ABSTRACT 001

A 75-YEAR RECORD OF NORTH SEA FOOD WEB DYNAMICS BASED ON THE STABLE ISOTOPIC COMPOSITION OF AMINO ACIDS FROM HARBOUR PORPOISE (*PHOCOENA PHOCOENA*)

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Animal tissues incorporate the stable nitrogen isotopic composition from underlying resources used into their biomass with a fractionation due to metabolism. These tissues reflect the baseline nitrogen isotope values supporting primary producers, the animal's position within the food web, and metabolism associated with tissue specific metabolic pathways. Within a long-lived tissue such as bone, collagen remains well preserved after death, allowing for the possibility of investigating long term ecosystem states through analysis of bones of known provenance. Here, collagen sourced from a museum archive and the tissue bank of the Dutch Stranding Network (n=170) were analyzed for nitrogen and carbon isotope ratios from bulk material and amino acids across historical (1950-2001) and recent (2009-2021) time periods. These results allow: 1) ID of modern and historical trophic position for harbour porpoise, 2) inference of ecosystem impacts that have led to changes in baseline nitrogen and trophic structure in the North Sea, and 3) ID of the dominant microbial support for food web carbon. Application of amino acids to provide a baseline integrated trophic position will provide a valuable multi-decadal baseline as well as trophic position for comparison against the more recent archive (2009-2021). The long history of industrial overfishing in the North Sea confounds interpretation of the multiple regime shifts and the multi-decadal impacts from climate change. We anticipate that integration of baseline changes across the 75-year period provides an opportunity to resolve the multiple anthropogenic stressors impacting the harbor porpoise's place in the food web structure in the North Sea.

ABSTRACT 002

Late Holocene Nearshore Marine Productivity Record, Climate Change, & Sociopolitical Dynamics on California's Northern Channel Islands

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The Northern Channel Islands of California were occupied by the Chumash and their predecessors for ~13,000 years. Over the past ~1,500 years, during the Middle to Late Transition (MLT) period, major changes in sociopolitical structure and subsistence strategies are apparent in the archaeological record, coinciding with the Medieval Climate Anomaly. While some proponents contend that regional social systems were steadily evolving towards increased hierarchy and political stratification over millennia, others argue it was spurred rapidly by climate instability.

Coastal California is a highly productive upwelling system. However, marine climate oscillations (e.g., ENSO or PDO cycles) strongly affect nutrients, productivity, and ecosystem structure. While marine climate records are traditionally reconstructed from sediment cores, these records integrate over broad regions and timescales, and may not capture local changes. In contrast, isotope paleo proxies preserved in shell from archaeological middens can capture ocean biogeochemistry and upwelling dynamics of a precise location and time. Archaeological shell archives therefore ideal for highly detailed coastal oceanographic paleo reconstructions at key maritime sites.

Here, we apply this approach to investigate marine conditions for the MLT and surrounding periods (2,000 to 250 cal BP and modern) on San Miguel Island. We measured $\delta^{13}C$ and $\delta^{15}N$ from the shell-bound organic matter of Mytilus californianus. Results show that the MLT exhibits both the most variable and lowest $\delta^{13}C$ and $\delta^{15}N$ values compared to all other time periods sampled, suggesting lower and highly variable marine productivity associated with reduced upwelling, supporting climate change as a key component of changing social organization.

ABSTRACT 003

A century long perspective on grey wolf ecology: comparing within and among individual diet

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Some carnivores are often classified as dietary generalists, but specialization between individuals can contribute to dietary variability and is often shaped by resource availability. Grey wolves (*Canis lupus*) are large, social carnivores and considered generalists at a population level but are known to specialize in some localities. In this study, we investigated changes to individual dietary variation in Swedish grey wolves during the past c. 100 years. We serially sampled dental collagen from the canine teeth of grey wolf individuals (n=38) and analyzed for carbon ($\delta^{13}C$) and nitrogen($\delta^{15}N$) stable isotope compositions. We also sampled a range of potential prey with varying foraging strategies and habitats from marine (e.g., seals), wetland (moose, beavers), and terrestrial (cervids, boar, badger, hares, foxes) habitats. The bone collagen of potential prey translated to a wide isotopic range for both $\delta^{15}N$ (0.5 – 16.0‰) and $\delta^{13}C$ (-26.7 – -15.7‰). Isotope values of grey wolves ranged widely ($\delta^{13}C$ = -23.8 - -19.0‰; $\delta^{15}N$ = 5.3 - 10.2‰) among individuals which supports grey wolves as generalist predators that make a variety of prey choices. We assessed isotopic niches with convex hull area among and within individuals and found no difference in varia/on between sex or among collection regions. We found a decreasing trend in convex hull area over /me from 1.93 to 0.58. Assessing the isotopic niches and diet variability in individual predators can offer insights into population level influences on complex food webs.

ABSTRACT 004

Individual amino acid isotopes in marine fossils: biogeochemical and ecological reconstruction on multi- million year timescales?

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In the past two decades compound-specific isotope analysis of amino acids (CSI-AA) has been employed across a steadily increasing range of disciplines. While most marine CSI-AA arguably remains focused on ecology, the technique has enormous potential for paleo and geochemical studies, with both $\delta^{15}N_{AA}$ and $\delta^{13}C_{AA}$ data from a range of archives allowing reconstruction of past algal assemblages, nutrient isotope baseline and cycling, as well as export production isotope values. However, the temporal reach of such applications is inherently limited by amino acid isotopic preservation. While sediments can offer contiguous records far into the past, sedimentary amino acids are intrinsically prone to degradation and diagenesis, in particular in oxic environments.

CSI-AA in marine fossils may provide a way to bypass temporal limits of other archives, potentially preserving AA isotope values on multi-million year time scales. This talk will first present an overview of recent data examining CSI-AA preservation in fossil and subfossil marine archives, including shell, subfossil coral, and foraminifera. We then show new data from a well preserved suite of ~ 70 MY nautiloid specimens from the Pierre Shale. Both $\delta^{15}N_{AA}$ and $\delta^{13}C_{AA}$ patterns in fossil Nacre align well with expectations for a marine heterotroph. While $\delta^{15}N_{AA}$ data yielded unexpectedly low TP values, $\delta^{15}N_{AA}$ also had better apparent preservation than $\delta^{13}C_{AA}$, consistent with other materials studied. Together, these results suggest the potential for excellent preservation of CSI-AA proxies at least through cretaceous in marine fossils, and we propose a set of criteria for evaluating CSI-AA data in very old materials.

ABSTRACT 005

Long-term evaluation of pre-moult foraging in Tawaki through stable isotope analysis of feathers over the last 150 years

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The spatial foraging patterns of seabirds are intrinsically linked to their ability to access dependable prey throughout their annual cycle. While flighted seabirds may cover longer distances during non-breeding periods to follow prey, penguins may be more limited in their capacity for rapid alterations in foraging range in both the breeding and non-breeding seasons. This pre-moult period is crucial not only for building fat stores to fuel the annual moult, but also for replenishing reserves lost during the breeding season. The Fiordland Penguin/tawaki (*Eudyptes pachyrhynchus*) embarks on one of the longest pre-moult journeys recorded for crested penguins. Yet the reasons embarking on such a journey when resources around coastal New Zealand are reaching peak remain a mystery. This study assessed the pre-moult foraging period of tawaki by analysing the bulk stable isotopes of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) derived from feathers. We collected feathers from live tawaki during the breeding season as well as from dated museum specimens to assess the stability of pre-moult foraging areas and prey resources over the last 150 years. Although we found differences among years, no consistent trend emerged over the study period as a whole. However, we do provide evidence of the role of continental resources to explain the remarkable pre-moult journey. Overall, we conclude that tawaki have not experienced drastic changes in foraging area or diet during the pre-moult period over the last 150 years. We propose that this unique strategy is key to tawaki population stability while other penguins are in decline.

ABSTRACT 006

DRIVERS OF RED DEER HABITAT CHANGES IN EUROPE OVER THE LAST 21 KA BP

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The habitat available to and used by red deer (*Cervus elaphus*) has changed significantly in Europe over the last 21 ka BP. The species largely inhabited open tundra steppes in the Late Pleistocene and forested areas during the Holocene Climate Optimum. Today, red deer occupy a wide spectrum of habitats from dense forests on the North European Plain to Mediterranean maquis scrub further south. In the recent past, the habitat of the species has been markedly shaped by human activity including anthropogenic transformations of the environment, hunting activity, translocations, and fencing. Prior to the human demographic explosion of the last few hundred years and the development of agriculture in Europe, red deer habitat was more strongly shaped by climatic and environmental conditions. Yet, it remains unclear exactly when and how humans began to influence red deer habitats in major ways, and to what extent the different drivers shaped red deer habitat use over time. To address this issue, we analysed stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope values from radiocarbon-dated bone collagen samples collected from the literature as proxies for foraging habitats. We first applied stable isotope niche modelling to reveal how red deer habitat changed in different parts of the continent over last 21 ka BP. Additionally, we used piecewise regression to test associations between the stable isotope composition of red deer bone collagen samples and climatic, environmental, and anthropogenic variables across multiple time bins at variable resolution. This approach allows us to detect subtle and temporally varying factors that have influenced the foraging niche of *Cervus elaphus* in Europe.

ABSTRACT 007

CONTRIBUTION OF STABLE ISOTOPES TO OCEAN ACIDIFICATION STUDIES IN SHALLOW VOLCANIC CO_2 VENTS

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Shallow volcanic CO_2 vents are naturally acidified areas due to the input of CO_2-volcanic fluids. They are considered proxies for future acidified oceans and natural laboratories where testing hypotheses on the effects of ocean acidification on different levels of the biological hierarchy. In the last decade, stable isotopes of carbon, nitrogen and sulphur have been analysed in shallow volcanic CO_2 vents from the Mediterranean Sea (Aeolian Archipelago, Italy) to investigate: i) the spatial extent of the area affected by volcanic input, ii) the origin (marine vs. volcanic) of nutrients exploited by primary producers, iii) nutrient transfer to upper trophic levels, and iv) the effects on local communities. Seawater pH measurements are affected by temporal variability in fluid emissions and hydrodynamics constraints, not allowing a proper assessment of the area affected by volcanic fluids, with implications on site selection (acidified vs control sites) for ocean acidification study. This limitation may be overcome by stable isotopes in sedimentary organic matter whose variability allowed the creation of isotopic distributional maps indicating the spatial influence of CO_2 vent. Close to the vent, primary producers showed altered isotopic values compared with control sites, suggesting the uptake of volcanic-derived nutrients. Analysis of animal communities revealed food web distortion with an overall simplification of the trophic structure and function. Stable isotopes can greatly contribute to the understanding of the effects of ocean acidification on communities and trophic functioning and their use should be promoted in ocean acidification studies in shallow volcanic CO_2 vents.

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ABSTRACT 008

Isotopic analysis of otoliths to determine early life habitat utilization of three fish species in Lake Michigan

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Habitat utilization by early-life stages of fish in freshwater river mouths remains under-described. In Lake Michigan, tributaries deliver seasonally warmer, nutrient enriched water into the relatively cool, oligotrophic lake. These river mouths represent dynamic mixing zones which may facilitate growth and survival of young fish. However, the relative contributions of river versus lake environments to support fish growth are not straightforward to distinguish. Prior studies have used stable isotope ratios of carbon, $\delta^{13}C$, and oxygen, $\delta^{18}O$, of otolith cores (indicative of early-life environment) and edges (indicative of recent environment) to assess riverine and lake habitat utilization of young fishes. We indexed these stable isotope ratios to describe habitat utilization for yellow perch (*Perca flavescens*), round goby (*Neogobius melanostomus*), and alewife (*Alosa pseudoharengus*) near three southern Lake Michigan river mouths. We used water temperature and the isotopic composition of the ambient water and potential prey to facilitate a priori predictions of habitat-specific $\delta^{18}O$ and $\delta^{13}C$ of otoliths. In general, habitat-specific a priori predictions generally matched observed otolith $\delta^{18}O$ and $\delta^{13}C$ of yellow perch and round goby, suggesting that these species generally remained in their distinct natal habitats into their juvenile and early adult life stages. In contrast, alewife otolith $\delta^{18}O$ and $\delta^{13}C$ values did not match habitat-specific a priori predictions, potentially because alewives move more between habitats than previously recognized or because of a greater contribution of metabolic derived isotopes than anticipated. This study demonstrates the complexity and need for further evaluation of isotopic contribution into otoliths under different environmental conditions.

ABSTRACT 009

Enamel nitrogen isotope ratios reflect a breastfeeding effect in wild chimpanzees and baboons from the Issa Valley (Tanzania)

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Nitrogen isotope ($\delta^{15}N$) analysis of animal hard tissues is a powerful tool for reconstructing dietary behavior and trophic position of fauna. Ecological studies indicate an increase in the $\delta^{15}N$ values of different tissues with trophic level, and similarly as the result of breastfeeding. While this method has not been applicable in dietary reconstructions in deep time due to protein preservation limitations, methodological advances now allow the analysis of $\delta^{15}N$ in tooth enamel.

Here, we present the first combined measurements of $\delta^{15}N$, $\delta^{13}C$ (carbon isotopes) and $\delta^{18}O$ (oxygen isotopes) in tooth enamel of modern free-ranging chimpanzees (*Pan troglodytes schweinfurthi*; n = 5) and sympatric yellow baboons (*Papio cynocephalus*; n = 11) from the miombo woodland site of Issa Valley, Tanzania. We analyzed first molars (which mineralize pre-weaning), and third molars (which mineralize post-weaning) from the same individuals to comparatively assess the breastfeeding effect in these isotope systems.

First molars show on average 1.9 ‰ (chimpanzees) and 1.1 ‰ (baboons) higher $\delta^{15}N$ values compared to the third molars of the same individual and detect a clear breastfeeding signal in contrast to $\delta^{13}C$ and $\delta^{18}O$. Therefore, the here presented results show that enamel-bound $\delta^{15}N$ data is a robust proxy for identifying weaning behavior in tooth enamel which potentially preserves over geological time scales. Our data illustrates the high potential of enamel-bound $\delta^{15}N$ as a proxy for reconstructing the timing of nursing in the social and biological evolution of modern and extinct mammalian species, including our early ancestors.

ABSTRACT 010

Linking declining Atlantic salmon (*Salmo salar*) populations with multidecadal changes in their marine foraging ecology

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Atlantic salmon (*Salmo salar*) populations have declined considerably over the last 50 years to the point where many populations are now threatened or endangered. This decline is believed to be largely attributed to low marine survival caused (in part) by changes in ocean temperature and prey abundance. We coupled stable isotope analysis with archived Atlantic salmon scales to investigate changes in Atlantic salmon marine resource use and trophic ecology of fish caught in the Northwest Atlantic Ocean from 1968-2019. There was a significant difference in bulk scale tissue $\delta^{13}C$ (range = -19.1‰ to -15.9‰, F = 7.5, $p<0.001$) and $\delta^{15}N$ (range = 7.1‰ to 12.3‰, F = 12.5, $p<0.001$) values across the study period, while trophic position estimates calculated from $\delta^{15}N$ of amino acids showed no significant difference (range = 3.0-4.1, F = 1.093, p = 0.367) over time. Generalized additive models (GAM) including sea surface temperature, fish condition, North Atlantic Oscillation and Atlantic Multidecadal Oscillation indexes explain 77.9% of the deviance in source amino acid $\delta^{15}N$ values, 58.5% of bulk tissue $\delta^{15}N$ values, and 46.1% of bulk $\delta^{1}C$ values. The results suggest that while changing ocean conditions in the northwest Atlantic are impacting primary production, Atlantic salmon trophic ecology has not undergone major secular shifts through time. Therefore, Atlantic salmon marine mortality is likely influenced by bottom-up controls and prey availability which may have implications for salmon survival in a warming ocean.

