon data are available in a related dataset.

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Coverage

Location: Santa Barbara Basin, CA, USA
Spatial Extent: **Lat**:34.2450389 **Lon**:-120.0592917
Temporal Extent: 2018-11-17 - 2021-10-28

Methods & Sampling

Samples were collected using a McLane Parflux 78H sediment trap deployed at depths >400 meters (m) in the central Santa Barbara Basin (34.2450389, -120.0592917). The sampling interval was 10 to 14 days, and samples were preserved in borate-buffered formalin solution. A 1/16th split of the sediment trap sample was used. Samples were rinsed with tap water over a 125-micron sieve, and foraminifera tests were removed from other trap material using a fine paintbrush. Foraminifera tests were dried on a micropaleontology slide, then species were identified by test morphology and sorted. Tests of the three most abundant species were removed to separate micropaleontology slides. These tests were inspected under a dissecting microscope to ensure no organic particles were adhered to the exterior or interior of tests. Any organic particles were gently removed with a wet brush. The removed tests were counted and weighed on a microbalance. Tests from multiple sediment trap samples were combined to achieve a sample of 5-10 milligrams (mg). This combined sample was gently rinsed with methanol three times, then dried.

Compound-specific stable isotopes were measured at the UC Santa Cruz Stable Isotope Lab. Tests were demineralized by adding ~1 milliliter (mL) 1N HCl to dissolve carbonate, then stored at 4 degrees Celsius (°C) overnight to complete the demineralization reaction. The HCl was then evaporated under N_2. The remaining organic matter was then hydrolyzed with ~ 1mL 6N HCl at 110°C for 20 hours after the vial was purged with N_2 to remove oxygen. Samples were purified by cation-exchange chromatography with DOWEX 50WX8-400 resin. Amino acids were measured as trifluoroacetyl isopropyl ester derivatives following Silfer et al. (1991). After drying under N_2, samples were esterified with a 1:5 mixture of acetyl chloride:isopropanol at 110 °C for 60 minutes. Samples were dried again under N_2, then trifluoroacetylation was completed using a 1:3 mixture of trifluoroacetic anhydride (TFAA) and dichloromethane (DCM) at 110 °C for 15 minutes. Inorganic salts were removed from samples by liquid-liquid extraction of derivatized amino acids in chloroform and an aqueous phosphate buffer. Trifluoroacetylation was completed again after liquid-liquid extraction. Samples were dried and dissolved in ethyl acetate for gas chromatography-isotope ratio mass spectrometry (GC-IRMS).

Amino acid stable isotopes were measured on a Thermo 1310 Trace gas chromatograph coupled to an Isolink II (Thermo combustion reactor 1000°C), Conflo IV, and Thermo Delta V Plus IRMS at the UCSC-SIL. Amino acids were were separated for δ15N analyses using a BPX5 column (60 m×0.32 mm, 1 µm film thickness; SGE Analytical Science, Trajan, Austin, TX, USA) and for δ13C analyses using a DB-5 column (50 m× 0.32 mm 0.52 µm film thickness; Agilent Technologies, Santa Clara, CA, USA). Samples were analyzed alongside a set of amino acid standards of known δ13C and δ15N values. The injector temperature was 250°C with He column flow rate of 2 mL/min. The GC temperature program for nitrogen isotope analysis was: initial temp = 70°C hold for 1 min; ramp 1=10°C/min to 185°C, hold for 2 min; ramp 2 = 2°C/min to 200°C, hold for 10 min; ramp 3 = 30°C/min to 300°C, hold for 6 min.

Data Processing Description

The $\delta^{13}C$ of amino acids was corrected for carbon added during derivatization using standards and following the methods of Silfer et al. (1991). Reproducibility was estimated by the standard deviation of triplicate injections of each sample. Accuracy was checked by analyzing an in-house long-term lab reference material (cyanobacteria) with every sample set.

BCO-DMO Curation Notes

- Imported original file "BCO-DMO_SBB_foram_CSI-AA_N.csv" into the BCO-DMO system.
- Added the following columns and populated with values provided in the metadata: Start_date, End_date, Lat, Lon.
- Saved the final file as "989777_v1_csi-aa_sbb_nitrogen.csv".

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Data Files

File
989777_v1_csi-aa_sbb_nitrogen.csv (Comma Separated Values (.csv), 848 bytes) MD5:528cb1c85f323ffaa95c734c6e7366c5 Primary data file for dataset ID 989777, version 1

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Related Publications

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
Methods

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Related Datasets

IsRelatedTo

Doherty, S. C., Christensen, S., Davis, C. V., McCarthy, M. D. (2025) **Compound-specific carbon stable isotopes of amino acids in planktic foraminifera from Santa Barbara Basin sediment traps from 2018 to 2021.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-11-26 doi:10.26008/1912/bco-dmo.986825.1 [view at BCO-DMO]
Relationship Description: Carbon and nitrogen compound-specific stable isotopes of amino acids (CSI-AA) were analyzed on the same sediment trap samples.

