Amino acid compound-specific isotope analysis (AA-CSIA) of tissue samples from four distinct trophic groups across the food web in the pelagic eastern tropical Pacific Ocean; samples collected on NOAA cruises from July to December 2006

Website: https://www.bco-dmo.org/dataset/679447
Data Type: Cruise Results
Version: 1
Version Date: 2017-01-30

Project
» CAMEO 2009 - A novel tool for validating trophic position estimates in ecosystem-based fisheries models (CAMEO_Trophic_Position)

Program
» Comparative Analysis of Marine Ecosystem Organization (CAMEO)

Contributors	Affiliation	Role
Olson, Robert	Inter-American Tropical Tuna Commission (IATTC)	Principal Investigator, Contact
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Abstract
Amino acid compound-specific isotope analysis (AA-CSIA) of tissue samples from four distinct trophic groups across the food web in the pelagic eastern tropical Pacific Ocean; samples collected on NOAA cruises from July to December 2006.

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Coverage

Temporal Extent: 2006-07-28 - 2006-12-08

Dataset Description

Amino acid compound-specific isotope analysis (AA-CSIA) of tissue samples from four distinct trophic groups across the food web in the pelagic eastern tropical Pacific Ocean: macrozooplankton (euphausiid crustaceans), micronekton (myctophid fishes), cephalopods (squids), and micronektonivores (tunas). Samples were collected onboard two NOAA research ships and numerous commercial tuna purse-seine vessels.

Related publication:

Hetherington E.D., Olson R.J., Drazen J.C., Lennert-Cody C.E., Ballance L.T., Kaufmann R.S., and Popp B.N. (2016). Spatial food-web structure in the eastern tropical Pacific Ocean based on compound-specific nitrogen isotope analysis of amino acids. Limnology and Oceanography. doi:10.1002/lno.10443

Methods & Sampling

Sampling Methodology: Zooplankton, small mesopelagic fishes, and squids were collected from July 28 to December 8, 2006 during the National Oceanic and Atmospheric Administration's (NOAA's) *Stenella* Abundance Research (STAR) surveys (Gerrodette et al. 2008). We defined our study area to include a subset of sample locations from the STAR surveys based on the presence of both east-west and north-south productivity gradients across the region, with greater surface chlorophyll *a* concentrations at the eastern end of the study area and along the equator, according to published oceanographic data. Zooplankton samples were collected with a cylindrical-conical bongo net (333 um mesh), fished to 200 m approximately two hours after sunset, and the samples were frozen within one hour of collection. Specimens of euphausiid crustaceans, *Euphausia distinguenda* (Ed) and *E. tenera* (Et) were sorted from the thawed zooplankton samples in the laboratory. Specimens of mesopelagic myctophid fishes *Myctophum nitidulum* (Mn) and *Symbolophorus reversus* (Sr) were collected by dipnet at night. Specimens of the squids *Dosidicus gigas* (Dg) and *Sthenoteuthis oualaniensis* (So) also were collected at night, using handlines and jigs. (See Olson et al. 2010, Philbrick et al. 2001 for detailed methods).

Three species of tuna, yellowfin (Ta.; *Thunnus albacares*), skipjack (Kp.; *Katsuwonus pelamis*), and bigeye (To.; *Thunnus obesus*) tunas, were sampled year-round during 2003-2005 by observers of the Inter-American Tropical Tuna Commission onboard purse-seine fishing vessels. Samples of dorsal white muscle were taken from each fish adjacent to the second dorsal fin. Fish of uniform size were used for analysis: skipjack tuna 450-550 mm, yellowfin tuna 500-700 mm, and bigeye tuna 450-550 mm. All samples were stored frozen until further processing in the laboratory.

