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

Website: https://www.bco-dmo.org/dataset/653106
Data Type: Other Field Results
Version: 1
Version Date: 2016-08-02

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
Koch, Paul L.	University of California-Santa Cruz (UC Santa Cruz)	Principal Investigator
McCarthy, Matthew D.	University of California-Santa Cruz (UC Santa Cruz)	Co-Principal Investigator
Ruiz-Cooley, Rocio I.	University of California-Santa Cruz (UC Santa Cruz)	Student
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Abstract
Compound-specific carbon isotopes from sperm whale skin tissue from the UC-Santa Cruz labs of P. Koch and M. McCarthy. The sperm whale skin tissue came from the California Current System from 1972 to 2005.

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Coverage

Spatial Extent: **N**:46.97 **E**:-117.35 **S**:32.47 **W**:-129.82
Temporal Extent: 1972-12-01 - 2005-07-31

Acquisition Description

Materials and methods for analysis are described in detail in the Ruiz_Cooly et al (2014). Skin tissue samples with enough material (3.5 mg) were selected for compound specific isotope analysis of amino acids (CSIA-AA). Data from 12 samples were obtained for individual amino acid (AA) d15N values, and 9

samples for d13C values. The Southwest Fisheries Science Center/Pacific Islands Fisheries Science Center Institutional Animal Care and Use Committee (IACUC) approved the original animal work that produced the samples. Sex was determined genetically using qPCR sexing assay by the PRD-Genetic Lab at NOAA. These samples consisted of 5 females, 2 males and 2 unidentified individuals possibly corresponding to females or juvenile males. Large adult males were not included.

The relative pattern of AA d15N and d13C values was highly consistent with past work from other organisms and tissues [1-3]. We grouped data as source- or trophic-AAs for d15N values, and essential- or non-essential-AAs for d13C values to increase power in the analysis and evaluate temporal variation. We calculated average values for each AA group. Regression analyses were conducted to evaluate linear relationship between time and each isotopic tracer for both bulk and individual-AA d15N and d13C values.

We hydrolyzed and prepared approximately 3.5 mg of skin as well as a control (Cyanno; bacteria tissue) [1] to quantify d15N values from source- and trophic-AAs and d13C values from essential- and non-essential-AAs. All derivatives were injected with an AA control, N-leucine, to verify accuracy during each run, and analyzed via gas chromatography-IRMS to obtain d15N and d13C values from individual AAs. Each sample was run 3–4 times to maximize accuracy among chromatograms. The associated analytical error among replicates typically <1.0‰ for AAs used in our analysis. For all samples, d15N values were obtained from a total of four source-AAs (phenylalanine, glycine, lysine, tyrosine), and five trophic-AAs (alanine, glutamate + glutamine, isoleucine, leucine, proline). For d13C values, the essential-AAs that we consistently determined were phenylalanine, valine and leucine, and the non-essential-AA were alanine, proline, aspartate + aspartamine, glutamate + glutamine, and tyrosine. Additional AAs were measured for both nitrogen and carbon, but either had chromatographic issues (lost values among samples, high variability) or are known to have unusual and variable isotopic values relatives to others AAs in their category (e.g., threonine).

Cited References:
1. McCarthy, et al, (2007)
2. Popp, et al. (2007
3. Sherwood, et al (2011)

Processing Description

Regression analyses were conducted to evaluate linear relationship between time and each isotopic tracer.

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 and NA with nd (no data)

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Related Publications

McCarthy, M. D., Benner, R., Lee, C., & Fogel, M. L. (2007). Amino acid nitrogen isotopic fractionation patterns as indicators of heterotrophy in plankton, particulate, and dissolved organic matter. Geochimica et Cosmochimica Acta, 71(19), 4727–4744. doi:10.1016/j.gca.2007.06.061
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 https://doi.org/10.1016/S1936-7961(07)01012-3
Methods

Ruiz-Cooley, R. I., Koch, P. L., Fiedler, P. C., & McCarthy, M. D. (2014). Carbon and Nitrogen Isotopes from Top Predator Amino Acids Reveal Rapidly Shifting Ocean Biochemistry in the Outer California Current. PLoS ONE, 9(10), e110355. doi:10.1371/journal.pone.0110355
Results

Sherwood, O. A., Lehmann, M. F., Schubert, C. J., Scott, D. B., & McCarthy, M. D. (2011). Nutrient regime shift in the western North Atlantic indicated by compound-specific 15N of deep-sea gorgonian corals. Proceedings of the National Academy of Sciences, 108(3), 1011–1015. doi:10.1073/pnas.1004904108
Methods

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Related Datasets

IsRelatedTo

Koch, P. L., McCarthy, M. D. (2016) **Compound-specific nitrogen isotopes from sperm whale skin tissue from the UC-Santa Cruz labs of P. Koch and M. McCarthy (Sperm Whale SI Ratios project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-08-02 http://lod.bco-dmo.org/id/dataset/653061 [view at BCO-DMO]

Koch, P. L., McCarthy, M. D. (2016) **Sperm whale skin bulk C and N isotopes from the California Current System, 1972 to 2005.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-08-02 http://lod.bco-dmo.org/id/dataset/653047 [view at BCO-DMO]

Koch, P. L., McCarthy, M. D. (2016) **Sperm whale skin tissue samples analyzed for C and N at UC-Santa Cruz: date and location of collection from the California Current System.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-08-02 http://lod.bco-dmo.org/id/dataset/653118 [view at BCO-DMO]

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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:	unitless
SWFSC_id	identification number assigned to sample at Southwest Fisheries Science Center	unitless
UCSC_id	identification number assigned to sample at UC Santa Cruz	unitless
year	year sample was collected	year
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
tissue	type of tissue sample	unitless
injections	number of times that the sample was injected and analyzed by gas chromatography-isotope ratio monitoring-mass spectrometry	each
d13C	delta 13 C. Isotope values are reported in conventional d-notation relative to the international standard V-PDB.	parts per thousand
d13C_stdv	standard deviation of delta C13	dimensionless (ratio)

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Instruments

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).

Dataset-specific Instrument Name	
Generic Instrument Name	Gas Chromatograph
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)

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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

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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.

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Funding

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

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