Compound-specific Carbon isotopes from sperm whale dentin from the UC-Santa Cruz labs of P. Koch and M. McCarthy (Sperm Whale SI Ratios project)

Website: https://www.bco-dmo.org/dataset/652952
Data Type: Other Field Results
Version:
Version Date: 2016-08-01

Project
» A novel approach for evaluating temporal and spatial changes in trophic structure of the mesopelagic eastern Pacific (Sperm Whale SI Ratios)

Contributors	Affiliation	Role
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Table of Contents

- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Dataset Description

To determine the effects of decalcification and the accuracy of untreated dentin analysis, compound-specific Carbon isotope analysis was performed on decalcified and raw sperm whale tooth dentin. The differences in the amino acid isotope values and molar composition are reported. The sperm whale tooth came from the California Current System.

Related Reference:
All sampling and analytical information are supplied in: Brault EK, Koch PK, Gier E, Ruiz-Cooley RI, Zupcic J, Gilbert KN, McCarthy MD (2014) Effects of decalcification on bulk and compound-specific nitrogen and carbon isotope analyses of dentin. Rapid Communications in Mass Spectrometry 28: 2744-2752.

Related Datasets:
Brault 2014 - Bulk Carbon and Nitrogen isotopes
Brault 2014: Compound-specific Nitrogen in sperm whale dentin

Methods & Sampling

Materials and methods for analysis are described in detail in the text. Briefly, a homogenized sample of sperm whale dentin was split into sub-samples. Three received "Conventional" extractraction (decalcification with 0.5N HCl, rinsing with water to neutrality, freeze-drying) and three were not treated ("Raw"). Samples were hydrolyzed with 6 N HCl for 20 h at 110°C, then trifluoroacetic anhydride (TFAA) derivatives were prepared. Samples were analyzed for amino acid carbon and nitrogen isotope composition on a Thermo Trace gas

chromatograph coupled to a Thermo Finnigan DeltaPlus XP isotope ratio mass spectrometer. Ideally, samples were injected 3x, and reported isotopic values represent means and standard deviations (stdv) in ‰ relative to the V-PDB standard. For several lysine (Lys) samples, the δ13C value is based on a single injection, so stdv is not calculated. Details on columns used, injection, and furnace ramp parameters are presented in the paper. The amino acid δ13C values were determined from the measured values of the amino acid with corrections based on an amino acid mixture standard for which isotopic values had been independently determined by offline elemental analyzer analysis. Using this approach, the δ13C values of 13 amino acids could be reproducibly quantified: alanine (Ala), glycine (Gly), threonine (Thr), serine (Ser), valine (Val), leucine (Leu), isoleucine (Ile), proline (Pro), hydroxyproline (Hpro), aspartic acid + asparagine (Asp), glutamic acid + glutamine (Glu), phenylalanine (Phe), and lysine (Lys). The amino acid molar percentages (Mol %) were determined from the peak areas using an external standard approach and based on the amino acid standard versus sample peak areas. For Mol %, data for Hpro and Pro are combined, and reported under Pro.

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- reformatted columns and rows to a simple flat file
- replaced hyphens with nd (no data)

[table of contents | back to top]

Data Files

File
compound_specific_C.csv (Comma Separated Values (.csv), 4.50 KB) MD5:c06b820adf6eee37dd52090bc2d656c9 Primary data file for dataset ID 652952

[table of contents | back to top]

Parameters

Parameter	Description	Units
amino_acid_type	Essential: an amino acid that cannot be synthesized de novo by the organism; non-essential: an amino acid that can be synthesized de novo by the organism	unitless

amino_acid	amino acid: Ala = Alanine Asp = Aspartate & Asparagine Glu = Glutamate & Glutamine Gly = Glycine Hpro = Hydroxyproline Ile = Isoleucine Leu = Leucine Lys = Lysine Phe = Phenylalanine Pro = Proline Pro_Hpro = Proline + Hydroxyproline Ser = Serine Thr = Threonine Tyr = Tyrosine Val = Valine	unitless
method	Conventional: removal of inorganic matrix by acid dissolution (see Brault et al. (2014) RCMS Raw: no pretreatment	unitless
sample	sample identification	unitless
injections	number of times that the sample was injected and analyzed by gas chromatography-isotope ratio monitoring-mass spectrometry	each
mol_pcent	mole percent = (moles of particular amino acid ÷ moles of all extractable amino acids) x 100. While Mol % sums to 100; not all amino acids in a protein can be extract and quantified.	percent
d13C	delta C13= ((13C/12Cstandard - 13C/12Csample) ÷ 13C/12Cstandard) x 1000; standard is Vienna PDB	dimensionless (ratio)
d13C_stdv	standard deviation of delta C13	dimensionless (ratio)

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	Thermo Trace gas chromatograph coupled to a Thermo Finnigan DeltaPlus XP 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	
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	Thermo Finnigan DeltaPlus XP isotope ratio mass spectrometer (Thermo Scientific, Bremen, Germany)
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).

[table of contents | back to top]

Deployments

lab_UCSC_Koch

Website	https://www.bco-dmo.org/deployment/652950
Platform	UCSC
Start Date	2012-03-01
End Date	2016-03-01
Description	whale isoptope studies

[table of contents | back to top]

Project Information

A novel approach for evaluating temporal and spatial changes in trophic structure of the mesopelagic eastern Pacific (Sperm Whale SI Ratios)

Coverage: California Current, Eastern Tropical Pacific, and the Peru-Humboldt Current

Description from NSF award abstract:
Anthropogenic and natural climatic perturbations drive changes in population dynamics of species, the structure and function of food webs, and biogeochemical processes. The PIs propose a comparative analysis

of three major ecosystems to investigate temporal change in the structure of mesopelagic food webs.

The PIs will investigate temporal changes in the structure of mesopelagic food webs in three major ecosystems: the California Current, Eastern Tropical Pacific, and the Peru-Humboldt Current over the past 50 years using a globally distributed apex predator as an indicator species. The predator is the sperm whale, *Physeter macrocephalus*, and the PIs will use stable isotope ratios of carbon and nitrogen as indicators of habitat and diet. Isotope values from bulk tissues of teeth and skin (C and N) as well as specific amino acids (N) will be used to address two primary objectives: (a) examine temporal patterns in the trophic position of sperm whales (as an indicator of changes in mesopelagic trophic structure) and baseline isotopic values (as indicators of nutrient cycling); and (b) use isotopic values, which vary among systems, to define the population structure of sperm whales from past and present times, and connectivity among populations.

This project will be conducted by researchers from academia and NOAA/NMFS with expertise in stable isotope analysis, trophic ecology, and ecosystem-based management of protected species. As such, it represents an opportunity for collaboration between scientists with complementary skills and from diverse institutions to compare structure and function of ecosystems across the eastern Pacific. Moreover, it represents a collaboration between academia and a federal agency with research and management responsibilities. The project will support a postdoctoral scholar (Iliana Ruiz-Cooley), a Ph.D. student, and undergraduate students to enhance their career and collaborative opportunities. The PIs anticipate that the results of their study will provide unique data to evaluate the effects of perturbations within and among mesopelagic ecosystems. This information may allow the scientific community to relate trends in climate to changes in trophic position of top predators and nutrient cycling, allowing more robust understanding of possible responses to future warming. Finally, as the first systematic applications of compound-specific stable isotope analysis to marine mammals, the project should be highly instructive for future evaluations of the feeding ecology, population structure and dynamics of endangered marine mammals. As such, this novel approach and unique historic perspective will be directly applicable for stock assessment and management.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1155728

[table of contents | back to top]