Total mercury and methylmercury concentrations measured across 10 tissues of the longnose lancetfish (Alepisaurus ferox) collected from the central and eastern North Pacific between 2018 and 2023

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Project
» Scripps Center for Oceans and Human Health: advancing the science of marine contaminants and seafood security (SCOHH)

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Abstract
This dataset contains total mercury and methylmercury concentrations measured across 10 tissues (brain, caudal white muscle, dorsal white muscle, gallbladder, gill filament, gonad, heart, intestine, liver, and stomach lining) of a globally distributed deep-sea fish, the longnose lancetfish (Alepisaurus ferox). Lancetfish specimens were collected by fisheries observers of the National Oceanic and Atmospheric Administration Pacific Islands Region and West Coast Region Observer Programs from 2018 to 2023 between 20 – 40° N and 115 – 160° W in the central and eastern North Pacific Ocean. The data were used to examine patterns of mercury bioaccumulation in lancetfish and evaluate the use of lancetfish as a biomonitoring species of mercury in the deep sea.

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Coverage

Location: Central and eastern North Pacific Ocean
Spatial Extent: **N**:40 **E**:-115 **S**:20 **W**:-160
Temporal Extent: 2018-01 - 2023-09

Dataset Description

This dataset is referred to as "Dataset S1" in the supplementary material of Chen et al. The data were used in Figures 1 and 2, and Table 1.

Methods & Sampling

Sample Collection: Whole lancetfish (n = 69) were collected by fisheries observers of the National Oceanic and Atmospheric Administration (NOAA) Pacific Islands Region and West Coast Region Observer Programs from 2018 to 2023 between 20 – 40° N and 115 – 160° W in the central and eastern North Pacific Ocean. Observers sampled lancetfish from the Hawaii-based shallow- and deep-set pelagic longline fisheries. Lancetfish were frozen whole at sea and capture location was recorded. In the lab, specimens were defrosted, measured to the nearest mm (FL), and weighed whole to the nearest 0.1 g.

The following components, hereafter referred to as “tissues”, were dissected from each fish when available: brain, caudal muscle, dorsal muscle, gallbladder, gill filament, gonad, heart, intestine, liver, and stomach lining. Only white muscle tissue was sampled; dorsal muscle was sampled posterior to the operculum at the base of the dorsal fin insertion and anterior to the vent, and caudal muscle was sampled posterior to the adipose fin and anterior to the caudal peduncle. Skin, bones, and cartilage were removed from white muscle tissues before analysis. Gonads were sampled whole and were not distinguished as testes or ovaries as lancetfish larger than 100 cm are simultaneous hermaphrodites (Bañon et al. 2022). Stomachs were emptied and rinsed with Milli-Q water to remove all contents. Following dissection, all tissues were gently rinsed with Milli-Q to avoid contamination between samples, placed in pre-weighed Whirl-Paks, and weighed before and after drying to measure moisture content. Tissues were frozen at -80˚C before being freeze-dried and homogenized within the Whirl-Pak or using an electronic mill (IKA Tube Mill 100 Control). Milling vessels and tools were cleaned with 95% ethanol between samples.

Data Processing Description

Analytical Methods: Total mercury (THg) concentrations were determined using a Nippon Instruments MA-3000 Direct Mercury Analyzer (DMA), which uses direct thermal decomposition, gold amalgamation, and cold vapor atomic absorption spectroscopy. For quality assurance and quality control, certified reference materials National Research Council Canada (NRCC) DORM-4 (fish protein) and NRCC TORT-3 (lobster hepatopancreas) were analyzed at the beginning and end of each analysis day. Around 20 mg of dried, homogenized tissues were weighed out for THg analysis, and replicate samples and DORM-4 were analyzed every seven samples. A blank boat was combusted after samples expected to have high THg concentrations (e.g., livers from large fish) to reduce any potential THg carryover to subsequent samples. The average variation of replicate measurements was 4.1%, and analyses of DORM-4 (average measured THg = 417 ± 26 ng Hg/g dry weight, n = 161) and TORT-3 (296 ± 15 ng Hg/g dry weight, n = 40) were within 1.2% and 1.5% of mean certified values, respectively. Only data collected between standard reference materials that were within the range of certified values were included in analyses.