Analytical Methodology: Methods are described in Hetherington et al. (2016). Briefly: Amino acid (AA) compound-specific isotope analysis (AA-CSIA) was conducted on a subset of 48 of the samples used for isotopic analysis of bulk muscle tissue or whole animals. The basis for sample selection was to represent the range of variability in bulk δ15N values and the range of sample locations along the transect. The d15N values of individual AAs were measured using an isotope ratio mass spectrometer (IRMS) (Delta PlusXP, Delta V Plus or MAT 253) interfaced with a gas chromatograph (Trace GC) through a GC-C III combustion furnace (980 degrees C), reduction furnace (650 degrees C), and liquid-N cold trap. All samples were analyzed in triplicate and the measured AA-d15N values were normalized to known d15N values of two coinjected internal reference compounds (norleucine and aminoadipic acid with d15N reference values of 19.06 ‰ and -5.8 ‰, respectively).

Data Processing Description

Data processing: Stable isotope analysis of carbon and nitrogen isotopes measures the ratio of the heavier, rare isotope to the lighter, more common isotope (13C:12C or δ13C;15N:14N or δ15N) expressed as parts per mil (‰) relative to a standard (air for N, V-PDB for C).

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Data Files

File
AA-CSIA.csv (Comma Separated Values (.csv), 9.11 KB) MD5:5cb2f93c6617f0a02501801ae17ff39e Primary data file for dataset ID 679447

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Related Publications

Bradley, C. J., Wallsgrove, N. J., Choy, C. A., Drazen, J. C., Hetherington, E. D., Hoen, D. K., & Popp, B. N. (2015). Trophic position estimates of marine teleosts using amino acid compound specific isotopic analysis. Limnology and Oceanography: Methods, 13(9), 476–493. doi:10.1002/lom3.10041
General

Choy, C. A., Popp, B. N., Hannides, C. C. S., & Drazen, J. C. (2015). Trophic structure and food resources of epipelagic and mesopelagic fishes in the North Pacific Subtropical Gyre ecosystem inferred from nitrogen isotopic compositions. Limnology and Oceanography, 60(4), 1156–1171. doi:10.1002/lno.10085
General

Gerrodette, T., Watters, G., Perryman, W., and Ballance, L. 2008. Estimates of 2006 dolphin abundance in the eastern tropical Pacific, with revised estimates from 1986-2003. NOAA Technical Memorandum NOAA-TM-NMFS-SWFSC-422. Available at https://swfsc.noaa.gov/publications/PubBIN#/search/
Methods

Hetherington, E. D., Olson, R. J., Drazen, J. C., Lennert-Cody, C. E., Ballance, L. T., Kaufmann, R. S., & Popp, B. N. (2016). Spatial food-web structure in the eastern tropical Pacific Ocean based on compound-specific nitrogen isotope analysis of amino acids. Limnology and Oceanography, 62(2), 541–560. doi:10.1002/lno.10443
Methods
,
Results

Olson, R. J., Popp, B. N., Graham, B. S., López-Ibarra, G. A., Galván-Magaña, F., Lennert-Cody, C. E., … Fry, B. (2010). Food-web inferences of stable isotope spatial patterns in copepods and yellowfin tuna in the pelagic eastern Pacific Ocean. Progress in Oceanography, 86(1-2), 124–138. doi:10.1016/j.pocean.2010.04.026
Methods

Philbrick, V.A. Fiedler P.C., Fluty J.T., and Reilly S.B. 2001. Report of Oceanographic studies conducted during the 2000 eastern tropical Pacific Ocean survey on the research vessels David Starr Jordan, and McArthur. NOAA Technical Memorandum NOAA-TM-NMFS-SWFSC-309. Available at https://swfsc.noaa.gov/publications/PubBIN#/search/
Methods

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Parameters

Parameter	Description	Units
species	Name of the species	unitless
sample_number	Sample identification number	unitless
date_analyzed	Date on which AA-CSIA analysis of corresponding sample was begun; formatted as yyyy-mm-dd	unitless
Alanine_Avg	mean d15N value of Alanine	parts per thousand (per mil, ‰)
Alanine_SD	standard deviation of d15N values of Alanine	parts per thousand (per mil, ‰)
Glycine_Avg	mean d15N value of Glycine	parts per thousand (per mil, ‰)
Glycine_SD	standard deviation of d15N values of Glycine	parts per thousand (per mil, ‰)
Threonine_Avg	mean d15N value of Threonine	parts per thousand (per mil, ‰)
Threonine_SD	standard deviation of d15N values of Threonine	parts per thousand (per mil, ‰)