ABSTRACT 011

Comparing Vertebrae and Eye Lenses for Stable Isotope Analysis in Elasmobranchs: A Case Study on the Leopard Shark (*Triakis semifaciata*)

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Life history patterns of long-lived and migratory species, such as elasmobranchs (i.e., sharks, skates, rays, and sawfish), are challenging to elucidate. To date, cartilaginous vertebral growth bands are the primary substrate for stable isotope analysis (SIA) to discern life history patterns (e.g., movement and trophic) in elasmobranchs. However, sampling vertebral bands presents preparation and technical challenges. Here, we present the first comparison of eye lens laminae and vertebral band SIA using the Leopard Shark (*Triakis semifasciata*), an endemic elasmobranch to the western Pacific. In addition, we compare Leopard Shark ecology and movement between four estuarine/coastal sites in Northern California, USA with SIA: San Francisco Estuary [n = 9], Drakes Estero State Marine Conservation Area [n = 10], Tomales Bay [n = 10], and Bodega Bay [n = 9]). There were similar patterns for $\delta^{13}C$ and $\delta^{15}N$ values in eye lens laminae and vertebral bands in six individuals, indicating eye lens laminae are a valid chronological tissue in elasmobranchs. In addition, eye lens laminae reflect isotopic composition during embryonic time with pre birth laminae enriched in ^{15}N relative to post-birth laminae, suggesting isotopic effects of maternal provisioning . Ecologically, the $\delta^{13}C$ values indicate distinct life history patterns and suggest the existence of separate subpopulations of Leopard Sharks at each site, which implies limited movement between estuarine or coastal sites later in their lives. Our results demonstrate that the use of eye lens laminae as a chronological tissue is valid and can provide insights into elasmobranch life history.

ABSTRACT 012

Assessing the feasibility of retrospective isotope analysis via avian eye lens through a feeding trial

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Isotope analysis of eye lenses has recently attracted considerable interest as a means of reconstructing the environmental conditions experienced by animals. This technique has mainly been applied to fish, but it could also be applied to other vertebrates. In this study, we developed and tested a novel approach for applying this technique to avian species through a feeding experiment. We conducted a feeding experiment with quails (*Coturnix japonica*) that lasted for 200 days, in which quails in the control group were continuously fed the C_3-based diet from hatching, whereas those in the comparison group were switched from a C_3-based to a C_4-based diet 10-40 days after hatching. The eye lenses were extracted, sectioned, and determined the carbon and nitrogen stable isotope ratios. The results showed that the $\delta^{13}C$ of the eye lenses of the experiment groups decreased from the center to the middle of the lens, followed by an increase after the diet change. In contrast, those of the control group showed a consistent decreasing trend and equilibrated at middle of the eye lens. The $\delta^{15}N$ of all groups decreased from the center to the outer lens. The high $\delta^{13}C$ and $\delta^{15}N$ observed in the center of the eye lenses of all quails was due to the C_4-based diet consumed by their mothers, whereas the high $\delta^{15}N$ in the center was due to ^{15}N fractionation through bioenrichment. These results indicate that the avian eye lens could become a useful tool for reconstructing chronological isotopic information of the early life history.

ABSTRACT 013

Preliminary investigation into the palaeoecologies and food web dynamics of Ireland’s late Pleistocene mammal fauna

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Cave sites in Ireland containing animal bones provide an excellent opportunity to study the dietary palaeoecology and community structure of late Pleistocene Irish fauna, enabling better understandings of how these animals may have been affected by climatic and environmental changes in the past. Here we present the first stable carbon and nitrogen isotope data from ancient collagen samples of a range of late Pleistocene mammals (reindeer, woolly mammoth, giant deer, horse, brown bear, fox, wolf, hare, and lemming) from the Castlepook, Shandon, and Foley caves in Ireland. Clear isotopic differences indicate niche partitioning among many of the taxa (e.g., large herbivores), consistent with patterns seen in other late Pleistocene contexts outside of Ireland. Mammoths, for example, are characterized by high δ^{15}N values relative to other herbivores, while reindeer have high δ^{13}C values related to lichen consumption. Isotopic differences among prey species allow for inferences about predator-prey interactions, such as the relative contributions of large and small mammals to wolves’ and foxes’ diets. More research is needed to fully explore how changing environmental conditions influenced animal ecologies throughout the late Pleistocene in Ireland. Ongoing excavation efforts at cave sites, however, continue to yield animal remains for further study.

ABSTRACT 014

The Nile and Its people: An Isotopic and archaeo-botanical study of the Impact of Climate Change and Dam Projects on Nile River Communities

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This paper examines the profound effects of human-induced climate change and large-scale dam projects on freshwater resources, floodways, cultural heritage and the livelihood of indigenous communities along the Nile River. The High Dam and its precedent Aswan dam construction led to significant environmental and socio-cultural disruptions. Unpublished ethnographic study by Nawal Hassan documented the submerging of 13 million palm trees impacting the Nubian communities in Egypt and Sudan by stripping them of critical resources for food and raw materials.This study integrates data from stable isotopes in Nile water and botanical materials (ancient, ethnographic, and modern) to trace climatic impacts on the Nile river and native plant biodiversity over time. Water samples from Ethiopia, Sudan, and Egypt reveal an increase in evaporative conditions downstream in Egypt (average $\delta^{18}O$ = 2.8‰ ± 0.4) in modern time compared to ancient oxygen isotopes of the Nile river implied from ancient freshwater mollusk ($\delta^{18}O$= -0.83‰). Particularly concerning is the drying trends in Lake Qarun, Fayum ($\delta^{18}O$ = +8‰). The study also includes isotopic analysis of desiccated botanical materials from ancient Egyptian tombs, and contemporary samples, which indicate a higher evaporative enrichment in plant species post-high dam construction. Ethnographic samples from museum collections, predating the dams, align more closely in oxygen isotope ratios with ancient botanical specimens, suggesting historically higher relative humidity and less arid conditions. The paper aims to provide a case study based on deep-time isotopic, and archaeological data to advocate for water justice and food sustainability among native communities along the Nile River.

ABSTRACT 015

EXPLORING THE POTENTIAL OF AMINO ACID δ^2H ANALYSIS AS A FORENSIC TOOL TO IDENTIFY REGION-OF-ORIGIN

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Hydrogen isotope (δ^2H) analysis of keratinaceous bulk tissues has been used as a forensic tool to reconstruct an individual's travel history or determine their region-of-origin. Recent controlled feeding experiments on organisms ranging from bacteria to mammals hints at the potential of amino acid (AA) δ^2H analysis to trace geographic origins. We expand on a recently published dataset of human scalp hair collected from known origin individuals (n=152) across the United States to evaluate how well AA δ^2H values reflect local geography. Our ongoing project collects metadata on age, sex, travel history, dietary preferences, and δ^2H of local tap water. δ^2H values of non-essential amino acids varied by up to 200‰ among individuals, likely reflecting a greater contribution of water in their synthesis and the potential for these dispensable compounds to exchange hydrogen with body water. Alanine, glycine, and glutamic acid δ^2H values were positively correlated with that of local tap water. In contrast, δ^2H values of essential AAs were relatively invariant and weakly correlated with tap water δ^2H, likely reflecting uniformity in the isotopic composition of food sources consumed across the country because of our regionally integrated supply chains and supermarket diet. Multivariate analysis of d2H for combinations of both non-essential and essential AAs resulted in successful (70–90%) reclassification to one of four regions-of-origin. Our findings suggest that amino acid δ^2H analysis could help improve geolocation models for human and wildlife forensics by simultaneously providing information about dietary and drinking water sources of hydrogen to keratinaceous tissues.

ABSTRACT 016

ORNITHOGENIC ENRICHMENT OF THE HIGH ARCTIC MARINE COASTAL FOOD WEB

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Nitrogen stable isotope ratio ($\delta^{15}N$) is the most commonly used proxy for estimating ornithogenic enrichment of biota and ecosystems. Elevated $\delta^{15}N$ values in the vicinity of a seabird colony result from the isotopic fractionation of N with progression through the marine food web of which seabirds are the top predators (feeding on large zooplankton and fish), and after ammonia volatilization from deposited guano.

Seabirds play a key role in Arctic terrestrial ecosystems by delivering great amount of organic matter and nutrients of marine origin to the colony surroundings, thus stimulating development of extraordinarily lush and rich tundra there. Considerable fraction of these nutrients is trapped by terrestrial ecosystem but the rest returns to the sea, possibly constituting a locally important resource for the marine coastal food web near the bird cliffs. However, the exact role and importance of the ornithogenic supplies for the marine nearshore communities remains unknown.

We present results of the studies conducted in the coastal zone beneath bird cliffs at Bjørnøya and Bellsund (Svalbard). Along distance from the cliffs (between 50 and 200 m) and depth (down to 22 m) we (i) tracked changes in seabird-derived resources for marine producers by measuring sea water chemistry, (ii) followed the flow of the ornithogenic nutrients concentrated around the colonies by measuring $\delta^{15}N$ in the successive trophic levels of the coastal food web (POM, SOM, and benthic producers and consumers of different feeding modes), and (iii) depicted changes in species composition of planktonic protists, mesozooplankton, and benthic algae and invertebrates.

ABSTRACT 017

Estimating southern hemisphere humpback whale skin isotopic incorporation rates: Implications for diet assessments

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Stable isotope analysis is a powerful tool for elucidating the diet and movement patterns of free-roaming mysticetes. Drawing meaningful conclusions based on isotope data is subject to understanding species- and tissue-specific isotope parameters such as isotopic incorporation rate. Metabolically active tissues like blubber, muscle, or skin are commonly used for stable isotope analyses of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) in mysticete research. In lieu of the possibility of conducting experimental trials on captive mysticetes under controlled conditions, we aimed to estimate the isotopic incorporation rates in Southern hemisphere humpback whale (*Megaptera novaeangliae*) skin using temporal variability in their primary prey item, Antarctic krill (*Euphausia superba*). Population G humpback whales were sampled at their feeding grounds off the West Antarctic Peninsula (WAP) at three different time points (January 2019, March 2019, January 2020), and at their breeding grounds off the coast of Colombia in August 2019. Antarctic krill were also sampled in the WAP region in both years. Humpback whale skin and whole Antarctic krill $\delta^{13}C$ and $\delta^{15}N$ were analysed and a generalized additive model of temporal variability trends was fitted to estimate the mean skin isotopic incorporation rate. Our findings underscore the significance of considering tissue isotopic incorporation rates in studies using isotope data to make inferences about the diet and foraging strategies of migratory mysticetes like Southern hemisphere humpback whales.

ABSTRACT 018

THE CHESAPEAKE BAY PLUME AS A TROPHIC SUBSIDIZER OF COASTAL BENTHIC FOOD WEBS

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The Chesapeake Bay plume is an important transitional zone that transports nutrients and organic matter from the estuary onto the continental shelf. This zone has been shown to be an area of enhanced biological activity in the water column, yet the magnitude and mechanisms by which the Chesapeake Bay plume influences benthic food web structure in the inner continental shelf ecosystem is poorly understood. In this project, my objectives are to use carbon and nitrogen stable isotope composition of basal resources, benthic invertebrates, and selected juvenile fish to 1) characterize the primary sources of production in the plume system (marine, autochthonous, and (or) estuarine), and 2) estimate the contribution of these energy sources to higher trophic level productivity. Sampling for basal resources, invertebrates, and fish occurred seasonally during 2022 and 2023 at multiple stations across an inshore-offshore gradient within the Chesapeake plume using a variety of gears. All prepared samples were analyzed for $\delta^{13}C$ and $\delta^{15}N$ signatures using a continuous flow IRMS coupled with an EA. Results of basal resource analyses will be discussed in the context of Objective 1 and as a possible small-scale isoscape of the Chesapeake Bay plume. Preliminary results of higher trophic level SIA will also be summarized and related to Objective 2. Findings from this study will elucidate the spatiotemporal role of the Chesapeake Bay plume as a structuring agent of the nearshore food web and provide insight into the potential importance of plume-derived material as a trophic subsidy of benthic and pelagic food webs.

ABSTRACT 019

Assessing the prevalence and ecological consequences of habitat connectivity between Maryland’s coastal lagoonsand coastal ocean for juvenile fish

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Coastal lagoons and adjacent shallow coastal ocean areas provide nursery habitats for many species of fish. Understanding how juveniles use these habitats is important given ongoing changes in hydrodynamics, habitat availability, and environmental conditions in shallow coastal areas due to human development, dredging, and climate change. The goal of this study is to evaluate the strength of ecological connectivity between the Maryland Coastal Bays (MCBs [lagoons]) and the adjacent coastal ocean (CO), with a focus on juveniles of three species: bay anchovy (*Anchoa mitchilli*), weakfish (*Cynoscion regalis*), and silver perch (*Bairdiella chrysoura*). Fishes and epibenthic invertebrates were trawled in the summer and fall of 2009 in both habitats (<20m). All fish were identified, measured, and counted. Juvenile specimens were collected for stomach contents, condition measures, and stable isotope (SI) analyses. Using random forest classification of the SI values, individuals were classified as recent migrants or residents of the MCBs or CO, and the proportion of residents to migrants was used as a metric of connectivity. Our results suggest strong bidirectional connectivity of MCB and CO habitats for bay anchovy and weakfish during summer months, and weak, unidirectional connectivity associated with seasonal migration for silver perch. Stomach contents and SI values from the focal species were analyzed to compare how these species might be differentially utilizing these habitats. Given the ongoing development of coastal areas and limited funds to protect and enhance habitats, understanding spatial use and connectivity of nursery areas for fish communities provides valuable information for natural resource managers.

ABSTRACT 020

Quantifying benthic-pelagic coupling in the Bay of Fundy: a comparison of stomach content, bulk and compound specific

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Marine food webs are typically comprised of distinct pelagic and benthic food chains, which can be coupled by both biotic and abiotic processes. This interaction and transfer of nutrients, energy, and mass between the pelagic and benthic food chains underpins food web processes that support higher level trophic consumers. Using the Bay of Fundy in Atlantic Canada as a study system we aimed to discern the degree of connectivity within a shallow temperate system by elucidating the source and fate of organic material within the Bay. We used a combined approach of stomach content and bulk stable isotope analysis (SIA) of carbon and nitrogen, to assess the diet of 18 fish and 11 invertebrate species in the Bay. This was complemented by compound specific stable isotope analysis (CSSIA) of carbon on a subset species to estimate how benthic and pelagic resources are coupled in this ecosystem. The combined bulk stable isotope and stomach content data suggests that pelagic detritus may not be fueling the benthic food chain, in contrast to observations in other systems. However, CSSIA data highlights a pelagic contribution at the base of the benthic food chain, indicating the presence of strong coupling processes that can be traced through multiple trophic levels in the Bays' food web. The Bay has some of the largest tides globally and the movement of such a large volume of water can resuspend deposited marine sediment and microbially processed pelagically derived organic detritus. This resuspended material may account for the discrepancy between the combined stomach content and bulk SIA and CSSIA of carbon. Our study exemplifies the limitations of each of these methods alone, and their use as a combined force may be useful for providing better resolution when considering coupling in other marine systems.

ABSTRACT 021

Elucidating dietary trends of the critically endangered flapper skate (*Dipturus intermedius*) using carbon and nitrogen stable isotope analysis from fin clippings, red blood cells and blood plasma

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The Critically Endangered flapper skate (*Dipturus intermedius*) is one of the most notable predators in British marine waters. After facing decades of targeted fishing and commercial bycatch, flapper skate populations have disappeared from most of their previous distribution. Significant knowledge gaps surrounding flapper skate ecology and their interactions with prey present roadblocks for the effective conservation of the species. Understanding the dietary patterns of predators such as the flapper skate is crucial for determining the functional role these species play in their respective niches. Due to the complexities of energetic pathways in marine systems, it is difficult to quantify these roles at an ecosystem level. Stable isotope analysis is a commonly used technique in defining the flow of resources through the food web and provides an opportunity to gain insight on the diet of the highly mobile and rare flapper skate. In this study, we use $\delta^{15}N$ and $\delta^{13}C$ stable isotope values to quantify trends in resource use in terms of isotopic niche space. We found evidence to suggest flapper skate exhibit seasonal variation in diet, likely owing to mobility between foraging sites and changes in prey availability. Implications of these findings can help guide future research for identifying specific regions and prey of dietary significance to further support the ecosystems flapper skates rely upon.