Havard, E., Cherry, K., Benitez-Nelson, C. R., Tappa, E., & Davis, C. (2024). Formaminiferal Flux acquired by the Santa Barbara Basin Sediment Trap Mooring between 2014 and 2021 (Version 1) [Data set]. Biological and Chemical Oceanography Data Management Office (BCO-DMO). https://doi.org/10.26008/1912/BCO-DMO.936276.1 https://doi.org/10.26008/1912/bco-dmo.936276.1

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Parameters

Parameter	Description	Units
Sample	Sample identifier	unitless
Start_date	Date when sample collection started	unitless
End_date	Date when sample collection ended	unitless
Latitude	Latitude of sample collection site	decimal degrees
Longitude	Longitude of sample collection site	decimal degrees
Ala	Alanine d15N	permille

Gly	Glycine d15N	permille
Thr	Threonine d15N	permille
Ser	Serine d15N	permille
Val	Valine d15N	permille
Leu	Leucine d15N	permille
Ile	Isoleucine d15N	permille
Pro	Proline d15N	permille
Asp	Aspartic acid d15N	permille
Glu	Glutamic acid/glutamine d15N	permille
Phe	Phenylalanine d15N	permille
Tyr	Tyrosine d15N	permille
Lys	Lysine d15N	permille
Ala_sd	Alanine standard deviation of replicate injections	permille
Gly_sd	Glycine standard deviation of replicate injections	permille
Thr_sd	Threonine standard deviation of replicate injections	permille
Ser_sd	Serine standard deviation of replicate injections	permille
Val_sd	Valine standard deviation of replicate injections	permille
Leu_sd	Leucine standard deviation of replicate injections	permille
Ile_sd	Isoleucine standard deviation of replicate injections	permille

Pro_sd	Proline standard deviation of replicate injections	permille
Asp_sd	Aspartic acid standard deviation of replicate injections	permille
Glu_sd	Glutamic acid/glutamine standard deviation of replicate injections	permille
Phe_sd	Phenylalanine standard deviation of replicate injections	permille
Tyr_sd	Tyrosine standard deviation of replicate injections	permille
Lys_sd	Lysine standard deviation of replicate injections	permille

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Instruments

Dataset-specific Instrument Name	Thermo 1310 Trace gas chromatograph coupled to an Isolink II and Conflo IV
Generic Instrument Name	Gas Chromatograph Mass Spectrometer
Dataset-specific Description	Amino acid stable isotopes were measured on a Thermo 1310 Trace gas chromatograph coupled to an Isolink II (Thermo combustion reactor 1000°C), Conflo IV, and Thermo Delta V Plus IRMS at the UCSC-SIL.
Generic Instrument Description	Instruments 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 by a mass spectrometer.

Dataset-specific Instrument Name	Thermo Delta V Plus IRMS
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	Amino acid stable isotopes were measured on a Thermo 1310 Trace gas chromatograph coupled to an Isolink II (Thermo combustion reactor 1000°C), Conflo IV, and Thermo Delta V Plus IRMS at the UCSC-SIL.
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	dissecting microscope
Generic Instrument Name	Microscope - Optical
Dataset-specific Description	Tests were inspected under a dissecting microscope.
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".

Dataset-specific Instrument Name	McLane PARFLUX 78HW-13 sediment trap
Generic Instrument Name	Sediment Trap
Dataset-specific Description	A McLane PARFLUX 78HW-13 sediment trap was used to collect samples.
Generic Instrument Description	Sediment traps are specially designed containers deployed in the water column for periods of time to collect particles from the water column falling toward the sea floor. In general a sediment trap has a jar at the bottom to collect the sample and a broad funnel-shaped opening at the top with baffles to keep out very large objects and help prevent the funnel from clogging. This designation is used when the specific type of sediment trap was not specified by the contributing investigator.

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Project Information

Collaborative Research: Constraining Planktic Foraminiferal Ecology Using Compound Specific Isotope Analysis of Amino Acids (Planktic Foraminiferal Ecology Using CSIA-AA)

NSF Award Abstract:
Current climate change is unique in human history. To understand how the Earth and life on it responds to comparable change it is necessary to look millions of years in the past. A huge amount of what we know about past climate comes from the fossils of marine plankton. Specifically, a group of single-celled organisms called foraminifera. Foraminifera make tiny fossil shells which capture the chemistry of the water they grew in. As a result, they can be used to reconstruct ancient ocean waters and climate. To use the fossil shells of foraminifera to their greatest effect, the ecology of the living creature must be understood. Variables like what the foraminifera ate, what depth it lived at, and whether it had symbionts will all impact how shell chemistry is interpreted. Compound-specific nitrogen and carbon isotopes of specific amino acids (CSI-AA) represent a unique approach to study these variables in living plankton. This proposal would test how well this approach can be applied to fossil shells. If successful, this would provide powerful ways to describe the ecology of long extinct planktic foraminifera. In doing so, one may better understand the records they hold of Earth's past. The project broader impacts include support for a postdoctoral researcher, development of a career-opportunities workshop to introduce students from Primarily Undergraduate Institutions to geoscience research, and content contributions to a summer program for at-risk STEM transfer students at UC Santa Cruz.

Specifically, this project will investigate and develop multiple aspects of CSI-AA to better understand the

species-level ecology of planktic foraminifera. This is key to generating paleoclimate and paleoceanographic records that can contextualize the Ocean’s future climate and trajectory. The proposed project will use CSI-AA to constrain three key aspects of planktic foraminiferal ecology: depth habitat, diet, and symbiosis. CSI-AA from shell-bound organics will be used in foraminifera for the first time to refine species-level inferences about these ecological traits. First CSI-AA applications in extant species will be ground-truthed using plankton tows, sediment traps, and recent sedimentary samples from the Santa Barbara Basin. Lessons learned will then be applied deeper into the fossil record to elucidate the trophic ecology of extinct foraminifera. Finally, amino acid molar ratios and racemization (the diagnostic shift between amino acid forms which occurs with fossil age) will be used to assess amino acid preservation in fossils and ultimately test the limits of this approach by targeting a suite of abundant species from the Miocene, Eocene, and Cretaceous.

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-2303608

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