Serine_Avg	mean d15N value of Serine	parts per thousand (per mil, ‰)
Serine_SD	standard deviation of d15N values of Serine	parts per thousand (per mil, ‰)
Valine_Avg	mean d15N value of Valine	parts per thousand (per mil, ‰)
Valine_SD	standard deviation of d15N values of Valine	parts per thousand (per mil, ‰)
Leucine_Avg	mean d15N value of Leucine	parts per thousand (per mil, ‰)
Leucine_SD	standard deviation of d15N values of Leucine	parts per thousand (per mil, ‰)
Isoleucine_Avg	mean d15N value of Isoleucine	parts per thousand (per mil, ‰)
Isoleucine_SD	standard deviation of d15N values of Isoleucine	parts per thousand (per mil, ‰)
Proline_Avg	mean d15N value of Proline	parts per thousand (per mil, ‰)
Proline_SD	standard deviation of d15N values of Proline	parts per thousand (per mil, ‰)
AsparticAcid_Avg	mean d15N value of Aspartic Acid	parts per thousand (per mil, ‰)
AsparticAcid_SD	standard deviation of d15N values of Aspartic Acid	parts per thousand (per mil, ‰)
Methionine_Avg	mean d15N value of Methionine	parts per thousand (per mil, ‰)
Methionine_SD	standard deviation of d15N values of Methionine	parts per thousand (per mil, ‰)
GlutamicAcid_Avg	mean d15N value of Glutamic Acid	parts per thousand (per mil, ‰)
GlutamicAcid_SD	standard deviation of d15N values of Glutamic Acid	parts per thousand (per mil, ‰)
Phenylalanine_Avg	mean d15N value of Phenylalanine	parts per thousand (per mil, ‰)
Phenylalanine_SD	standard deviation of d15N values of Phenylalanine	parts per thousand (per mil, ‰)
Tyrosine_Avg	mean d15N value of Tyrosine	parts per thousand (per mil, ‰)
Tyrosine_SD	standard deviation of d15N values of Tyrosine	parts per thousand (per mil, ‰)
Lysine_Avg	mean d15N value of Lysine	parts per thousand (per mil, ‰)
Lysine_SD	standard deviation of d15N values of Lycine	parts per thousand (per mil, ‰)
Arginine_Avg	mean d15N value of Arginine	parts per thousand (per mil, ‰)
Arginine_SD	standard deviation of d15N values of Arginine	parts per thousand (per mil, ‰)
Histidine_Avg	mean d15N value of Histidine	parts per thousand (per mil, ‰)

Histidine_SD	standard deviation of d15N values of Histidine	parts per thousand (per mil, ‰)

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Instruments

Dataset-specific Instrument Name	cylindrical-conical bongo net
Generic Instrument Name	Bongo Net
Dataset-specific Description	Zooplankton samples were collected with a cylindrical-conical bongo net (333 um mesh), fished to 200 m approximately two hours after sunset.
Generic Instrument Description	A Bongo Net consists of paired plankton nets, typically with a 60 cm diameter mouth opening and varying mesh sizes, 10 to 1000 micron. The Bongo Frame was designed by the National Marine Fisheries Service for use in the MARMAP program. It consists of two cylindrical collars connected with a yoke so that replicate samples are collected at the same time. Variations in models are designed for either vertical hauls (OI-2500 = NMFS Pairovet-Style, MARMAP Bongo, CalVET) or both oblique and vertical hauls (Aquatic Research). The OI-1200 has an opening and closing mechanism that allows discrete "known-depth" sampling. This model is large enough to filter water at the rate of 47.5 m3/minute when towing at a speed of two knots. More information: Ocean Instruments, Aquatic Research, Sea-Gear