ABSTRACT 022

Tracing variability in production sources fueling pelagic food webs with carbon isotope fingerprints

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Zooplankton is a key component of pelagic ecosystems, influencing global carbon export and burial. Global biogeochemical models face uncertainties in zooplankton dietary ecology, particularly the proportional contribution of fresh primary production compared to microbial secondary production. CSIA fingerprinting is ideally suited to resolving these issues. We applied unique fingerprints of amino acid $\delta^{13}C$ values among evolutionarily distinct groups of producers to quantify proportional contributions of different production sources to zooplankton and POM at Long-Term Ecological Research site Promontory of Portofino in 2023. We assessed absolute contributions of carbon sources in and their variability with depth and seasonality (summer vs. winter). All samples were dominated by microalgal and autotrophic-bacterial carbon sources, providing conclusive evidence that the zooplankton foodweb is fueled by autotrophs even at times of low production (e.g., summer). This result suggests that primary productivity remains the main source of production, emphasizing stability in the role of zooplankton in capturing newly fixed carbon production and exporting it to depth – at least in the study site. Our results conflict partly with foodweb models inferring increased microbial contributions over time, highlighting the importance of drawing on multiple lines of evidence. CSIA-derived estimates of the relative contributions of essential carbon compounds synthesized via autotrophic compared to heterotrophic microbial sources are expected to be increasingly important as global change disrupts biogeochemical pathways, potentially favoring different biosynthetic energy channels. Application of CSIA fingerprinting to all consumers also allows us to test whether changes in basal carbon cycling and molecular biosynthesis are propagated proportionally through foodwebs.

ABSTRACT 023

Characterizing the functional roles of Micronesian fishery species targeted via spearfishing

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Herbivorous fishes are critical for promoting coral reef ecosystem health and resilience. Despite this monolithic nomenclature, herbivorous fishes possess a wide range of feeding strategies that shape the benthic community structure and function of reef systems. Such feeding strategies can vary both within and among species. In Ulithi Atoll, Federated States of Micronesia, herbivorous fishes are an important protein source for local communities and are primarily caught via spearfishing. However, consistent and target-driven spearfishing may lead to the unsustainable harvest of these fishes, leading to declines in herbivory and the potential for ecosystem phase shifts. As such, understanding the functional role of herbivorous target species will provide insight into how reef ecology may respond to the growing impacts of spearfishing on fishery catch quantity and composition. In this study, we used amino acid carbon isotope fingerprinting to characterize and assess variation in the functional roles of three commonly speared species in Ulithi that have been nominally classified as “reef herbivores”: *Ctenochaetus striatus*, *Naso lituratus*, and *Chlorurus spilurus*. Isotopic fingerprinting revealed universally high reliance on macroalgal derived food chains, suggesting a similar, ecologically critical functional role of algal removal among the three species. The model also predicted high functional redundancy among all individuals, with little intraspecific, interspecific, and geographical variation in carbon sourcing. These results have important implications for predicting the ecological impact of harvesting these fishery species on reef health and will be returned to Ulithian communities with the hopes of supporting local education, reef governance, and food security.

ABSTRACT 024

Stable isotope analysis of specimens of opportunity provides baseline ecological data for elusive wildlife

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Widely dispersed, rarely encountered species are difficult to study in situ, which hinders developing effective species conservation approaches. Stable isotope analysis of specimens of opportunity provides an avenue to address knowledge gaps in elusive animal ecology. Here, we use stable isotope analysis to investigate the ecology of an elusive marine species, Stejneger's beaked whale (*Mesoplodon stejnegeri*). We analyzed opportunistically collected samples from whales stranded throughout the species' range (n=20). Whales were sampled for four tissue types (kidney, liver, muscle, and skin) with different integration timelines; however not every whale could be sampled for each tissue type. We evaluated median and mean $\delta^{13}C$ and $\delta^{15}N$ isotope values across tissue types, calculated the mean difference in isotope values between tissue type pairs pooled from all animals, and calculated intra-animal offset values between tissue type pairs. We observed low (≤1.0‰) median and mean $\delta^{13}C$ and $\delta^{15}N$ variation across tissue types. Similarly, mean offset values between paired tissue types when tissues were pooled from all animals were low ($\delta^{13}C$ =0.1–0.6‰; $\delta^{15}N$ =0.1–1‰). Intra-animal offset values between tissue pairs were also low ($\delta^{13}C$ =0.4–0.8‰; $\delta^{15}N$ =0.5–1‰). Observed low intra- and inter-individual variation suggests Stejneger's beaked whales are temporally consistent in resource and habitat use. Species that display high resource and habitat use fidelity may be particularly sensitive to environmental change, necessitating the need for collecting baseline ecological data. Our results are some of the first insights into the ecology of this highly elusive species, which will be useful in developing a scientifically grounded conservation plan.

ABSTRACT 025

Establishing the extent of migratory connectivity between moulting and non-breeding sites of a waterbird species, using bulk carbon and nitrogen stable isotope analysis of feathers

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Each year, 300,000 common shelduck (*Tadorna tadorna*) migrate cyclically between breeding, moulting and non-breeding sites within their northwest European distribution. The spatial and temporal extent of these migratory movements, and thus connectivity between sites, is uncertain. Shelduck encounter many anthropogenic obstacles during these migrations, and the lack of knowledge regarding these movements presents challenges when producing evidence based environmental impact assessments for new developments. It is particularly challenging to assess how shelduck may be impacted by offshore wind farms when traversing shelf seas. We analysed bulk carbon and nitrogen stable isotopes in 210 moulted secondary feathers, collected from the tidelines of seven of the eight known moult sites across northwest Europe. We used kernel utilisation density estimation to identify area specific isotope clusters for each of these moult sites. We then sampled feathers from non-breeding shelduck in the UK and were able to assign the stable isotope signatures of these to the moult site isotope clusters. This allowed us to establish the extent of connectivity between moulting and non-breeding sites for UK non-breeding populations of this species. The results and effectiveness of this approach will be discussed. These insights into movement and connectivity have aided our understanding of the proportion of the shelduck population that conducts migrations across northwest European shelf seas. This in turn aids us in estimating the proportion of the population that may be exposed to offshore wind farms on migration.

ABSTRACT 026

CONSIDERING DYNAMICS IN ISOTOPIC MIXING MODELS, A REQUIRED EFFORT

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The use of isotopic mixing models (MM) to estimate the diet of a consumer is common practice, but assuming isotopic equilibrium (i.e., everything is constant) within the studied system (referred to as Static MM). However, real-world scenarios rarely meet this assumption, leading to potential biases in diet estimation. To mitigate this, previous studies suggested averaging source values over the incorporation time window (ΔT) to account for isotopic sources variability (SMM_ΔT). Furthermore, a Dynamic MM capable of addressing all system dynamics was developed but only for 1 isotope and 2 sources. This study aims to generalize these models for all setups of studied isotopes and sources as well as to identify and quantify factors contributing to bias in model estimation. In-silico experiments and tests with in-situ datasets were conducted to validate the models. We formalized the bias (β), the difference between real diet and its estimation on a sampling time-window, using the time model for all three MM. Factors contributing to bias include consumer initial value (or diet switch), variability in source isotopic values, and especially the ΔT times the isotopic incorporation rate (λ). Inaccurate ΔTλ relative to general isotopic dynamics could result in biases of up to 94%, underscoring the importance of accounting for λ in MMs. Under proper ΔTλ conditions, the consumer initial value could introduce a 10% bias in static models, whereas source dynamics could lead to biases of up to 50% for SMM and 20% for SMM_ΔT. Results showed no bias in the DMM. Bias from dynamic in-situ and experimental datasets will be presented to identify bias-generating situations and produce methodological guidelines.

ABSTRACT 028

A review of the precision and accuracy of compound-specific isotope analysis of amino acids

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Compound specific stable isotope analysis of amino acids (CSIA-AA) has allowed for in-depth studies of many different physiological, ecological, and environmental phenomena. The vast information obtainable using CSIA-AA has driven the exponential growth of this field since its mainstream introduction in the early 1990s. This growth, however, has been accompanied by the development of several distinct analytical approaches. In this talk, we outline the CSIA-AA process and identify areas of its workflow with the highest potential to introduce measurement error. Through a meta-analysis of CSIA-AA publications, we found that rather than experimental application, the primary determinant of methodology lies in the geographic location of the analyst, likely reflective of the academic lineages of CSIA-AA practitioners rather than application specific method development. The relative nascency of CSIA-AA gives it incredible expansion potential, but such expansion would greatly benefit from comprehensive experimentation optimizing every portion of the analytical process. Uniform guidelines can ensure the highest achievable accuracy and precision for intra- and interlaboratory analyses, alike. The goal of this talk and its corresponding workshop are to improve data comparability and work towards the adoption of standardized methodologies that uniformly generate highly accurate, precise, and reproducible data. We make recommendations for areas that would benefit from further investigation (e.g., procedure optimization, error mitigation, and data handling methods). The creation and implementation of guidelines for optimal approaches to CSIA-AA – as has been done for applications like forensic science – can help realize the full potential of this rapidly growing field.

ABSTRACT 029

COLLAGEN TO COLLAGEN PREY-PREDATOR TROPHIC DISCRIMINATION FACTORS (Δ13C, Δ15N) IN LATE PLEISTOCENE CAVE HYENA

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The spotted hyena was an important large carnivore in Pleistocene ecosystems in Africa, Europe, and Asia. Having numerous fossil records and posing important threats and competition to early humans, the hyena is of particular interest in Quaternary studies, including isotopic paleoecology. Hyenas are obligate carnivores, adapted to crush and digest bones of their prey, and absorb organic matter from bones more efficiently than any other carnivore. This discrepancy in the nutrient resource use between hyenas and most of other carnivores leads to differences in the isotope flux and, consequently, possible variation in the $\Delta^{13}C$ and $\Delta^{15}N$ trophic discrimination factors (TDFs). The TDF is a key parameter in isotope-based estimation of the use of dietary resources by animals, particularly in mixing models used for quantitative diet reconstruction. In paleoecology, one of the most popular TDFs is prey bone collagen compared to carnivore bone collagen TDF because bones are usually the only preserved tissues. In our paper, we assess the collagen-to-collagen TDF ($\Delta^{13}C$ and $\Delta^{15}N$) for the Pleistocene cave hyena and a wide spectrum of its prey. We analyze a fossil hyena den bone accumulation in Perspektywiczna Cave (Poland). Using proteomicsto confirm the taxonomical identification, we retrieve the proportion of prey species in hyena diet. This study brings new data on this large carnivore's dietary habits and allows for more accurate use of isotopic signals in modeling the past hyena diets. The project is funded by the EU Horizon 2020 MSCA, grant agreement No 101023317.

ABSTRACT 030

Unravelling stable isotope trends with a novel host-parasite pair database

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Stable isotopes have been used infrequently over the last two decades to characterize host-parasite trophic relationships. The main reason for the scarcity of data is the lack of obvious patterns in stable isotope values of parasites versus their host tissues, which is a key to understanding any host-parasite system dynamics.

To circumvent this and to leverage the potential of stable isotopes in parasitology, we proposed at the 2021 IsoEcol conference to perform a worldwide meta-analysis on a wide range of host-parasite stable isotope data, including δ 15 N, δ 13 C and δ 34 S values. Based on a large number of host-parasite pairs collected worldwide, we hypothesised that generalizable patterns could be identified and would inform future research in the field.

After two years of collecting datasets and ready-to-analyse samples, our new database comprises 2340 entries, representing 515 unpublished parasite-host pairs. As our project concludes, we are excited to present our findings and summarise our imminent data article.

ABSTRACT 030 cont’d

ABSTRACT 031

What can plant $\delta^{13}C$, $\delta^{18}O$, $\delta^{15}N$, and $\delta^{34}S$ tell us about water and salt stress during oil sands fen reclamation?

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Alberta has over 900 km^2 of active oil mining that primarily occurs over fen peatlands. Post-extracted fens are contaminated with sodium sulphate ($NaSO_4$) and have fluctuating water tables. Although fen reclamation projects are designed for biodiversity and carbon sequestration, the main project in the region has become a near-monoculture of water sedge (*Carex aquatilis*) despite initially diverse plantings. Variation in plant cover could be caused by competition or environmental stress. We tested these hypotheses in a greenhouse experiment that manipulated salinity, water availability, and diversity using *Carex aquatilis* and Baltic rush (*Juncus balticus*). *Carex* grew best under wet-low salt conditions; Juncus grew best and out-competed *Carex* in dry-low salt conditions. Both species had lowest growth under high-salt, regardless of water availability. To identify potential mechanisms underlying growth responses, we measured $\delta^{13}C$ and $\delta^{18}O$ to integrate carbon-water metabolism, and $\delta^{15}N$ and $\delta^{34}S$ to assess nutrient and salt uptake. *Carex* leaf $\delta^{13}C$ increased with salinity while *Juncus* leaf $\delta^{13}C$ was similar across treatments except for being more depleted under wet-low salt. Leaf $\delta^{18}O$ did not vary substantially across treatments for *Carex*; *Juncus* had relatively enriched $\delta^{18}O$ in dry-high salt conditions. Leaf $\delta^{15}N$ did not vary substantially across treatments, but root $\delta^{15}N$ was relatively enriched in high salinity treatments for *Carex*. For both species, leaves and roots were relatively depleted in $\delta^{34}S$ in high-salt and enriched in wet-low salt conditions. Juncus appears more resilient than *Carex* to water limitation and salinity, possibly through tighter stomatal control and by limiting root salt uptake.

ABSTRACT 033

Multi-metric isotope tools to explore mixotrophy in coral holobionts

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Mixotrophs, with their energy source flexibility, are some of the most widespread organisms on the planet. Yet the degree of their trophic plasticity can be challenging to assess due to difficulties in quantifying carbon and nitrogen cycling in mixotrophs. We examined trophic plasticity in mixotrophic corals from shallow and mesophotic reefs in American Samoa using multiple isotope metrics: 1) Host Evaluation: Reliance on Symbionts (HERS), which quantifies the relative trophic strategy of mixotrophic holobionts (both host and symbiont) from multiple outputs of the Stable Isotope Bayesian Ellipses in R (SIBER) framework, 2) Amino Acid Carbon Isotope Fingerprinting, which calculates the relative contribution of carbon to corals from internal autotrophic symbionts, external heterotrophic plankton, and microbially-reprocessed detritus, 3) Source Amino Acid Nitrogen Index, which examine baseline nitrogen cycling dynamics fueling coral production, and 4) Trophic Position Index, which estimates the degree of autotrophy vs heterotrophy internally indexed to baseline nitrogen isotope variation using trophic and source amino acids. We found that each metric told a unique but complementary story about the sources and cycling of organic matter fueling these complex mixotrophic coral holobionts. Shallow reef *Montipora* stood out as distinct from the light-limited *Montipora* (mesophotic) and *Leptoseris* (shallow cave and mesophotic) in bulk isotope space, Phe $\delta^{15}N$ patterning, and trophic dynamics. Conversely, carbon cycling patterns aligned more by genera than light limitation. As a result, internal carbon and nitrogen exchanges between host and symbiont within the coral holobiont were not coupled and told different stories about coral mixotrophy.