We analyzed tissues known to play roles in methylmercury (MeHg) accumulation and excretion for MeHg. We selected sets of dorsal muscle, stomach lining, intestine, and liver samples from 10 lancetfish representing a range of masses (116.0 – 3920.8 g) for MeHg analysis (n = 40 samples total). We also analyzed brains from 33 whole lancetfish for MeHg. MeHg concentrations were determined using species-specific isotope dilution mass spectrometry following microwave-assisted acid digestion. This method quantifies the MeHg concentration of a sample based on the recovery of an isotopically labeled Me201Hg solution added during sample preparation. A stock Me201Hg solution was synthesized from 201HgII (96.3% purity) (Gilmour and Riedel, 1995; Hintelmann et al., 2000; Hintelmann and Ogrinc, 2002) and diluted to a 13 ng/mL working solution. The MeHg concentration of the Me201Hg working solution was periodically quantified using reverse isotope dilution with standards prepared from a certified 1000 ppm MeHg (II) chloride standard (Alfa Aesar). Exact concentrations were used to calculate MeHg concentrations in the samples after signal deconvolution of Me201Hg and Me202Hg peak areas.

To prepare samples for analysis, around 20 mg of tissue were weighed into acid-cleaned 50 mL PTFE-TFM pressure vessels with 10 mL of 5 M nitric acid and 85 µL of the 13 ng/mL Me201Hg working solution. The volume of Me201Hg added was selected to target a 202Hg/201Hg mixing ratio of 0.23 to minimize uncertainty in signal deconvolution (Heimbürger et al., 2015; Rousseau et al., 2013). Samples were digested using an

Anton Paar Multiwave 5000, which heated the samples to 70˚C for 10 minutes after a 5-minute ramp-up period. After digestion, sample digestates were diluted with 30 mL of Milli-Q water and stored at 4˚C.

MeHg in each sample was derivatized for analysis using ascorbic acid-assisted direct ethylation (Munson et al., 2014). 100 µL of sample digestate were added to a clean 60 mL amber borosilicate glass vial with 45 mL of Milli-Q water. Sample pH was adjusted to 4.8 using 2 M acetate/glacial acetic acid buffer before ascorbic acid (2.5% w/v) was added. Samples were ethylated with sodium tetraethylborate (1% NaTEB in 2% potassium hydroxide), and ethylation was allowed to proceed for at least 10 minutes before analysis. All reagents were prepared using Milli-Q water as needed. Samples were purged with Hg-free ultra-high purity argon gas, volatile Hg species were separated via gas chromatography using a Tekran 2700 Methyl Mercury Auto-Analysis System, and Me201Hg and Me202Hg were detected using an Agilent 8900 triple quadrupole inductively coupled plasma mass spectrometer (ICP-MS). Replicate samples, DORM-4, and TORT-3 were analyzed in each batch prepared for microwave digestion. The average variation of replicate measurements was 6.7%, and analyses of DORM-4 (average measured MeHg = 363 ± 24 ng Hg/g dry weight, n = 9) and TORT-3 (128 ± 8 ng Hg/g dry weight, n = 9) were within 2.3% and 6.9% of mean certified values, respectively.

Data Analysis: Because MeHg analysis is costly and time-consuming, we analyzed a subset of tissues for MeHg to confirm the relationship between THg and MeHg concentrations. THg and MeHg concentrations were highly correlated in dorsal muscle, liver, stomach lining, and intestine (Spearman's rank correlation, r = 1.00, 0.99, 0.98, and 0.83, respectively). However, we analyzed all brains for MeHg, so comparisons of measured MeHg concentrations between tissues were skewed by uneven sample size. To address this issue, we fit a generalized additive model (GAM) using restricted maximum likelihood estimation, a gaussian family distribution, and an "identity" link function using the mgcv package (version 1.9.0; Wood, 2011) to predict percent MeHg from lancetfish mass by tissue type using paired MeHg and THg measurements (Table S1). Percent MeHg was calculated as the MeHg concentration divided by the THg concentration of the same sample. We then used the GAM to estimate MeHg concentrations of dorsal muscle, stomach lining, intestine, and liver samples from fish with measured brain MeHg concentrations. We only measured MeHg in brain due to low sample mass, and thus do not report percent MeHg.

All mercury concentrations are reported in ng Hg/g on a wet-weight basis using percent moisture data obtained from the freeze-drying process. All data processing was performed in R Statistical Software (version 4.3.2; R Core Team, 2023).