Dataset-specific Instrument Name	gas chromatograph (Trace GC)
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	The d15N values of individual AAs were measured using an isotope ratio mass spectrometer (IRMS) (Delta PlusXP, Delta V Plus or MAT 253) interfaced with a gas chromatograph (Trace GC) through a GC-C III combustion furnace (980 degrees C), reduction furnace (650 degrees C), and liquid-N cold trap.
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	dipnet
Generic Instrument Name	Hand Net
Dataset-specific Description	Specimens of mesopelagic myctophid fishes Myctophum nitidulum (Mn) and Symbolophorus reversus (Sr) were collected by dipnet at night.
Generic Instrument Description	A hand net (also called a scoop net or dip net) is a net or mesh basket held open by a hoop. They are used for scooping fish near the surface of the water.

Dataset-specific Instrument Name	handlines and jigs
Generic Instrument Name	Handline and Jig
Dataset-specific Description	Specimens of the squids Dosidicus gigas (Dg) and Sthenoteuthis oualaniensis (So) also were collected at night, using handlines and jigs.
Generic Instrument Description	Handline fishing, or handlining, is a fishing technique where a single fishing line is held in the hands. A handline is a relatively large diameter line that can be pulled by hand, and it has a jig attached at the end. Handlines are frequently used for catching fish or squid that are schooling near the surface, thus a long haul by hand is not necessary.

Dataset-specific Instrument Name	isotope ratio mass spectrometer (IRMS)
Generic Instrument Name	Isotope-ratio Mass Spectrometer
Dataset-specific Description	The d15N values of individual AAs were measured using an isotope ratio mass spectrometer (IRMS) (Delta PlusXP, Delta V Plus or MAT 253) interfaced with a gas chromatograph (Trace GC) through a GC-C III combustion furnace (980 degrees C), reduction furnace (650 degrees C), and liquid-N cold trap.
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	purse-seine fishing
Generic Instrument Name	Purse-seine Fishing Gear
Dataset-specific Description	Three species of tuna, yellowfin (Ta.; Thunnus albacares), skipjack (Kp.; Katsuwonus pelamis), and bigeye (To.; Thunnus obesus) tunas, were sampled year-round during 2003-2005 by observers of the Inter-American Tropical Tuna Commission onboard purse-seine fishing vessels.
Generic Instrument Description	A purse seine is a large wall of netting deployed in a circle around an entire school of fish. The seine has floats along the top line with a lead line of chain along the bottom. Once a school of fish is located, a skiff pulls the seine into the water as the vessel encircles the school with the net. A cable running along the bottom is then pulled in, "pursing" the net closed on the bottom, preventing fish from escaping by swimming downward. The catch is harvested by bringing the net alongside the vessel and brailing the fish aboard.

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Deployments

SWFSC1630

Website	https://www.bco-dmo.org/deployment/675238
Platform	NOAA Ship David Starr Jordan
Report	http://dmoserv3.whoi.edu/data_docs/CAMEO_Trophic_Position/06FinalCruiseReptDSJ.pdf
Start Date	2006-07-28
End Date	2006-12-07

SWFSC1631

Website	https://www.bco-dmo.org/deployment/675265
Platform	NOAA Ship McArthur II
Report	http://dmoserv3.whoi.edu/data_docs/CAMEO_Trophic_Position/0FinalCruiseReptMAC.pdf
Start Date	2006-07-28
End Date	2006-12-07

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Project Information

CAMEO 2009 - A novel tool for validating trophic position estimates in ecosystem-based fisheries models (CAMEO_Trophic_Position)

Website: http://cameo.noaa.gov/pres_bpopp.html

Coverage: Subtropical North Pacific Ocean

(*From NSF Award Abstract*)