ABSTRACT 034

Trophic plasticity and acclimatization of corals under contrasting water quality

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Trophic plasticity is a fundamental mechanism underpinning coral health. Scleractinian corals rely on autotrophy through their symbiosis with dinoflagellates, but they are also able to use heterotrophic feeding to supplement their energetic and metabolic needs. In particular, the ability to upregulate heterotrophy has been shown to aid coral survival during episodes of bleaching, low light, or ocean acidification. Nutritional flexibility across taxa, however, is not well understood, and it is unclear how trophic plasticity affects a species' resilience to various environmental stressors. Here, we conducted a transplantation experiment to assess coral trophic plasticity and acclimatization in response to contrasting water quality. Three genera of corals (*Acropora*, *Porites*, and *Platygyra*) were collected and transplanted to three low impact sites (LI) and three high impact (HI) sites. After six months, transplants were collected and processed for $\delta^{15}N$ and $\delta^{13}C$ stable isotope values, chlorophyll a concentration, and symbiont density. For each genus and site, Stable Isotope Bayesian Ellipses in R (SIBER) and the novel metric Host Evaluation: Reliance on Symbionts (HERS), were used to determine trophic strategy by quantifying the amount of isotopic niche overlap between paired coral hosts and symbionts. Corals from HI sites were more heterotrophic than respective genera from LI sites, and *Acropora* exhibited the greatest trophic plasticity while *Platygyra* had the largest overall host and symbiont niche separation. The results of this study elucidate differences in coral responses to changing ecosystems and provide a framework for evaluating the trophic plasticity of symbiotic organisms.

ABSTRACT 035

Integration of fatty acids and nitrogen isotopes offers a powerful biochemical framework for estimating heterotrophic nutrition in a mixotrophic coral

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Mixotrophic reef-building corals rely on nutrition from their endosymbiotic dinoflagellates and through heterotrophy (feeding) on particulate organic matter and zooplankton in the water column. Heterotrophy plays a vital role by provisioning corals with essential nutrients that aid in the resistance and recovery from thermal stress. In a warming ocean, the ability of corals to feed will likely play a role in determining the trajectory of reefs worldwide. Yet, we still have a limited understanding of heterotrophic feeding patterns of corals in the wild. To fill this knowledge gap, we conducted a feeding experiment with the common coral, *Stylophora pistillata*, in the northern Red Sea. Corals were fed along a gradient from full autotrophy to full heterotrophy using *Artemia nauplii* to validate fatty acid (FA), isotopic, and elemental biomarker responses to variations in coral nutrition. FA and isotopic biomarkers showed strong responses to heterotrophic nutrition, with 22 of 30 biomarkers changing significantly as a function of diet. We identified three essential FA biomarkers that reliably track heterotrophic nutrition into coral host tissues. Nitrogen isotope and essential fatty acid data showed clear integration into coral tissues while carbon isotope data did not correlate significantly with heterotrophy. Our data reveal that nutritional proxies based on bulk carbon isotope data alone ($\delta^{13}C$) may underestimate the contribution of heterotrophy to mixotrophic corals. These results emphasize the value of combined isotopic and FA approaches as a powerful biochemical framework for evaluating heterotrophic resource supply to corals on reefs worldwide.

ABSTRACT 036

Trophic structure of cold-water coral communities along the U.S. Atlantic and Gulf of Mexico margins

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Cold-water coral (CWC) environments depend on the flux of organic matter transported via rapid currents for energy and essential nutrients. While photosynthetically-derived particulate organic matter (POM) is a food subsidy for CWC in the U.S. mid-Atlantic canyons, trophodynamic patterns across the region remain unknown. This study expands on our previous work by examining the spatial variability and interspecific patterns in the stable isotope ($\delta^{13}C$ and $\delta^{15}N$) values of CWCs and associated species, and estimates the dominant nutritional resources across CWC environments throughout U.S. Atlantic and Gulf of Mexico regions. POM isotopic composition overlapped among coral communities, indicative of isotopic consistency in basal carbon sources. However, significant differences among feeding groups suggested spatial variability in the isotopic composition of nutritional inputs and/or in food selection by suspension feeders. Co-located corals had lower isotopic values than sponges, which may be a function of food resource use and roles of their microbiomes. Isotopic niche comparisons indicate overlapping niches across regions, suggesting consistency of isotopic composition of food resources over space and time. Potential drivers of isotope niche space include variation in terrain, including slope, profile and plan curvature, that are linked to local hydrodynamics, nutrient flow, and food supply. Results presented will include newly developed isotope maps (i.e., isoscapes), illustrating faunal isotope variability over different spatial scales and seafloor features. Isoscapes provide road maps to understanding changing food resource use by residents with changing food availability, habitat use by migratory species, and decipher complex trophic relationships in CWC ecosystems.

ABSTRACT 037

Combined in situ niche analysis and pulse-chase labelling experiments unravel energy acquisition strategies in cold-water corals

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Cold-water corals (CWCs) are reef-building foundation species occurring worldwide in the aphotic zone of the ocean. Those reefs are considered biodiversity hotspots in the deep-sea. In the absence of endogenous production, CWCs mostly depend on exported photosynthetic production for their nutrition. Energy acquisition is therefore a major challenge for CWCs. In this context, we investigated feeding habits of three syntopic CWC species forming reefs in the Lampaul Canyon (Bay of Biscay) at depths ranging from 800 to 1200 m: *Desmophyllum pertusum*, *Madrepora oculata* and *Solenosmilia variabilis*. Specifically, we tackled the following questions: 1) What is the realized trophic niche of CWCs in the Lampaul Canyon?; 2) Do the three species rely on the same resources?; and 3) Are the trophic niches of CWCs overlapping with those of associated fauna, particularly suspension feeders?

Joint carbon, nitrogen and sulfur stable isotope analysis showed that CWCexhibit marked resource segregation with associated fauna. However, coral niches largely overlapped. Species-specific trends in niche size were present, suggesting variable trophic diversity. Fatty acid analysis highlighted the importance of zooplankton for CWC feeding, which could favor this resource for its high nutritional value. Furthermore, pulse-chase experiments in pressurized tanks suggested that all species are, to some extent, able to function as holobionts. They notably obtain part of their nitrogen from mutualistic relationships with the microbiome living in the mucus secreted by the polyps. Ultimately, reliance upon these multiple, non-mutually exclusive ecological mechanisms could be a key factor to facilitate CWCs future survival under changing environmental conditions.

ABSTRACT 038

How seabird-derived nitrogen influences the nitrogen cycling in coral reefs through time: A case study from Surprise Island in New Caledonia

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Seabirds transfer nitrogen (N) from the ocean to their nesting sites into adjacent reefs through guano. This transfer provides nitrogen to the reef while enhancing the productivity, biomass and functioning of the recipient ecosystems. Invasive rodents can significantly impact and decrease seabird populations, through direct predation or habitat modification, therefore reducing nitrogen supply to reefs. Potentially, reef productivity, biomass, and functioning are lower near rat-infested islands, highlighting the importance of rat control as a crucial component of coral reef conservation and restoration.

The timescales for the rebound of guano-N supply, and subsequent change in the coastal N-cycle, after rat removal events, are currently unknown. This study explores the N-cycle through time by examining the nitrogen trapped inside a coral skeleton. As the coral grows and produces its skeleton, nitrogen is trapped inside the organic matrix, reflecting the isotopic composition of nitrate NO_3^--$\delta^{15}N$ at the time of growth, at a monthly resolution, while protecting it from degradation.

Preliminary results suggest that coral skeleton $\delta^{15}N$ does record seabird derived-N, and that it is a powerful tool to reconstruct the history of this N supply to the reef. Here, we explore the historical variability of guano input into a coral ecosystem after a rat eradication event in 2005 by analyzing the *Porites* CS-$\delta^{15}N$ at Surprise Island (New Caledonia) in the past 20 years and address the questions: Does rat eradication on seabird islands influence N enrichment processes in adjacent coral reefs? What are the timescales for the return of guano-nitrogen into corals?

ABSTRACT 039

Estimated maternal isotopic niche in southern bluefin tuna larvae (*Thunnus maccoyii*) influence growth variability in the Eastern Indian Ocean

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Southern bluefin tuna (Thunnus maccoyii, SBT) is a commercially important highly migratory species widely distributed in temperate regions of the Southern Hemisphere with one known spawning ground in the eastern Indian Ocean. Larvae were sampled during an oceanographic survey (January-March 2022), as part of the 2nd International Indian Ocean (IO) Expedition, coinciding with the SBT spawning peak. SBT larvae were identified according to morphological, meristic and pigmentation characteristics and integrated with genetic identification. An isotopic maternal transmission model developed using aquaculturally reared Atlantic bluefin tuna larvae was used to generate estimates of maternal nitrogen and carbon isotopic signatures from values measured in SBT pre-flexion larvae. SBT maternal isotopic niche widths were estimated by stable isotope Bayesian ellipses in R-software (SIBER package) and by Kernel utilization density (rKIN package) from pre-flexion larval isotopes in relation to their specific growth curve. Results are discussed in terms of daily growth variability and compared with other top predator larvae to assess

species-specific differences, from generalist to selective trophic behaviors. This pioneering methodology determines maternal (transgenerational) influences on larval survival, growth and condition with direct effects on recruitment, which is necessary for understanding how larvae respond to varying spatio-temporal dynamics in their environment and identify quality SBT nursery habitat characteristics in the IO. This study was funded by INDITUN project PID2021/122862NB/100 MCIN/AEI/10.13039/501100011033 (UE-FEDER) and BLOOFINZ-IO (USA-NSF).

ABSTRACT 039 cont’d

ABSTRACT 040

Stable isotopes analyses as trophodynamics tracers in Southern bluefin tuna (*Thunnus maccoyii*) larvae in the Eastern Indian Ocean

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The present study uses stable isotopes of nitrogen and carbon ($\delta^{15}N$ and $\delta^{13}C$) as trophic indicators for larvae of Southern bluefin tuna (*Thunnus maccoyii*, SBT). SBT is a commercially significant, highly migratory species found throughout temperate regions of the Southern Hemisphere, with only one known spawning ground in the eastern Indian Ocean (IO). Larvae and zooplankton were collected during the spawning peak, from January to March 2022, in an oceanographic survey conducted as part of the 2nd International Indian Ocean Expedition. SBT larvae were identified according to morphological, meristic and pigmentation characters, integrated with genetic identification. SBT isotopic niche widths were estimated by stable isotope Bayesian ellipses in R-software (SIBER package) and by Kernel utilization density (rKIN package) from nitrogen and carbon isotopes values analyzed in postflexion larvae. SBT trophic position value was estimated by means of both frequentist model and tRophicPosition package Bayesian model (Markov Chain Monte Carlo simulations) at both individual and population levels, using the microzooplankton fraction (55-200 μm) as isotopic baseline for primary consumers. The results are discussed in terms of larval daily growth variability and compared with larvae of other top predators in the region to evaluate species-specific distinctions. Understanding the relationship between growth and trophodynamics is essential for comprehending how larvae respond to spatio-temporal environmental dynamics, and to identify key features associated with quality SBT nursery habitat in the IO.

This study was funded by INDITUN project PID2021/122862NB/100 MCIN/AEI/10.13039/501100011033 (UE-FEDER) and BLOOFINZ-IO (USA-NSF).

ABSTRACT 040 cont’d

ABSTRACT 041

Partitioning the sources of sediment organic carbon in South African seagrass meadows

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In seagrass sediments, allochthonous carbon sources account for 50 – 90% of the sediment organic carbon (SOC), where non-seagrass carbon is derived from external organic matter (OM) advected into the meadow sediments or trapped by the seagrass canopy. Identifying the SOC origin is essential to ensure the accurate estimation of the climate change mitigation potential of seagrass ecosystems, as greenhouse gas (GHG) accounting protocol requires climate change mitigation estimates to exclude allochthonous carbon, yet the ratio of allochthonous to autochthonous SOC in South African seagrass populations has not been investigated. In this study, we measured the SOC and $\delta^{13}C$ ratios in *Zostera capensis* seagrass meadows in the Berg River and Breede River estuaries and applied Bayesian mixing models to disentangle the SOC contributory sources. Sediment organic carbon differed not only between estuaries, but also revealed intra-estuarine variation, with autochthonous carbon accounting between 35 ± 0.23% (SE) and 42.3 ± 0.18 % of total meadow SOC. Other sources of SOC included saltmarsh, macroalgae, reed and grass species. Our work highlights the importance of accounting for allochthonous carbon in disentangling the drivers of high carbon stock variability in estuarine environments and contributes to improving the accuracy of South African seagrass carbon stock estimates in global GHG abatement schemes.

ABSTRACT 042

Using carbon isotope analysis of essential amino acids to reveal the importance of kelp-derived energy for rocky reef food webs and consequences of kelp forest decline in the Gulf of Maine

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Kelp forests support productive communities across many temperate coastlines; however, ecological linkages between kelp and consumers in the North Atlantic have not been quantified. As this region warms and its kelp forests collapse into red algal turf reefs, the consequences for local food webs remain unknown. Here, we measure carbon isotope ratios of essential amino acids ($\delta^{13}C_{EAA}$) to assess whether consumers on Gulf of Maine reefs utilize kelp-derived energy. Sampling across a habitat gradient from healthy kelp forests to degraded turf reefs, we assess how energy flow through food webs changes with kelp decline. First, we measured $\delta^{13}C_{EAA}$ values for local primary producers (n=44) including kelps, red algae, and particulate organic material. Using linear discriminant analysis, we found that kelp $\delta^{13}C_{EAA}$ values are distinct from those of phytoplankton and red algae with an 89% reclassification rate, enabling us to trace energy flow from producers to consumers. Next, we measured $\delta^{13}C_{EAA}$ values of secondary consumers (two abundant reef fishes; n=67) from both kelp forest and turf reef habitats. These data suggest that fishes living in kelp forests utilize kelp-derived energy to a high degree, and that each species adapts to the decline of a kelp-based energy channel in different ways. The $\delta^{13}C_{EAA}$ values of nearshore invertebrate grazers and filter feeders (n=19) shed light on mechanisms by which kelp-derived energy may enter food webs. This study demonstrates that kelps provide key energetic resources to consumer communities, and reveals a mechanism by which kelp forest collapse alters energy flow through coastal food webs.

ABSTRACT 043

THE TROPHIC ECOLOGY OF NORWEGIAN FJORD COMMUNITIES AND FOOD WEB RESPONSES TO OXYGEN LOSS AND INCREASING JELLYFISH BIOMASS

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Decreases in dissolved oxygen and increases in jellyfish biomass are two global phenomena that have recently been observed in multiple marine systems and are hypothesized to be related to anthropogenic drivers including climate change and eutrophication. However, our understanding of how these changes affect trophic relationships within an ecosystem is still limited. Between 2011-2018, the western Norwegian fjord, Masfjord, experienced a period of rapid deoxygenation followed by a deep-water oxygen renewal event in 2021. Meanwhile, the biomass of the deep-sea jellyfish, *Periphylla periphylla*, began to rapidly expand in Masfjord in 2018 and has remained at high levels. In this study, we use community composition and stable isotope data to examine how oxygen loss and increasing jellyfish biomass affect the trophic ecology of Masfjord. First, we describe the trophic structure of the fjord community by analyzing tissue samples of 329 individuals from 39 representative mesopelagic, demersal, and benthic species from Masfjord and surrounding fjords for $\delta^{13}C$ and $\delta^{15}N$. We find clear separation in $\delta^{13}C$ and $\delta^{15}N$ signatures of species feeding on benthic versus pelagic resources, find that diel vertical migrators occupy an important intermediate trophic position in the fjord food web, and find that *P. periphylla* occupies a distinct trophic niche from other jellyfish. Changes in the community composition of Masfjord are assessed using a 12-year (2011-2022) depth-stratified time series. By combining stable isotope and community data, we provide the first insights into how changes in oxygen and jellyfish biomass impact the biomass trophic spectra of deep-sea marine communities.

