Concentration and δ15N of Amino Acids in Size-fractionated Particles

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Project
» Collaborative research: Using individual amino acids N isotopes in sinking particles and surficial sediments to reconstruct euphotic zone N sources and trophic structure (Amino Acids N Isotopes)

Contributors	Affiliation	Role
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Abstract
This dataset includes the concentration and δ15N of bulk N and amino acids in size-fractionated particles. Particle samples were collected aboard the R/V Sally Ride (cruise SR2011) from December 23 – 30, 2020 with a McLane large volume pumping system (WTS-LV). These data assess the nitrogen sources utilized by different phytoplankton communities inhabiting the two chlorophyll maxima and the transformation of particulate organic matter within the oxygen-deficient zone.

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Coverage

Location: Eastern tropical North Pacific oxygen deficient zone
Spatial Extent: **N**:17.29 **E**:-104.27 **S**:14.02 **W**:-107.78
Temporal Extent: 2020-12-22 - 2020-12-30

Methods & Sampling

Two particle fractions were collected at five stations in the eastern tropical North Pacific region. At each station, seawater was filtered sequentially through a 53-micrometer (µm) Nitex mesh and then a pre-combusted 142-millimeter (mm) diameter glass fiber filter (GF-75: 0.3 µm retention size; or GF/F: 0.7 µm nominal retention size) with the McLane pump in situ. These filters were promptly frozen upon retrieval.

Each 53 µm Nitex mesh was immersed in approximately 100 milliliters (ml) of MilliQ water and subjected to a 5-minute sonication. The solution was filtered onto pre-combusted 47-mm glass fiber filters (GF/F, 0.7 µm pore size), which retain the > 53 µm particle fraction.

The GF-75 and GF/F filters (0.3 or 0.7 – 53 µm fractions) were subsampled, packed in tin capsules, and analyzed for concentration and δ15N of bulk materials by an elemental analyzer isotope-ratio mass spectrometer at the UC Davis Stable Isotope Facility. Bulk δ15N analysis was not performed for the > 53 µm

fraction due to the limited amount of collected material.

The sample pre-treatment procedures for δ15N-amino acids were based on the method detailed in Zhang et al. (2021). The glass fiber filters underwent hydrolysis with 6N HCl for 22 hours at 110 degrees Celsius (°C). Hydrophobic impurities were eliminated from the hydrolysates through liquid-liquid extraction using n-hexane/dichloromethane (6:5, v/v), followed by evaporation to dryness in a vacuum evaporator (RapidVap, Labconco). The samples were subsequently redissolved in 0.05N HCl and further purified via cation-exchange resin, following procedures adapted from Takano et al. (2010) to remove metal ions and salts. The purified amino acids in the samples were completely dried under vacuum.

Amino acids in the samples were separated and collected as individual fractions using an ICS-5000+ Ion-exchange chromatography system with the instrumental method adapted from Zhang et al. (2021). For each sample, Phe, Glu, and their corresponding IC procedural blanks were collected from 1 to 3 replicate injections. The IC-collected fractions were sequentially converted to NO2- and N2O through a two-step process involving hypochlorite oxidation and azide reduction, as described in McIlvin and Altabet (2005); Zhang et al. (2007); Zhang and Altabet (2008); and Zhang et al. (2021). δ15N-N2O was determined with a GV IsoPrime IRMS.

Data Processing Description

Concentrations of Phe and Glu in the particle samples were determined by calibrating them against the chromatographic peak areas of a set of amino acid standard mixtures at varying concentration levels between 1 and 5 millimolar (mM).

The δ15N of Phe and Glu were calibrated by three replicate injections of multiple amino acid isotopic standard mixtures with distinct δ15N values were carried out as outlined in Zhang et al. (2021). Trophic position (TP) was calculated from δ15N of Phe and Glu with an empirical formula proposed by Chikaraishi et al. (2009).

Standard deviations were reported for samples with δ15N measurements obtained from replicate IC injections. The error propagated from uncertainties of the instrument, calibration, and correction was calculated for samples collected from a single injection.

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

SR2011

Website	https://www.bco-dmo.org/deployment/955215
Platform	R/V Sally Ride
Start Date	2020-12-16
End Date	2021-01-06
Description	More information is available from R2R: https://www.rvdata.us/search/cruise/SR2011

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Project Information

Collaborative research: Using individual amino acids N isotopes in sinking particles and surficial sediments to reconstruct euphotic zone N sources and trophic structure (Amino Acids N

Isotopes)

Coverage: Gulf of California, Equatorial Pacific, Sargasso Sea

NSF Award Abstract:
Nitrogen is a limiting nutrient over most of the surface ocean. Fixed nitrogen (N) such as nitrate controls absorption of atmospheric carbon dioxide and production of organic matter by marine plants and algae. Nitrogen availability, use patterns, and biological community structure in the surface ocean help determine the amount of organic matter passed onto higher organisms. Nitrogen availability also controls how much organic matter sinks into deep waters. This project will reconstruct past sources of nitrogen, use patterns, and trophic structures in surface waters of the Gulf of California, equatorial Pacific, and Sargasso Sea. The tool employed by the principal investigators from Texas A&M University in Corpus Christi and University of Massachusetts Dartmouth is nitrogen isotope ratios of individual amino acids. The investigators will measure isotope ratios in sinking particle samples collected by sediment traps such as those used by the Ocean Flux Program in the Sargasso Sea. This study will train graduate students in stable isotope biogeochemistry and oceanography. This project will also provide research funds for students in the McNair program. McNair students come from underrepresented and economically challenged backgrounds to pursue degrees in STEM fields at Texas A&M University Corpus Christi, a Hispanic and Minority Serving Institution. Data from this project will be made available to the public through the Biological and Chemical Oceanography-Data Management Office (www.bco-dmo.org).

There is great interest in reconstructing past climate-forced variations in nitrogen sources, their patterns of utilization, and euphotic zone community structure using compound specific N isotope ratios in amino acids liberated from preserved proteinaceous materials in sediments and coral skeletons. However, it has not yet been verified whether 1) the nitrogen isotope ratios of individual amino acids produced in the euphotic zone are transported with fidelity by sinking particles to deep-sea corals and sediments and 2) the nitrogen isotope ratios of individual amino acids liberated from sedimentary organic matter have been altered by diagenesis. Through analysis of sediment trap material collected over time, this project seeks to verify that nitrogen isotope ratios in individual amino acids reflect the 1) overall spatial contrast in N sources, utilization patterns, and trophic structures among the Gulf of California, equatorial Pacific, and Sargasso Sea and 2) temporal variations in nitrogen sources, utilization patterns, and trophic structures within both the Gulf of California and equatorial Pacific due to seasonal upwelling and/or El Nino-Southern Oscillation. This study will also test if the nitrogen isotope ratios of total hydrolysable amino acids in sedimentary organic matter from the three locations retain the unaltered nitrogen isotope patterns carried by sinking particles. This project will, for the first time, compare nitrogen stable isotope ratios in amino acids collected from sediment trap samples with surficial sediments from deep-sea oxic sites to verify whether total hydrolysable amino acids in deep-sea sediments preserve unaltered nitrogen isotope signals produced in overlying euphotic zone, which can provide insights on addressing diagenetic alteration of bulk N isotope ratios that have hindered paleo-nitrogen cycle reconstruction.

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