Evidence increasingly demonstrates that selective removal of marine life can induce restructuring of marine food webs. Trophic structure is the central component of mass balance models, widely used tools to evaluate fisheries in an ecosystem context. Food web structure is commonly determined by stomach contents or by bulk tissue stable isotope analyses, both of which are limited in terms of resolution and versatility. The investigators will refine a tool, Amino Acid Compound-Specific Isotopic Analyses (AA-CSIA), which can be broadly applicable for quantifying the time-integrated trophic position (TP) of consumers. Differences in source and trophic nitrogen isotopic composition for specific amino acids will provide an unambiguous and integrated measure of fractional trophic TP across multiple phyla, regardless of an animal's physiological condition or of the biogeochemical cycling at the base of the food web. AA-CSIA will allow testing of the efficacy of trophic position estimates derived from ecosystem-based models and promote the evolution of these models into decision-support tools.

This project has three goals: 1. To validate the application of AA-CSIA across multiple marine phyla under differing physiological conditions. 2. To compare the application of AA-CSIA across systems with contrasting biogeochemical cycling regimes. 3. To develop the use of AA-CSIA TP estimates for validating trophic models of exploited ecosystems. The investigators will test and refine the approach using a combination of laboratory feeding experiments and field studies across regions with differing biogeochemical cycling regimes. They will determine the applicability of the AA-CSIA approach in a variety of marine organisms assessed in controlled studies. Subsequently, ecosystem components will be sampled from the eastern tropical Pacific, coastal California and the subtropical Pacific gyre. They will also test the effects of sample preservation on the isotopic composition of individual AA to determine whether the approach can be used on archived samples. This tool will allow testing of the efficacy of ecosystem-based models currently used to gain insight into the ecological effects of fisheries removals and improve the reliability of future models required to manage marine resources. In addition to the goal of developing AA-CSIA for use as a TP indicator, the information obtained through this project will provide important species-specific biological data on the feeding behavior of marine organisms that could have implications for their resilience to anthropogenic pressures and climate change.

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Program Information

Comparative Analysis of Marine Ecosystem Organization (CAMEO)

Website: http://www.nsf.gov/geo/oce/programs/CAMEO_Webpage.jsp

CAMEO Science Plan (2012).

The Comparative Analysis of Marine Ecosystem Organization (CAMEO) program was implemented as a partnership between the NOAA National Marine Fisheries Service and National Science Foundation Division of Ocean Sciences. The purpose of CAMEO was to strengthen the scientific basis for an ecosystem approach to the stewardship of our ocean and coastal living marine resources. The program supported fundamental research to understand complex dynamics controlling ecosystem structure, productivity, behavior, resilience, and population connectivity, as well as effects of climate variability and anthropogenic pressures on living marine resources and critical habitats. CAMEO encouraged the development of multiple approaches, such as ecosystem models and comparative analyses of managed and unmanaged areas (e.g., marine protected areas) that can ultimately form a basis for forecasting and decision support. Central to the program was the emphasis on collaborations between academic and private researchers and federal agency scientists with mission responsibilities to inform ecosystem management activities. (adapted from CAMEO website)

This funding opportunity implemented CAMEO research by supporting the development of research tools and strategic approaches through the following types of proposals:

1. Development of strategies and methodologies for comparative analyses that can be applied consistently across spatial and temporal scales and ecosystems, and that facilitate the design of decision support tools for marine populations, ecosystems and habitats.

2. Development of models that address key scientific questions by comparing ecosystems and ecosystem processes. Models that are geographically and temporally portable, and that incorporate assessment of modeling skill, are particularly encouraged.

3. Retrospective studies that analyze, re-analyze or synthesize existing information (historic, time-series, ongoing program, etc.) using a comparative approach.

4. Studies that integrate the human dimension within ecosystem dynamics. The CAMEO program seeks to promote interdisciplinary research using comparative approaches to link marine ecosystem research with the social and behavioral sciences in new and vital ways.

To guide program priorities, a Science Steering Committee was formed through Dr. Linda Deegan and the initial Scientific Planning Office at the Marine Biological Laboratory in Woods Hole, MA. This Committee was designed to provide scientific advice and broad direction to NOAA and NSF regarding the CAMEO program.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1040810

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