ABSTRACT 044

Reconstructing seasonal changes in phytoplankton community composition using carbon isotope

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The Northwest Atlantic Ocean off Nova Scotia is undergoing some of the most rapid warming of any ocean region on Earth. To better predict how this warming will affect future marine productivity patterns, we need better paleo-proxy data from the past. Recently, compound-specific isotope analysis of carbon-13 in amino acids (δ^{13}C-AA) has been shown to differentiate among phylogenetically different groups of microalgae, for example, diatoms, dinoflagellates, and cyanobacteria. These δ^{13}C-AA fingerprints are well preserved in organic archives like marine sediments and annually-banded corals, thus opening up the possibility of tracking long-term changes in phytoplankton community compositions over climate-relevant timescales. However, the ability of δ^{13}C-AA to track proportional abundances of different microalgae groups within natural phytoplankton communities has not been fully tested. We collected samples of filtered POM from the Northwest Arm in Halifax, Canada, over a seasonal phytoplankton bloom in 2024 to test whether the seasonal transition from large-cell, diatom-based production in spring to small-cell, flagellate-based production in summer is reflected in δ^{13}C-AA signatures of seawater filtrates. Preliminary results from the spring 2024 plankton bloom season will be presented.

ABSTRACT 045

EVIDENCE OF CAPITAL BREEDING IN LOGGERHEAD SEA TURTLES USING COMPOUND-SPECIFIC ISOTOPE ANALYSIS

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Reproduction requires substantial investment of nutritional resources, and as a result, most sea turtle species do not nest annually. Reproductive investments have long thought to be financed from stored resources in sea turtles, and early studies classified them as capital breeders. A growing body of evidence suggests that sea turtles may be more plastic in their ability to rely on energy acquired during the reproductive period. However, the evidence is mixed and not always clear in establishing whether foraging occurs and if acquired nutrients are routed to the production of eggs. We address two objectives in a nesting population of loggerhead turtles to answer a longstanding question of where sea turtles fall on the capital vs. income breeding spectrum. First, we assess whether loggerheads fast during the nesting season. Second, we assess the source of nutritional allocations to the proteins in egg yolk and albumen. Samples of nesting female plasma and eggs (yolk and albumen) were collected at Wassaw Island, Georgia. Additionally, plasma was obtained from juvenile and adult loggerheads in the coastal waters off the coast of South Carolina and Georgia to represent foraging individuals. Amino acid carbon and nitrogen isotope analysis revealed that females were likely not feeding during the nesting season. Additionally, multivariate analysis of amino acid isotope data indicated that the nutritional allocations to yolk and albumen were similar, likely lipid-derived, and effectively differentiated plasma from egg components. This approach provides a promising method for determining the nutritional status of reproduction in sea turtles.

ABSTRACT 046

Integration of pelagic and benthic sources reflected in the stable isotopic signatures of coastal juvenile fish (age 0 and age 1 Atlantic cod)

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The complex nature of eelgrass beds makes them a prime nursery habitat for juvenile fish including Atlantic cod. These areas of high productivity provide shelter from predators following settlement and are an important link between the early life of juvenile Atlantic cod and their successful recruitment to adult populations. We used multiple isotopes ($\delta^{13}C$, $\delta^{15}N$ and $\delta^{34}S$) to track changes in feeding behaviour of juvenile Atlantic cod (age 0 and age 1) collected from eelgrass habitats along the northeast coast of Newfoundland, Canada over a two year period. Shifts in isotopic signatures indicate a continuous shift from the time they enter the eelgrass habitat through the year. The isotopic signatures of newly settled age 0 cod reflect a pelagic zooplankton-based diet, but the integration of benthic material in their diet is reflected by small shifts in $\delta^{13}C$ and $\delta^{34}S$ and a slight increase in trophic level over the summer/fall period. Juvenile cod are expected to spend their first winter in these inshore areas, and by spring age 1 fish exhibit more pronounced shifts in isotopic signatures and were generally isotopically distinct from co-habiting age 0 fish. While $\delta^{15}N$ values plateaued in spring, age 1 juveniles exhibited large increases in $\delta^{13}C$ (~+3‰) and decreases in $\delta^{34}S$ values (~-5‰). The range of values observed for age 1 fish varied between years which reflected changes in availability of prey. Comparing different cohorts and areas along the coast; however, indicates that the same trends are present across years and larger spatial scales.

ABSTRACT 047

Host Isotopic Composition and the Microbiome

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The holobiont concept in biology is increasingly used as a paradigm to assess the impact of the microbiome on a host organism.[1] Caution regarding the evolutionary constraints on a host and its microbiome has led to a description of the system as “an ecosystem on a leash”.[2] This study utilizes gnotobiotic (germ-free) mice and conventionalized control mice to examine the impact of the microbiome on four natural abundance isotopic systems (carbon, nitrogen, hydrogen and oxygen) in a number of tissues and gut contents. The leash of the host seems particularly strong in relation to carbon and nitrogen isotopes in all tissues where no differences are observed between groups of mice. The efficiency of host digestion in the upper portion of the GI tract accounts for the isotopic identity among the animal tissue. Compound specific amino acid $\delta^{15}N$ of cecal contents vary between germ free and conventionalized mice and illustrate both the impact of microbes and the inclusion of the gut wall in fecal matter. Oxygen isotopes are significantly different between groups in number of tissues, including the liver and bone carbonate, reflecting differences in the metabolic rate of germ-free vs conventionalized animals. Hydrogen isotopes continue to reveal differences in the just weaned animals that was noted in previous work on human teeth.

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ABSTRACT 048

The role of the gut microbiome in supplying essential amino acids to granivorous rodents in the Chihuahuan Desert, New Mexico

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The mammalian gut contains an incredibly diverse community of microbes that directly affect host fitness, immunity, and development. For example, the gut microbiome converts recalcitrant dietary molecules (e.g., cellulose) into compounds that are more easily metabolized or assimilated (e.g., short-chained fatty acids) by the host. Recent laboratory and field experiments have shown that gut microbes synthesize and supply essential amino acids (AA_{ESS}) to help their hosts maintain protein balance. Although there are limited studies for wild mammals, emerging isotopic evidence suggests herbivores and omnivores faced with seasonal or persistent protein limitation assimilate AA_{ESS} synthesized by gut microbes. We use carbon isotope ($\delta^{13}C$) analysis of AA_{ESS} in red blood cells from granivorous desert rodents (*Dipodomys*) to quantify seasonal and annual variation in the relative contributions of AA_{ESS} derived from gut microbes versus dietary plant sources. We present data for 24 individuals that were captured at least three separate times across three consecutive years (2021-2023). Our preliminary findings suggest rodents assimilate greater proportions of AA_{ESS} from C_4 plants (e.g., grasses) in years with higher C_4 seed production and greater proportions of AA_{ESS} from gut microbes during seasons and years with less C_4 seed production. Future work incorporating 16S rRNA gene sequencing will allow us to characterize how the composition and function of the mammalian gut microbiome interact with variation in primary production to influence host protein metabolism.

ABSTRACT 049

Impacts of plant phenology on desert rodent foraging strategies

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Foraging is a fundamental aspect of animal ecology with direct consequences for body condition, reproduction, and, ultimately, survival. Traditionally, specialist versus generalist foraging strategies have been defined at the population level, however an increasing number of studies have found that individual variation in foraging strategies might be key to understanding how rodents interact with resource landscapes. We investigated how individual diet specialization among seed-caching granivores in the family *Heteromyidae* responded to variation in seasonal phenology of plant fruiting in the northern Chihuahuan Desert. We measured blood plasma carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope values for animals that were captured more than three times per season (n=563) from 2013-2023 to calculate individual diet specialization using a relative individual niche index (RINI) metric. We then calculated resource diversity and availability using monthly plant phenology data. Using these data, we evaluated the interactions of seasonal fruiting plant richness, fruit biomass estimates, phenotypic diversity, and inter/intra-specific competitors on RINI. In agreement with theoretical predictions, preliminary results suggest that intraspecific competition yields a higher prevalence of individual diet specialization, while greater interspecific competition results in more generalist diets. Conversely, there was no significant effect of fruiting plant richness on RINI, suggesting more research on individual caching behavior (caching style, hoard size/composition) may be required to untangle the impacts of resource landscapes on desert rodent foraging strategies.

ABSTRACT 050

Tracing aquatic and terrestrial origins of fatty acids to aerial insectivorous birds: insights from bulk and compound-specific stable isotope analyses

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Fatty acids are vital for the development, growth, and health of young birds. Beneficial fatty acids such as long-chain omega-3 highly unsaturated fatty acids (LC-HUFA) may be acquired through diet and possibly internally synthesized. We used δ^2H measurements of tail feathers and fatty acid profiles of blood plasma of nestlings to investigate terrestrial versus aquatic origins of diets of purple martin (*Progne subis*), tree swallow (*Tachycineta bicolor*), and barn swallow (*Hirundo rustica*) nestlings in southern Ontario, Canada. We expected lower tissue δ^2H values to indicate higher inputs of aquatically derived prey. Compared to barn swallows, purple martin and tree swallows had greater inputs of aquatically derived prey and lakeshore birds had higher omega-3 fatty acid levels in their blood plasma compared to inland nestlings. Barn swallows had highest feather δ^2H values and also the highest plasma omega-3 docosahexaenoic acid (DHA), possibly converted from its more readily available short-chain precursor. Following these findings, we fed barn swallow and purple martin nestlings a ^{13}C labeled omega-3 or omega-6 oil to track internal fatty acid synthesis. Using δ^{13}C compound-specific stable isotope analysis, we concluded that both barn swallows and purple martins can synthesize their own omega-3 and -6 LC-HUFAs and that omega-3 conversion efficiency was higher than previously reported for riparian tree swallows. By combining fatty acid with bulk and compound-specific stable isotope techniques it is possible to disentangle complex nutritional dynamics among sympatric species.

ABSTRACT 051

Native trees provide more essential amino acids to macroinvertebrate consumers than nonnative trees in a large arid land river

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The coupling of “fast” and “slow” energy channels is known to confer food web stability across a variety of ecosystems. In river food webs, this energetic coupling can be met with nutrient-rich “fast” autochthonous (algal) and recalcitrant “slow” allochthonous (terrestrial) resources. Additionally, microbial biofilms may enhance the nutritional quality of allochthonous resources for macroinvertebrate consumers, potentially facilitating trophic linkages within slow energy channels. We used essential amino acid (AA_{ESS}) carbon isotope ($\delta^{13}C$) analysis to quantify proportional contributions of AA_{ESS} derived from algae, terrestrial plants, and microbes to macroinvertebrates across a series of mesocosm and in-situ leaf pack experiments in the middle Rio Grande of central New Mexico, USA. In our 12-week mesocosm experiments, we found that leaves of native cottonwood trees (*Populus fremontii wislizeni*) contributed greater mean proportions of AA_{ESS} (40.9–81.1%) to Chironomidae larvae than those of nonnative Russian olive trees (*Elaeagnus angustifolia*; 18.0–50.3%). We also found that microbial biofilms were notable sources of AAESS to macroinvertebrates inhabiting native grass (*Sporobolus contractus*) leaf packs (7.6–25.6%). Our in-situ experiments demonstrated variation in allochthonous resource use across macroinvertebrate taxa, where Chironomidae larvae assimilated the greatest mean proportions of AA_{ESS} from native cottonwood leaves (36.4–65.1%) and Ephemeroptera and Trichoptera larvae obtained the majority of their AA_{ESS} from algae (81.7–94.1%). Our work suggests native plants are more palatable sources of AA_{ESS} to local macroinvertebrates and highlights the potential widespread impacts nonnative plants may exert on river food webs across western North America, where nonnative plants often dominate riparian habitats.

ABSTRACT 052

VARIATION IN STABLE CARBON ISOTOPES OF FATTY ACIDS WITH SEASONAL AND SEX DIFFERENCES IN GREY SEAL (*HALICHOERUS GRYPUS)* DIET

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Marine predator diets provide essential information on trophic relationships and the overall structure and function of marine ecosystems. Inherent difficulties and limitations of observing foraging behaviour to determine diet of aquatic species has led to the development and use of indirect methods using biomarker approaches, such as fatty acid (FA) and stable isotope analysis. Analyses of both FA profiles and bulk stable carbon and nitrogen isotopes have been applied to evaluate grey deal diets in the past; however, both techniques are limited due to alternations in the dietary markers made by the predator before and after incorporation into tissues. Here, we present a novel approach of examining predator diet using FA carbon isotopes as the basis of a new biomarker estimation technique. Recent findings indicate that carbon isotopes ($\delta^{13}C$) of specific polyunsaturated FA are not modified when assimilated into storage tissues, thus combating the major limitation of both the FA and bulk stable isotope methods when used alone. This technique will be applied to the grey seal (*Halichoerus grypus*), a significant marine predator from the Northwest Atlantic (NWA). Recent (2023-2024) and archived (2000) blubber samples will be evaluated for their $\delta^{13}C$ values in individual FA, to characterize diet variations across years, seasons (n=66), and sexes (n=132). This research will address knowledge gaps in grey seal diet in the NWA to understand trophic relationships and ultimately will help to evaluate the impacts of grey seals on commercially important fisheries stocks.

ABSTRACT 053

ISOTOPIC DISSECTION OF THE DOGFISH *MUSTELUS CANIS* AND *SQUALUS ACANTHIAS*: EXPLORATION OF NOVEL TISSUES AND MATERNAL-PUP RELATIONSHIPS

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Stable isotope analysis (SIA) has greatly increased understanding of the trophic ecology of elasmobranchs and their ecosystem roles. Here, we seek to further understand the influence of elasmobranch physiology on the utility of SIA of these important consumers. Traditional tissues (muscle, fin, and liver) along with some novel tissues (brain and heart) were dissected from two species of dogfish, *Mustelus canis* and *Squalus acanthias*, and subjected to both bulk and compound specific isotope analysis of amino acids (CSIA-AA). Traditional tissues were also extracted from five well-developed fetuses and their two mothers. Inter-tissue relationships were assessed on both a broad (bulk) and fine scale (CSIA) to validate nutrient or amino acid sources among tissues of individuals and during prenatal development. Interestingly, maternal-pup amino acid nitrogen isotope differences varied depending on uterine location and carbon ‘source’ amino acids differed between mothers and pups but not between the two pup cohorts. Tissue-specific trophic level calculations show the possibility to determine ontogenetic trophic changes across time within the same individual by analysing multiple tissues with different turnover rates.

ABSTRACT 054

Position Specific Isotope Analysis (PSIA) of Amino Acids — Extracting the Highest Resolution ^{13}C / ^{12}C Isotope Records from Biosphere Samples

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The fundamental isotope information in biosphere samples is recorded is at the level of individual atoms or positions within molecules, not at the bulk or individual compound levels which average the position-level information. Advances in automation are accessing this highest resolution, atomic-level $^{13}C/^{12}C$ data via position specific isotope analysis (PSIA). Here we summarize technical developments and results from a decade of PSIA research into amino acids.

Using the reaction with ninhydrin to quantitatively cleave the C1 carboxyl group from pure amino acids, we successfully validated online results against off-line results. The online ninhydrin reaction gave very precise results for individual amino acid reference materials (0.05 ‰ or better SD). We next separated amino acid mixtures by HPLC, finding that peak integration and baseline assignments were critical to obtaining reproducible results. Analysis of several mammalian samples showed amino acids were, unsurprisingly, recording isotopic information from diet but also, remarkably, the metabolic response to diet. Using the new HPLC-PSIA system, we studied metabolic patterns across food webs, estimating comparative growth rates and glucose sources for humans, ungulates, whales, fish and invertebrates. Work in progress concerns isotope indicators of disease metabolism.

Our research measured the isotopic composition of carboxyl C1 carbons of amino acids, but not the other positions that constitute most (75%) of amino acid carbon. Robust $^{13}C/^{12}C$ predictions for all the carbon positions in amino acids may be possible using a combination of current technologies, including PSIA, CSIA (compound specific isotope analysis), and tracer addition experiments with metabolic flux analysis.