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Data Files

File
948929_v1_lancetfish.csv (Comma Separated Values (.csv), 52.80 KB) MD5:072dc21734e7b6eb4865a79811c908b5 Primary data file for dataset ID 948929, version 1

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Related Publications

Bañón, R., Roura, Á., García-Fernández, C., Alonso-Fernández, A., & de Carlos, A. (2022). Coastal habitat evidences and biological data of Alepisaurus ferox (Aulopiform; Alepisauridae) from northwestern Iberian Peninsula. Marine Biodiversity, 52(2). https://doi.org/10.1007/s12526-022-01261-9
Methods

Chen, R. S., Schartup, A. T., Paulson, E. T., & Choy, C. A. (2024). Diet shifts drive mercury bioaccumulation and distribution in tissues of the longnose lancetfish (Alepisaurus ferox). Scripps Institution of Oceanography, University of California San Diego. https://doi.org/10.1016/j.marpolbul.2025.117590
Results

Gilmour, C. C., & Riedel, G. S. (1995). Measurement of Hg methylation in sediments using high specific-activity203Hg and ambient incubation. Water, Air, & Soil Pollution, 80(1–4), 747–756. https://doi.org/10.1007/bf01189726 https://doi.org/10.1007/BF01189726
Methods

Heimbürger, L.-E., Sonke, J. E., Cossa, D., Point, D., Lagane, C., Laffont, L., Galfond, B. T., Nicolaus, M., Rabe, B., & van der Loeff, M. R. (2015). Shallow methylmercury production in the marginal sea ice zone of the central Arctic Ocean. Scientific Reports, 5(1). https://doi.org/10.1038/srep10318
Methods

Hintelmann, H., & Ogrinc, N. (2002). Determination of Stable Mercury Isotopes by ICP/MS and Their Application in Environmental Studies. Biogeochemistry of Environmentally Important Trace Elements, 321–338. https://doi.org/10.1021/bk-2003-0835.ch021
Methods

Hintelmann, H., Keppel-Jones, K., & Evans, R. D. (2000). Constants of mercury methylation and demethylation rates in sediments and comparison of tracer and ambient mercury availability. Environmental Toxicology and Chemistry, 19(9), 2204–2211. https://doi.org/10.1002/etc.5620190909
Methods

Munson, K. M., Babi, D., & Lamborg, C. H. (2014). Determination of monomethylmercury from seawater with ascorbic acid-assisted direct ethylation. Limnology and Oceanography: Methods, 12(1), 1–9. doi:10.4319/lom.2014.12.1
Methods

R Core Team (2023). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Rousseau, T. C. C., Sonke, J. E., Chmeleff, J., Candaudap, F., Lacan, F., Boaventura, G., Seyler, P., & Jeandel, C. (2013). Rare earth element analysis in natural waters by multiple isotope dilution – sector field ICP-MS. Journal of Analytical Atomic Spectrometry, 28(4), 573. https://doi.org/10.1039/c3ja30332b
Methods

Wood, S. N. (2010). Fast stable restricted maximum likelihood and marginal likelihood estimation of semiparametric generalized linear models. Journal of the Royal Statistical Society: Series B (Statistical Methodology), 73(1), 3–36. https://doi.org/10.1111/j.1467-9868.2010.00749.x
Methods

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Parameters

Parameter	Description	Units
specimen_id	unique identifier assigned to individual fish	unitless
date	fish collection date, in the format YYYY-MM	unitless
latitude	fish collection location. Location data are provided in 5x5 degree cells. The coordinate represents the lower left corner of the 5x5 degree cell	degrees
longitude	fish collection location. Location data are provided in 5x5 degree cells. The coordinate represents the lower left corner of the 5x5 degree cell	degrees
FL_mm	fork length of whole fish	millimeters (mm)
whole_mass_g	wet weight of whole fish	grams (g)
size_class	lancetfish size class, where individuals <1.8 kg are considered "small" and individuals ≥1.8 kg are considered "large"	unitless
tissue_type	tissue type analyzed	unitless
percent_moisture	moisture content of the tissue	percentage (%)
THg_wet_ng_g	THg concentration reported as ng Hg/g on a wet weight basis	nanogram per gram (ng/g)
hg_notes	notes on whether measurements are averaged from replicate measurements of the same sample	unitless
MeHg_wet_ng_g	methylmercury (MeHg) concentration reported as ng Hg/g on a wet weight basis	nanogram per gram (ng/g)
mehg_type	"measured" or "predicted" to distinguish between measured MeHg concentrations and MeHg concentrations predicted with a generalized additive model using percent MeHg and mass	unitless
percent_mehg	MeHg content of the tissue, as a percentage of THg content	percentage (%)