ABSTRACT 055

Bulk and amino acid $\delta^{13}C$ and $\delta^{15}N$ reveal foraging strategies of California Sea lions during a harmful algae bloom: Implication for mass strandings

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Neurotoxic domoic acid (DA)-producing *Pseudo-nitzschia* spp. blooms are increasing in severity and frequency along the California coast, and have induced mass mortality/stranding events of California Sea Lions (CSL; *Zalophus californianus*). We performed postmortem examinations, stomach content analysis, DA quantification, and $\delta^{13}C$ and $\delta^{15}N$ stable isotope analyses (SIA) in bulk tissue and compound specific SIA of amino acids (CSIA-AAs) on well-preserved dead CSLs and their prey. Strandings occurred along California beaches during spring 2022. SIA was quantified in liver for CSL and muscle for squid. A total of 677 intact market squid (*Doryteuthis opalescens*) were recovered from 10 CSL stomachs with similar size range (mean mantle length = 10.54 cm±1.03). Standard ellipse area (SEA) estimates suggest that CSLs behaved as specialists during their last days of life, while market squid were opportunistic consumers. AAs $\delta^{13}C$ and $\delta^{15}N$ values for both predator and prey revealed moderate variation in trophic proxies ($\delta^{15}N_{Tro\text{-}Src}$) and foraging sites ($\delta^{13}C_{E.AAs[Ile,\ Leu,\ Phe,\ Val]).}$ DA measurements indicate higher DA levels in CSL feces than gastric juice and prey tissue samples, indicating low DA concentrations in prey. While stomach content and SIA bulk placed CSL and squid in the same geographic area for the last days of life, CSIA-AA provided further details. The lower $\delta^{13}C_{E.AAs}$ values suggest squid cohorts were migrating from offshore towards the CSL foraging area. Our multidisciplinary approach suggests DA-intoxication was likely not the cause of death, but perhaps underwater entrapment during fisheries operations.

ABSTRACT 056

Lipid origins and dynamics of the migratory monarch butterfly (*Danaus plexippus*): New perspectives using compound specific stable isotopic (^{2}H and ^{13}C) analysis of essential and non-essential fatty acids

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Annual migration is a challenging aspect of the life history of many insects. In North America, the eastern populations of the monarch butterfly (*Danaus plexippus*) are iconic migrants. These monarchs traverse up to 4000 km to overwinter in high-altitude Oyamel fir (*Abies religiosa*) colonies of central Mexico. However, their migratory phenomenon is threatened by habitat loss, pesticides, pathogens, and climatic changes. A crucial, but poorly understood, aspect of monarch migration is where and how they acquire lipids that fuel their migratory movements and sustain a 3-month overwinter fast. Using compound-specific stable isotopic (^{2}H and ^{13}C) analyses (CSIA) we aim to determine, for the first time, the spatial origins of lipids in resident, migrating, and overwintering monarchs. Preliminary δ^2H analysis comparing wing chitin (proxy for natal origin) and fatty acids in heads of overwintering monarchs (collected December to February 2022/2023) showed no link between non-essential fatty acids and the natal origin of surviving monarchs. However, alpha-linolenic acid (ALA) δ^2H values correlated (R^2= 0.65-0.82) with wing δ^2H values, reflecting retention of this essential fatty acid from the natal site across fall migration and overwintering use. Some non-essential fatty acid δ^2H values declined in February compared to the previous month despite lipid mass fractions remaining consistent, suggesting potential biosynthesis of fatty acids from local nectar feeding at the overwintering grounds before remigration. Further CSIA aims to establish baseline isotopic mapping of monarch lipids across North America to allow more precise inferences on the source of nonessential fatty acids accumulated during the migratory period.

ABSTRACT 057

Isotope Geolocation of the Defoliating Spruce Budworm in the Boreal Forest: Testing the transmission of isotopes from trees to insect wings

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The eastern spruce budworm moth (Choristoneura fumiferana) is the most severe pest in North American boreal forests, substantially defoliating spruce and fir stands. Repeated outbreaks every 30-40 years, lead to adverse socio-economic effects, heightened risk of forest fires, increased CO2 emissions, and diminished carbon capture capacity. Outbreaks are believed to stem from irregular migrations events of large swarms of gravid moths traveling long distances from their original sites to colonize new areas.

Isotopes offer an effective approach for tracking the migration and population interconnectivity of insect species, but the relationships between the isotopic composition of spruce budworm moths and their host plants under different environmental conditions remains uncertain. We aim to explore the cycling of hydrogen, carbon, nitrogen, sulfur, and strontium isotopes from host trees to moths, to assess the possibility in applying those isotopes for provenance. In collaboration with National Resources Canada, we conducted field rearing experiments raising spruce budworms on selected trees across Eastern Canada, representing diverse environmental, climatic, and geological conditions. We measured hydrogen, carbon, nitrogen, sulfur, and strontium isotopes on the tissues of adult moths raised in field conditions as well as on their host tree; and found strong correlations between the tree and moth isotope composition. This demonstrates that several isotopes transmit from host trees to moths in a predictable manner, particularly sulfur and strontium. This research lays the foundation for utilizing multi-isotope geolocation to track the migration of spruce budworm throughout eastern Canada, advancing our comprehension of the pest's ecology and enhancing management approaches.

ABSTRACT 058

Reconstructing historical ecology of North Pacific transient killer whales using stable isotope analysis

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Populations of transient killer whales (KWs; *Orcinus orca*) along the west coast of North America occupy different habitats, as evidenced by transients in central California that rarely venture north (hereafter ‘CA’) and transients that range from Alaska through Oregon and occasionally California (hereafter ‘AK’). We aimed to characterize the long-term diet of KWs from CA and AK and address a long-standing hypothesis that AK-KW predation contributed to marine mammal declines in the Bering Sea over the last century.

We used stable isotope analysis of KW teeth from both CA and AK populations to reconstruct transient KW diets and understand their ecosystem impacts. We bisected 42 teeth and counted their annual growth layers to determine individual KW ages. We sampled dentin from every 3rd year to create a longitudinal dataset of the bulk (n = 299) and compound-specific (n = 30) $\delta^{13}C$ and $\delta^{15}N$ values from KWs over approximately 150 years to address potential: 1) population-wide shifts in KW diet over time, 2) ontogenetic shifts in KW diets, and 3) ecosystem impacts of KW predation.

We found that both populations of KWs had similar isotopic profiles overall and consisted of individual specialists. We detected a significant difference in AK-KW $\delta^{15}N$ values over time, suggesting their diet choices could have contributed to the declines of Bering Sea marine mammals. In contrast, CA-KW $\delta^{15}N$ values did not vary with time, but there were significant ontogenetic changes in their diets. Our framework provides insight into the long-term ecology of two transient KW populations.

ABSTRACT 059

Identifying the Geographic Origins of Kingston's Irish Emigrant Typhus Victims Using C, N, S, Sr Stable Isotope Analysis

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This ongoing research is conducted following the 2021-2022 ASI exhumation of typhus victims buried at Kingston Health Sciences Centre. These remains were part of a larger mass grave containing the remains of Irish Great Famine immigrants. The aim of this research is to identify the probable geographic origin in Ireland for each of the 38 individuals included in this analysis. Strontium ($^{87}Sr/^{86}Sr$) and sulfur ($\delta^{34}S$) isotope analyses are well suited to address such questions regarding residential mobility. Ireland has two well studied isoscapes (for $\delta^{34}S$ and $^{87}Sr/^{86}Sr$) that vary independently of one another. By identifying isotope ratios incorporated into the immigrants' teeth, these data can be compared to an overlay of these two isoscapes. With the addition of contextual dietary clues provided by $\delta^{13}C$ and $\delta^{15}N$ data to this comparison, it is possible to positively identify, or rule out, their place or origin. This study implements incremental enamel and dentin samples to track dietary or migratory changes throughout an individual's childhood. Children were much more mobile in their childhood than adults, and immigrants to Canada were of incredibly diverse geographic origins within Ireland, much more than originally assumed through interpretation of historical evidence.

ABSTRACT 060

Geographic relationships between human tooth enamel and tap water $\delta^{18}O$ values

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Although there is a strong, fundamental expectation that $\delta^{18}O$ values in drinking water and animal tissues covary over space-time, isotopic geolocation methods – whether for ecological, archaeological, or forensic studies – still require reference data verifying and quantifying this relationship. We explore how variations in research design and sampling affect the relationship estimated between human tooth enamel and drinking water $\delta^{18}O$ values, and how this affects isoscape predictions.

Previously published tooth enamel $\delta^{18}O$ data from North America demonstrate a robust relationship between local tap water and tooth enamel (n=515, R^2=0.43). Substantial differences in methodology exist among studies, however, and limiting our analysis to data from the single largest study (which also reduced geographic extent) produces a dramatic increase in R^2 (n=178 , R2=0.71). Culling the dataset to remove individuals who lived in multiple locations during the period of tooth formation further improved this relationship (n=118, R^2=0.85).

Our results suggest that inter-study variation in sample preparation and research design are barriers to isoscape development and application. Using the model including all data and a 95% confidence level for sample assignment, a user could generally exclude ~30% of North America as the origin of a tooth sample. The same analysis conducted using the strongest model would allow exclusion of ~60% of the contiguous United States, offering much greater forensic utility. The remarkably strong relationship in the vetted dataset reinforces the primacy of drinking water as the source of $\delta^{18}O$ variation in modern human bodies.

ABSTRACT 061

Triple-oxygen isotope analysis reveals how migratory songbirds derive water in the desert heat

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Each fall, billions of migratory birds cross through the Sonoran, Mojave, and Chihuahuan deserts during their southward migration on their way to wintering grounds in Mexico and Central America. These habitats are drastically different from their summer breeding grounds in the temperate northern latitudes of Canada and Alaska. The heat and aridity present new challenges to songbirds as they stop to refuel in desert habitats prior to continuing their journey south. As such, migrants must balance water budgets to account for thermoregulatory demands while refueling in the American desert southwest. One physiological mechanism to offset the lethal risk of dehydration in arid environments is to increase the contribution of metabolic water to total body water (BW) reserves. We used the novel Triple-oxygen Isotope Analysis method to assess fractional inputs of pre-formed meteoric (i.e. drinking) and metabolic waters to the BW pools in multiple species of migratory songbirds caught during fall migration in New Mexico, USA. Using cavity ring-down spectroscopy we measured oxygen isotopes (^{16}O, ^{17}O, and ^{18}O) of BW distilled from blood samples to determine $\Delta'^{17}O_{BW}$ of all individuals. $\Delta^{17}O$ values of pre-formed and metabolic water are known constants which diverge significantly; where an individual's $\Delta'^{17}O_{BW}$ falls between these two extremes reflects the extent of reliance on metabolic water. Our data shows that across all migratory songbirds, $\Delta'^{17}O_{BW}$ values indicate substantial metabolic water contributions. Reliance on metabolic water is also influenced by diet type with obligate insectivores showing the greatest dependence, while generalists and granivores intake more pre-formed water.

ABSTRACT 062

ASSESSING COLLAGEN TURNOVER RATE RANGES FOR ACCURATE BONE ANALYSIS

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Understanding tissue turnover is critical to isotopic analysis. Collagen, which makes up the majority of the organic fraction of bones, is frequently analyzed in archaeology and palaeontology, but few studies have quantified the rate of bone collagen turnover, especially across multiple skeletal elements. This study aims to address this gap by assessing bone collagen turnover rates for multiple human skeletal elements using the bomb carbon dating method. Seven donors between the ages of 54 and 78 were sampled from the facility for Research in Experimental and Social Thanatology / Recherche en Sciences Thanatologiques [Experimentales et Sociales] in Québec. Collagen turnover rates varied substantially among the skeletal elements samples. The sampled skeletal elements can be ranked from slowest to fastest turnover rates in the following order: Ulna, Humerus, Femur, Rib, Pelvis, Vertebra. While the rib and femur have often been considered bones with "fast" and "slow" turnover rates in palaeodietary studies, their turnover rates were very similar. Studies seeking multiple bones to reconstruct temporal variation in life history should consider the vertebra and ulna instead as alternatives, as these elements exhibit distinctly fast and slow turnover rates, respectively. In some cases, it is inaccurate to refer to collagen as reflecting a "lifetime average" of dietary intake, as the rate of synthesis of collagen is unevenly weighted throughout life. This research presents the most comprehensive list of bone collagen turnover rates for multiple human skeletal elements.

ABSTRACT 063

Investigating Water Balance in Captive Eastern Collared Lizards

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The need to obtain water exerts selective pressure on ectotherm ecology and behavior. Sources include exogenous free water (i.e., meteoric water) and endogenous metabolic water (synthesized de novo during the biochemical reactions of metabolism). In particular, cytochrome c oxidase in the mitochondria uses atmospheric oxygen to synthesize water. Metabolic water production is directly linked to the rate of energy production, presenting the opportunity to investigate these dynamics using stable isotopes. The $\Delta^{17}O$ values of animal body water ($\Delta^{17}O_{BW}$) enable a novel assessment of exogenous and endogenous water inputs into the body water pool. Meteoric water values vary but are typically about 41 per meg. While there is no measured $\Delta^{17}O$ value of water produced by cytochrome c oxidase, we assume it has the $\Delta^{17}O$ value of atmospheric oxygen of -441 per meg. To quantify how different oxygen fluxes influence the $\Delta^{17}O_{BW}$ in an ectotherm, we continuously monitored food and water intake, O_2 consumption, and CO_2 production of captive Eastern Collared Lizards (*Crotaphytus collaris*; n = 8) and repeatedly measured $\Delta^{17}O_{BW}$ in blood samples. We manipulated 1) temperature to increase metabolic rate and 2) water content of food items to decrease dietary water intake. Preliminary analyses suggest greater effects of temperature than food water intake. Values of $\Delta^{17}O_{BW}$ were -95 to -125 per meg (mean -111 per meg) at 25 °C, and -78 to -112 per meg (-98 per meg) at 35 °C.

ABSTRACT 064

Exploring the potential of amino acid δ^2H values for tracing metabolic fluxes and energy flow in food webs

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Pioneering research has shown that δ^{13}C and δ^{15}N values of individual amino acids (AAs) can trace energy flow through food webs and estimate relative trophic positioning. However, comparatively few studies have measured δ^2H values of AAs. Here, we show that AA δ^2H values can differentiate among basal resources and provide insights into metabolic fluxes and physiology. We present AA δ^2H and δ^{13}C values of terrestrial and aquatic (freshwater and marine) primary producers. Terrestrial and freshwater aquatic samples from New Mexico, including C3, C4, CAM plants and freshwater algae, exhibited >450‰ range in AA δ^2H values, from -300‰ (isoleucine) to +170‰ (proline). Linear discriminant analysis using δ^2H values of ten measured AAs yielded a 91% successful reclassification rate among C_3, C_4, CAM and algae; a second model using only five AAs considered 'essential' for consumers yielded a 100% reclassification rate. Essential AAs exhibited the lowest δ^2H values, which we hypothesize is due to biosynthesis from ^{2}H-depleted NADPH and limited rates of subsequent catabolism. AAs diRered further in the correlation among δ^2H and δ^{13}C values. For instance, serine and glycine in terrestrial plants exhibited strong correlations in these values, which may reflect synthesis from initial products of photosynthesis (e.g., 3-Phosphoglyceric acid). In contrast, aspartic and glutamic acid showed weak correlations of δ^{13}C and δ^2H values, which may reflect their role as central metabolic intermediates. Analysis of marine producers is ongoing; samples (n=29) include intertidal and subtidal brown algae, filamentous and foliose red/green algae, and particulate organic material from the Gulf of Maine.

ABSTRACT 065

Examining how increases in metabolic rate and drinking water effect the triple oxygen isotopes of captive deer mice (*Peromyscus maniculatus*) body water

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Maintaining water balance is critical to animals for facilitating metabolic reactions, digestion, waste expulsion, and other functions. Some metabolic reactions consume water, while others produce water, like those via cytochrome c oxidase in the mitochondria. This inherent link between water balance and metabolism provides an opportunity to study animals via stable isotopes. Here, we explore a recently developed method for assessing the contributions of different water sources to animal body water, by interpreting natural abundance measurements of the triple oxygen isotope system (^{16}O, ^{17}O, and ^{18}O; $\Delta^{17}O$). The basis for this method is the unique $\Delta^{17}O$ values of oxygen influxes and effluxes for animals that can be modeled using $\Delta^{17}O$ measurements of biological samples. For example, water generated via cytochrome c oxidase uses atmospheric oxygen which has a $\Delta^{17}O$ of ~ -441 per meg. In contrast, the $\Delta^{17}O$ value of freshwater drinking sources is commonly ~ 40 per meg. To quantify how different oxygen fluxes influence $\Delta^{17}O$ in animal body water ($\Delta^{17}O_{BW}$), we continuously monitored food and water intake, O_2 consumption, and CO_2 production of captive deer mice (*Peromyscus maniculatus*) and repeatedly measured $\Delta^{17}O_{BW}$ in blood samples. We manipulated 1) temperature to increase metabolic rate, and 2) dietary salt content to increase drinking water intake. Our results suggest that increased metabolic rate lowered $\Delta^{17}O_{BW}$, and that increased drinking water intake increased $\Delta^{17}O_{BW}$. These data help provide an empirical basis for interpreting $\Delta^{17}O_{BW}$ in wild animals, and we encourage further research to improve the accuracy and precision of modeling oxygen fluxes.

ABSTRACT 066

Migratory cyclicity informs amino acid nitrogen isotope incorporation in the African elephant *Loxodonta africana*

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Accurate interpretation of an organism's isotopic composition relies heavily on the assumption of steady state, such that isotope values of tissues reflect that of the ambient environment and not other ecological or physiological processes. This assumption can often be violated owing to limited appreciation of isotope incorporation and the diversity of metabolic 'pools' that may contribute to tissue synthesis. We present amino acid (AA) nitrogen isotope ($\delta^{15}N$) records from the tail hair of an African elephant (*Loxodonta africana*) that frequently migrated between semi-arid lowland of Samburu National Wildlife Reserve and the highland Imenti Forest on Mount Kenya. These two regions have drastically different baseline $\delta^{15}N$ values: Samburu is ~10‰ higher than Mount Kenya. We used this unique degree of baseline isotopic variation to perform a 'natural' diet switch experiment to estimate $\delta^{15}N$ incorporation for 13 AAs. We observe that incorporation in most AAs is best described by a two 'pool' reaction progress variable. Trophic and physiological AAs exhibited higher contributions from a short pool (41% – 75%) with faster incorporation (T50 = 5 –37 days). Source AAs exhibited higher contributions from a long pool (50% – 64%) with slower incorporation (T50 > 365 days). This could be problematic for estimating the relative trophic position of migratory animals that move among ecosystems with inherently different baseline isotope compositions. These findings underscore the complexity of nitrogen isotope incorporation in organic tissues, the importance of considering contributions from multiple metabolic pools, and how these vary across trophic, physiological, and source AAs.

ABSTRACT 067

Non-invasive determination of critical dissolved oxygen thresholds for stress physiology in fish using triple-oxygen stable isotopes and aquatic respirometry

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We lack robust, non-invasive methodologies to augment our understanding of critical dissolved oxygen thresholds that trigger adaptive physiological responses in aquatic organisms. The triple oxygen-isotope ($^{18}O/^{17}O/^{16}O$) fractionation of O_2 associated with respiring organisms correlates with the proportion of oxygen used during respiration. In this experiment, we measured the oxygen isotope fractionation of dissolved O_2 in aquatic respirometry experiments to determine the response of wild sticklebacks (*Gasterosteus aculeatus*) adapted and experimentally acclimated to hypoxic and normoxic conditions to evaluate how their utilization of oxygen responded to progressively acute hypoxia. After initially following progressive ^{18}O enrichment caused by preferential uptake of ^{16}O known to all respiring organisms at dissolved oxygen concentrations below 3-5 mg O_2/L, we observed a systematic mixing of ^{16}O and ^{17}O from fish with the remaining O_2 pool for all populations. We propose this apparent reversal in oxygen isotope fractionation came from a change in the oxygen metabolism of the fish, thereby highlighting the usefulness of measurements of dissolved O_2 isotopes. Contrary to expectations and despite limited sample size, we observed stronger oxygen isotope fractionation in sticklebacks adapted to hypoxia but acclimated to normoxia than their conspecifics adapted to normoxia or acclimated to hypoxia. This contradicted the expectation that adaptation to hypoxia would reduce oxygen isotope discrimination by sticklebacks due to more efficient oxygen uptake. These preliminary experimental results underscore the innovative prospect of using dissolved O_2 isotopes as a non-invasive proxy to determine metabolic thresholds in fish and other aquatic organisms quantitatively. This proxy advances our comprehension of crucial oxygen responses and adaptation mechanisms in varying oxygen environments.

ABSTRACT 068

METHOD DEVELOPMENT FOR MEASURING TRIPLE OXYGEN ISOTOPE VALUES IN BLOOD AND ITS APPLICATIONS TO SMALL MAMMALS

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Understanding how animals maintain water balance is becoming increasingly important as precipitation and temperature patterns shift in response to climate change. To understand how animals may be affected by desert expansion, the relationship between current desert animals and water must be investigated. Previous studies investigating water balance have used dehydrated diets and water deprivation to understand how animals compensate for water deficiency. Some of these studies show that desert animals have adapted to water deprivation by decreasing water loss. Recently, triple oxygen isotope analysis has been proposed as a method to examine water balance and characterize environmental conditions (e.g. aridity). Traditional methods, such as fluorination of distilled blood water, for measuring triple oxygen values at high precision are labor intensive and analytically challenging. We are developing a new method that utilizes the equilibration of whole blood with CO_2 or direct analysis of exhaled CO_2 collected from wild animals, from which the triple oxygen isotope composition can be measured via tunable infrared laser direct spectroscopy (TILDAS, Aerodyne Corp). By testing this new method against traditional methods of cryo-distilled blood water, we are validating this method as an easier and more accessible way to measure the triple oxygen isotope values of body water. We will highlight an application of this method by presenting data for three small mammal species from the family *Heteromyidae* to demonstrate how seasonality affects the balance of metabolic, meteoric, and plant water utilized by animals in a seasonal desert ecosystem.

ABSTRACT 069

A multi-tissue isotope approach to assess interactions between a native, threatened and a non-native, invasive fish species in a large prairie river

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Many threatened fishes face combined effects of habitat loss, overfishing, and competition with invasive species. In the Qu'Appelle River, Saskatchewan, Canada, long-lived bigmouth buffalo (*Ictiobus cyprinellus*) are in decline and now federally-threatened. Their recovery may be impeded by invasive common carp (*Cyprinus carpio*). Here we use $\delta^{13}C$ and $\delta^{15}N$ in bigmouth buffalo and common carp muscle tissue, along with bulk and amino-acid $\delta^{15}N$ of otoliths to examine their modern and historical food web interactions in two riverine lakes. Modern bigmouth buffalo and common carp occupy different isotopic niches. Bigmouth buffalo had greater evidence of open water feeding (% pelagic = 78 ± 28%), and higher trophic positions (3.6 ± 0.4) relative to common carp (% pelagic = 52 ± 24%, trophic position = 3.2 ± 0.4). Otoliths allowed a glimpse into century-old isotope patterns, and outer bands of otoliths, representing recent growth, were correlated with those of muscle tissue. Bulk otolith $\delta^{15}N$ increased over time but was highly variable within and among individuals, indicative of interannual baseline $\delta^{15}N$ variation that may have masked trophic shifts. Amino acid $\delta^{15}N$ in otoliths confirmed that bigmouth buffalo trophic positions (3.1 ± 0.1) were elevated relative to common carp (2.6 ± 0.2), but estimates were lower than those calculated with bulk muscle tissue. Together, this information suggests that otoliths can provide useful information on interactions of co-occurring species. Our evidence shows that there may be sufficient isotopic niche differentiation to allow these two species to co-exist in their feeding ecology.

ABSTRACT 070

ENVIRONMENTAL DRIVERS OF SIZE-RELATED DIETARY CHANGES BY SALMONIDS IN FENNOSCANDIAN COLD-WATER LAKES

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Sustainable management of subarctic lake ecosystems and their valuable salmonid species demands a holistic understanding of the food web dynamics of these systems. One key factor shaping subarctic lake food webs and the within and between species dynamics is the size-related dietary niche shifts of salmonid species. Multiple studies show that such niche shifts are common among salmonid species, but understanding how these shifts vary under different environmental conditions remains incomplete. Our study elucidates how the diet of Arctic charr (*Salvelinus alpinus*), and brown trout (*Salmo trutta*) evolves with increasing body size across diverse lake types in Sweden, Finland, and Norway. We examine the influence of lake size, fish community composition, and productivity on the size-related shifts in trophic position ($\delta^{15}N$) and littoral reliance ($\delta^{13}C$) of charr and trout, employing generalized linear mixed-effects models. By elucidating the dynamics of size-related dietary niche shifts, our findings offer valuable guidance for developing effective management strategies for these ecosystems and their salmonid species.

ABSTRACT 071

Enhancing Population Delineation in Sockeye Salmon Through Integrated Strontium Isotope and Genetic Analysis

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Effective conservation and management of remaining wild fisheries depend on accurately identifying and monitoring distinct populations. Traditional genetic methods often fall short as they typically lack habitat-specific data, a gap that becomes particularly evident in revealing populations of sea/river-type Sockeye salmon (*Oncorhynchus nerka*). This ecotype, characterized by its climate resilience and vital role in fisheries, presents challenges in population tracking due to subtle gene flow, which dilutes genetic markers. Our study focuses on a significant Pacific Rim Sockeye fishery, employing a combination of river strontium (Sr) isotope predictions, otolith Sr isotope measurements, and Bayesian assignment models. This approach integrates a comprehensive 4-year radiotelemetry genetic dataset (n=1,994) to map these populations' natal habitats and, thus, population structures more precisely. We identified distinct subpopulations with unique natal habitat Sr isotope signatures previously indiscernible using conventional genetic approaches. These findings challenge existing management practices and introduce a novel method for longitudinal monitoring of Sockeye salmon subpopulations, enhancing our understanding of their stability and dynamics over multiple spawning seasons.

ABSTRACT 072

Fluctuating waters: Hydropower impacts on food webs in Fennoscandian lakes

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Hydropower is one of the largest human stressors in European rivers and lakes, with damming and water level regulation (WLR) decreasing freshwater biodiversity and productivity. However, the potential impacts of WLR on freshwater food webs remains poorly described. We demonstrate how WLR can influence the lateral (littoral–pelagic energy flow) and vertical (food chain length) structuring of lake food webs, using $\delta^{13}C$ and $\delta^{15}N$ data from predatory fishes and their putative benthic and pelagic prey from Norwegian lakes and hydropower reservoirs. Our case study of allopatric Arctic charr (*Salvelinus alpinus*) populations in two mountain lakes indicated a pelagic niche shift and a slight niche compression in a heavily regulated lake as compared to a nearby unregulated lake. Our larger-scale results from 28 reservoirs demonstrated contrasting responses of charr and brown trout (Salmo trutta) to increasing WLR (regulation amplitude 2–67 m), with charr showing minor responses while trout shifted to a more pelagic niche and a lower trophic position with increasing WLR. Our results provide further evidence that WLR can influence the structure and function of food webs in hydropower reservoirs. Although charr and trout can adapt to altered environmental conditions, the potential short- and long-term impacts of WLR on population and community dynamics, as well as the lost ecosystem services provided by affected freshwater ecosystems, should be better accounted for in the sustainable management of hydropower systems.

ABSTRACT 073

Understanding the response of freshwater food-webs to environmental changes: a global stable isotope approach

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Global environmental changes are reshaping biological diversity, impacting the functioning of ecosystems and disrupting key ecosystem services provided to humans. At the centre of these modifications is food-web architecture that links the structural characteristics of biological diversity to the emerging properties of ecosystems. Yet, we are lacking of global understanding of the effects of global environmental changes on food-webs. Here, we use a macroecological approach based on an unprecedented stable isotope ($\delta^{13}C$ and $\delta^{15}N$) global database (13,400 observations) from > 800 freshwater ecosystems located

worldwide (65 countries). The Fooδ-webs project, funded by the French biodiversity synthesis centre (CESAB), aims to i) investigate the patterns and drivers of food-web topology at the global scale, ii) determine the importance of intraspecific variability in food webs, iii) understand how energy transfer efficiency is modulated by global changes and iv) develop food-web based metrics to assess ecosystem structure and function. The Fooδ-webs project will analyse, synthesise and share truly unique stable isotope databases recovered from a robust systematic literature review and the collation of data from scientists all around the world. During this presentation, information about the existing databases and first results obtained related to the link between stable isotope structure and food web topology, stable isotope niche and morphological traits and baseline variability obtained at the global scale will be presented.

ABSTRACT 073 cont'd

ABSTRACT 074

Ecosystem responses to environmental drivers in Fennoscandian cold-water lakes as captured by the stable isotope compositions of large salmonid fishes

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Cold-water lakes can exhibit diverse ecosystem structures and functioning despite close proximity, implying that local, as well as regional-scale environmental drivers strongly influence ecosystem processes. Previous small-scale studies have suggested a multitude of potentially confounding drivers that can shape cold-water lake ecosystems, such as climate, topography, community structure, and anthropogenic modifications, as expressed through resident, generalist salmonid fishes. To disentangle the sensitivity of cold-water lakes to various environmental drivers, we collated over 7500 stable isotope measurements from across 135 Fennoscandian lakes to estimate relative effect sizes of different drivers on salmonid isotope compositions using Bayesian GLMMs. We find that the isotopic responses of brown trout (*Salmo trutta*) and Arctic charr (*Salvelinus alpinus*) to biotic factors (fish community composition and body size) match the known vertical and lateral flexibilities of the feeding ecologies of these two species. Warmer climates and catchment productivity coincided with increased pelagic reliance and potentially higher trophic positions of fishes, while lake topography (size and shape complexity) had limited observable effects. Artificial water level regulation also induces greater pelagic reliance, acting synergistically with global warming to negatively impact these vulnerable cold-water ecosystems. In addition, decreases in $\delta^{15}N$ values over the growing season are observed region-wide along with a pelagic shift in Arctic charr. Positive correlations with baseline measurements where available indicate that unexplained differences in lake isotopic baselines are at least partially captured by the models, highlighting the strength of the Bayesian GLMM approach to the analysis of large isotope datasets.

ABSTRACT 075

Tracking insect dispersal through sulfur isotopes – An example with a forest pest, the spruce budworm moth (*Choristoneura fumiferana*) in eastern Canada

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The eastern spruce budworm moth (*Choristoneura fumiferana* (Clem.)) is a major pest species of the boreal forest. Its devastating outbreaks defoliate, reduce growth and increase mortality of balsam fir and spruce stands, and have severe impacts on the Canadian economy and ecological dynamics. Dispersal from high-density (outbreak) sites to low-density (endemic) sites is a key driver of the extent and magnitude of outbreaks. Yet, traditional methods of animal tracking have been difficult to implement in this small, wind-assisted, high-gene flow, insect. Isotope geolocation is a promising avenue to identify the source and arrival locations of these dispersal events. Sulfur offers an independent and complementary geolocation tool to more established isotopes like hydrogen ($\delta^{2}H$) and strontium ($^{87}Sr/^{86}Sr$), but development of techniques for its analysis and validation for its use in insects needs testing. We show that $\delta^{34}S$ varies predictably in space and reliably transmits its local value through food chains, thus is an effective isotope system to track budworm moth regional dispersal. We illustrate the use of this tool by tracing the natal origin of immigrants captured at two sites in Nova Scotia using $\delta^{34}S$ continuous surface geographic assignment and validate it by comparing our predictions to independent wind dispersal trajectory models (i.e., HYSPLIT).