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Instruments

Dataset-specific Instrument Name	Nippon Instruments MA-3000 Direct Mercury Analyzer
Generic Instrument Name	Automated Mercury Analysis System
Dataset-specific Description	Nippon Instruments MA-3000 Direct Mercury Analyzer: used to collect total mercury concentration data from lancetfish tissues
Generic Instrument Description	Examples include Tekran Models 2600 and 2700

Dataset-specific Instrument Name	Tekran 2700 Methyl Mercury Auto-Analysis System
Generic Instrument Name	Automated Mercury Analysis System
Dataset-specific Description	Tekran 2700 Methyl Mercury Auto-Analysis System: uses gas chromatography to separate mercury species in samples
Generic Instrument Description	Examples include Tekran Models 2600 and 2700

Dataset-specific Instrument Name	IKA Tube Mill 100 Control
Generic Instrument Name	Homogenizer
Dataset-specific Description	IKA Tube Mill 100 Control: used to homogenize lancetfish tissues
Generic Instrument Description	A homogenizer is a piece of laboratory equipment used for the homogenization of various types of material, such as tissue, plant, food, soil, and many others.

Dataset-specific Instrument Name	Agilent 8900 triple quadrupole inductively coupled plasma mass spectrometer (ICP-MS)
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	Agilent 8900 triple quadrupole inductively coupled plasma mass spectrometer (ICP-MS): used to detect Me201Hg and Me202Hg to quantify methylmercury concentrations
Generic Instrument Description	An ICP Mass Spec is an instrument that passes nebulized samples into an inductively-coupled gas plasma (8-10000 K) where they are atomized and ionized. Ions of specific mass-to-charge ratios are quantified in a quadrupole mass spectrometer.

Dataset-specific Instrument Name	LABCONCO Benchtop Freeze Dryer
Generic Instrument Name	Lyophilizer
Dataset-specific Description	LABCONCO Benchtop Freeze Dryer: used to freeze dry tissues
Generic Instrument Description	A lyophilizer, also known as freeze dryer or liofilizador, is a device that is used to freeze-dry material.

Dataset-specific Instrument Name	Anton Paar Multiwave 5000
Generic Instrument Name	Microwave Digestion Platform
Dataset-specific Description	Anton Paar Multiwave 5000: microwave used to digest tissues
Generic Instrument Description	Microwave digestion is a chemical technique used to decompose sample material into a solution suitable for quantitative elemental analysis

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Project Information

Scripps Center for Oceans and Human Health: advancing the science of marine contaminants and seafood security (SCOHH)

Coverage: Scripps Center for Oceans and Human Health

The Scripps Center for Oceans and Human Health (SCOHH) is a five-year effort to advance the science and community engagement surrounding seafood pollutants, on a rapidly changing planet. The project brings together a multidisciplinary team of biomedical and oceanographic researchers with expertise in fish ecology, microbiology, marine chemistry, climate modeling, technology development, bioaccumulation, genomics, toxicology, and public health. The Center?s scientific goals and focus are guided by the needs of society, established through bidirectional community engagement, and led by a proven community engagement team. The proposed research program of SCOHH spans four main areas:

1. Climate change impacts on the human intake of seafood micronutrients and contaminants.
2. The marine microbiome as a source for the synthesis, transformation, and distribution of seafood contaminants.
3. Mechanisms of bioaccumulation and developmental toxicity of seafood pollutants.
4. Bidirectional public engagement and literacy surrounding seafood risks and benefits.

The outcomes of the SCOHH will inform policies, consumption guidelines, and individual decisions to lower risk and enhance greater benefits associated with seafood consumption. Internally, SCOHH will take deliberate measures to enhance engagement with community partners. The Center is jointly supported by NSF?s Division of Ocean Sciences and by the National Institute for Environmental Health Sciences (NIEHS).

The central scientific theme of SCOHH is to advance knowledge of marine contaminants and seafood security. Natural and anthropogenic contaminants such as mercury, DDT, and PCBs drive seafood consumption advisories. Yet understanding of their sources, microbial transformations, toxicity, and potential for climate driven change remain incomplete. The SCOHH team will study and track the distribution of essential micronutrients and harmful contaminants in marine food webs to the three billion people who consume seafood globally, the roles that the marine microbiome play in their production and transport, and the developmental toxicity of seafood pollutants and their interactions with transporters that determine uptake and bioaccumulation.

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-2414798
National Institute of Environmental Health Sciences (NIEHS)	P01ES035541

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