ABSTRACT 076

Resource use partitioning amongst three sympatric beaked whale species revealed through isotopic niche analysis of specimens of opportunity

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Quantifying how species use resources is important for creating effective management plans; however, collecting data on rare and hard-to-find species can be difficult. One solution is to use stable isotope analysis on specimens of opportunity, such as natural mortalities or museum specimens. Beaked whales are prime examples of elusive species, and little is known about their ecology. To address this, we quantified relative isotopic niches, and from this inferred resource use partitioning, amongst three sympatric species of beaked whales in the northeast Atlantic Ocean. We measured carbon and nitrogen stable isotope values in kidney, liver, muscle, and skin tissues from Cuvier's (*Ziphius cavirostris*), northern bottlenose (Hyperoodon ampullatus), and Sowerby's (*Mesoplodon bidens*) beaked whale carcasses stranded along the Scottish coast. Results showed that Cuvier's and Sowerby's beaked whales had low-to-moderate levels of isotopic niche overlap across tissue types, whereas northern bottlenose whales occupied a distinct isotopic niche. Quadratic discriminant analysis of isotope values assigned more than 80% of tissue samples to the correct species, indicating that these beaked whale species demonstrate short- and long-term resource partitioning. Cuvier's and Sowerby's beaked whales forage at the same trophic level but from different deep-sea communities, while northern bottlenose whales forage at a higher trophic level and demonstrate low foraging plasticity.

ABSTRACT 077

INFLUENCE OF FASTING AND OPPORTUNISTIC FEEDING ON SKIN STABLE ISOTOPE VALUES OF MIGRATING WHALES

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Humpback whales (*Megaptera novaeangliae*) migrate between low-latitude breeding grounds and high-latitude feeding grounds, with increasing evidence that they utilise supplemental feeding sites in temperate regions while migrating. Feeding behaviour and diet while migrating is often unknown, and the impact that temperate feeding and/or fasting has on bio-chemical tracers used to investigate diet remains unclear. This study (1) determined whether prey consumption at supplemental feeding sites could be detected by analysing carbon and nitrogen stable isotope ratios in whale skin; (2) obtained information on whale diet during migration; and (3) ascertained the impact of potential fasting on whale stable isotope values. Skin and diet samples were taken from the eastern Australian humpback whale population on Antarctic feeding grounds and at two sites on the southward migration route (a sub-tropical site and a temperate site) across two years. At the sub-tropical site, $\delta^{13}C$ and $\delta^{15}N$ values were consistent with the last place of foraging five months earlier. However, higher whale skin $\delta^{15}N$ values in 2011 than 2012, suggested that in some years, (potentially when blubber reserves were insufficient), $\delta^{15}N$ values may be influenced by fasting. In both years, whale skin $\delta^{13}C$ and $\delta^{15}N$ values at the temperate site were higher than those from the Antarctic and sub-tropical sites, indicating that a feeding signal from temperate zones, with whales feeding on fish and krill, had likely been incorporated. Importantly, supplemental feeding during migration could affect the interpretation of whale diet on Antarctic feeding grounds if whales are sampled early in the season.

ABSTRACT 078

EXPOSURE OF STELLER SEA LION PUPS TO MERCURY CHANGES THROUGH STAGES OF GESTATION AND SUCKLING; CORRELATIONS WITH STABLE ISOTOPE RATIOS RECORDED ALONG THE VIBRISSAE

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Steller sea lion pups on Kiska Island, Alaska, have the highest median concentration of total mercury ([THg]) in their natal fur than pups from any other rookery in Alaska. Over 75% of pups sampled on Kiska Island have fur [THg] above 20 ppm, which is the lower toxicological threshold for potential negative health effects. Vibrissa (mystacial whiskers) were collected from 10 pups on Kiska Island in 2023. To determine if mercury exposure was uniform throughout gestation into the nursing period, we serially sampled vibrissa, designating alternating segments for carbon and nitrogen stable isotope ($\delta^{13}C$, $\delta^{15}N$, respectively), and [THg] quantitation throughout the length of the vibrissa. Segments grown near the root of the vibrissa that showed depleted $\delta^{13}C$ were assumed to represent tissue grown after the lipid-rich milk diet began at birth (0 to 4 segments per pup; 1.8±1.3 segments). The remainder of the vibrissa represented growth during gestation; late gestation segments follow adjacent to nursing segments, and mid-gestation segments were those nearest to the tip. [THg] was significantly correlated to both $\delta^{15}N$ and $\delta^{13}C$ during mid- and late gestation ($p<0.02$) suggesting that when mothers ate higher trophic level prey, the fetus was exposed to higher [THg]. Vibrissa [THg] ranged widely among pups (5.35 to 73.77 μg/g; $p<0.0001$), but much smaller differences were seen within pups between mid- and late gestation [THg] ($p<0.0001$). [THg] were significantly lower in segments grown after birth ($p=0.044$) when mean $\delta^{13}C$ was lower than in late gestation ($p=0.014$), but $\delta^{15}N$ had not changed significantly ($p=0.978$).

ABSTRACT 079

Sophisticated Bayesian isoscape modeling does not excuse inconsistent sampling - a case study in the Mediterranean Sea

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The potential of any spatial applications of isotope tracers depends on the nature, scale and predictability of spatial variation. The Mediterranean Sea (MS) encompasses strong biogeochemical and climatic gradients, but the scale of variation is unclear.

We compiled the first dataset of georeferenced CN isotope data across the MS. The dataset contains multiple, broad sample categories representing the base of pelagic food-webs (pico-nanoplankton, phytoplankton, POM, zooplankton, suprabenthos, and surface sediment). Data were obtained opportunistically and spatio-temporal coverage reflects non-targeted sampling. We applied Bayesian hierarchical models (INLA) to generate isoscapes across the MS, accounting for sample category.

At spatial ranges >6 km, the isoscape models revert to the mean value. While, theoretically, this could imply that variance across 100s of km is dominated by local effects, most likely the failure to resolve broad isotopic gradients reflects inappropriate reference samples. Systematic, coordinated, targeted sampling is required to improve isotopic signal to noise ratios for modeling to effectively capture local variances at <10 km resolution.

More broadly, compilations of isotopic data are increasingly available, enabling meta-analyses to ask macroecological questions from opportunistic datasets. Such datasets are inevitably biased, with uneven sampling. Statistical approaches partitioning variance into fixed and random effects are designed to address such problems, but are not magic bullets, and not all problems can be solved through increasing data volume. We caution users to carefully consider the sources of bias in opportunistic datasets and the signal to noise requirements of target analyses before embarking on ambitious macroecological studies using data compilations.

ABSTRACT 079 cont’d

ABSTRACT 081

IT'S NOT ZERO: AN UPDATED REVIEW OF TROPHIC DISCRIMINATION IN $\Delta^{34}S$

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For >50 years, stable isotope ecologists have largely relied on carbon and nitrogen stable isotopes (when not focusing on water isotopes). However, there has been a notable recent increase in the use of sulfur stable isotopes ($\delta^{34}S$). This partly reflects recent advances easing the analysis of $\delta^{34}S$, and the fact that sometimes $\delta^{13}C$ and $\delta^{15}N$ provide insufficient resolution to solve the problem at hand. Although not a panacea, the addition of $\delta^{34}S$ (e.g. for mixing models) can notably improve performance and understanding of the problem at hand. It is often assumed that there is little isotopic change (trophic discrimination) between the diet and a consumer's tissues, i.e. the TDF ($\Delta^{34}S$) = 0 ‰. Conversely, controlled studies in bears and rats have shown clear negative relationships between the $\delta^{34}S$ in food and consumer $\Delta^{34}S$, and some researchers have used these relationships to estimate TDFs in other taxa.

Here, I report an updated meta-analysis of published $\Delta^{34}S$ estimates (n = 168) that includes different taxa (birds, fish, invertebrates, mammals), tissues (blood, brain, collagen, egg, feather, fin, hair, liver, muscle), habitat (terrestrial, aquatic) and diet type (animal, plant, mixed). The results revealed that contrary to expectations, in almost all cases mean (or median) TDFs were different to zero. Most taxa had negative $\Delta^{34}S$ values, but fish showed a positive $\Delta^{34}S$. When examined across studies, a negative relationship between consumer $\Delta^{34}S$ and dietary $\delta^{34}S$ was apparent, but it had limited predictive power, invalidating its use as a general relationship.

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ABSTRACT 082

A NEW INDIVIDUAL MODEL FOR TROPHIC POSITION ESTIMATION USING STABLE ISOTOPES: HOW THE ERROR AND UNCERTAINTY PROPAGATES THROUGH FOOD WEBS

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Stable isotopes have demonstrated their utility as tools to capture the complexity of trophic interactions, identify habitat use or energy sources and infer the trophic position (TP) of secondary and higher consumers. TP is an important concept that describes the ecological role of consumers in food webs. However, current methods for estimating TP using $\delta^{15}N$ are limited and do not exploit the full potential of the isotopic approach. For example, researchers typically use point estimates of trophic enrichment factors and isotopic baselines, and often do not explicitly include intra-population variation, i.e., that exhibited by individual consumers. We present an update to the R package *tRophicPosition*. This widely-used package incorporates a Bayesian model for the calculation of TP using single or multiple baselines within the powerful approach of Markov Chain Monte Carlo simulations provided by JAGS and the statistical language R. Previously, the new package only provided estimations of population-level TP: the new version importantly allows researchers to estimate TP at the level of individual consumers using the powerful approach of greta. We show the core of the new model included in the package, the theory behind it, and the functions created to estimate TP and produce figures. We also discuss how error, baselines and observational uncertainty propagates through trophic webs. Finally, we demonstrate the capabilities of the updated *tRophicPosition* individual-level model using a series of contemporary and archaeological consumers from the Altiplano of Chile and the SE Pacific.

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ABSTRACT 083

A Niche By Any Other Name

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Ecologists often struggle to distill tangible and intangible aspects of communities, populations, and organisms into quantitative, intercomparable, metrics. For this reason, countless measurements and proxies have been devised to describe seemingly every aspect of an organism's ecological niche. One popular framework -particularly for dietary studies- is the, "isotopic niche," wherein variance in consumer stable isotope compositions is interpreted as being reflective of individual-level resource selection (i.e., prey choice), and population-level variability (i.e. generalist vs specialist). However, variance in consumer stable isotope compositions may contain a significant non-dietary component. Thus, care is required to avoid erroneous conflation of isotopic niche breadth and trophic niche breadth as measured by more traditional methods, such as gut content analysis. Our present work explores incongruence of the isotopic and trophic niche. Specifically, we demonstrate how spatial variability in the stable isotope composition of prey items can skew trophic-centered interpretations of the isotopic niche. To do this, we used carbon and nitrogen stable isotope measurements of invertebrates from lakes in Finland alongside simulation modeling to investigate the relationship among isotopic niche characteristics and more traditional gut content-derived measures of the trophic niche in hypothetical consumers. Our results indicate that covariance of trophic and isotopic niches is strong when resource selection gradients are parallel to isotopic gradients. However, our analyses also indicate that while expansions in the isotopic niche can be correlated to increased trophic niche breadth, the two quantities are not inexorably linked. Therefore, interpretation of the isotopic niches as a direct analog of the trophic niche should be done cautiously.

ABSTRACT 084

BORN TO BE WILD? ISOTOPIC TURNOVER REVEALS BIOENERGETICS OF FARMED FISH RELEASED INTO NATURAL ENVIRONMENTS

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The introduction of juvenile fish raised through aquaculture into natural water systems is a commonly practiced technique on a global scale. This is done to enhance declining natural populations, sustain recreational fishing activities, or simply to meet the demand for food consumption. However, once released into the wild, these young fish quickly encounter various new environmental factors that affect their growth. Growth is a vital aspect of their adaptation to the wild, with their ability to consume food and efficiently convert it into growth determining their fitness. Measuring the growth of tagged fingerlings in the wild is relatively straightforward, but assessing growth efficiency, a key variable to explain how growth varies among different sites, poses a challenge. To tackle this issue, the turnover of stable isotopes in the natural environment can serve as a valuable indicator of growth efficiency as it allows calculation of metabolic turnover. However, for this method to be effective, the fingerlings must possess a distinct isotopic composition compared to the natural consumers in the receiving environment. Bycatch from marine fisheries, often utilized as a food source in aquaculture, exhibits notable differences in $\delta^{13}C$ and $\delta^{34}S$ compared to food items from most freshwater ecosystems. In a multiple-lake study, we demonstrate that the bioenergetics of transplanted brook trout, as inferred from the turnover of $\delta^{13}C$ and $\delta^{34}S$, reflects a gradient in both competition and food quality. This highlights the potential of stable isotope turnover as a tool for estimating growth efficiency and understanding ecological dynamics in transplanted populations.

ABSTRACT 086

INTER- AND INTRA-SPECIFIC DIETARY SPECIALIZATION IN SMALL CARNIVORE MAMMALS IN SOUTHEAST ASIA

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The islands of the Sunda Shelf within the Southeast Asia is a biodiversity hotspot. Several threats like deforestation and agricultural practices threaten the region and its biota. Several species of small carnivore mammals co-exist across different habitats in Southeast Asia, but limited information is available regarding their feeding ecology and to what degree they compete for resources. We sampled fur material of 17 Southeast Asia carnivore species from museum collections that were originally collected in the Sunda Shelf region and the continental portion of Southeast Asia. Samples were cleaned and analysed for the stable isotope measurements of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$). Isotopic niches, defined as the Bayesian estimate for the standard ellipse area (SEAB) that includes the data of a predefined group, were determined for each carnivore species from each biogeographical region by using the R package SIBER. Overall, the posterior distribution of SEAB covered a range between 5 and 15 ‰^{2} for most species. We found that $\delta^{15}N$ and $\delta^{13}C$ values were significantly different between Felidae and Viverridae, mainly related to the lower $\delta^{13}C$ and $\delta^{15}N$ values of the fruit eating Viverridae. Interestingly, isotope values of species classified as 'endangered' according to the IUCN Red List were significantly different from those of other conservations status groups, which indicates contrasting feeding niches of the endangered species in this region. For instance, the flat-headed cat (*Prionailurus planiceps*) shows a specialist behavior based on its isotopic niche compared to other closely related species and conservation measures to protect its habitat in key areas should be considered.

ABSTRACT 087

CASTE-SPECIFIC ROUTING OF MICROBIAL RESOURCES IN COLONIES OF FUNGUS - GROWING TERMITES

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Herbivorous and detrivorous consumers, such as termites, often complement their low-protein diets with nutrients originating from fungi and bacteria. However, the role of microbial components in termite nutrition remains poorly resolved. In the fungus-growing termite symbiosis, the fungal symbiont (*Termitomyces* sp.) degrades lignocellulose of foraged plant matter in 'fungus combs' that serve as the principal food source for the host insect colony. However, it remains elusive whether the proteins in the combs originate mostly from the decaying plant matter or the fungus, and how plant-fungal dynamics are reflected to the diet compositions of the various termite castes. Gut bacteria, abundantly present especially in guts of termite workers, could provide an important third nutritional component. In this study, we quantified the relative contributions of plant, fungal, and bacterial essential amino acids (EAA) in the nutrition of the Kenyan fungus-cultivating termite *Macrotermes michaelseni* using an approach combining EAA $\delta^{13}C$ fingerprinting and Bayesian mixing modeling. Our results indicate that comb EAAs were mostly of fungal origin (32-55 %), with plants and bacteria having smaller (< 36 %) and relatively equal contributions. Termite workers and soldiers had much higher bacterial diet contributions than the reproductive queen and king, and most of the EAAs in eggs and larvae were derived from the fungus. Soldier termites had the lowest fungal contribution, and their nutrition was mostly from plants. These findings indicate that, within *Macrotermes* colonies, the proteinaceous fungal food is efficiently routed to reproduction, whereas gut bacteria provide supplementary nutrition mainly for the adult sterile castes.

ABSTRACT 088

MAPPING FOOD WEB DYNAMICS OF MAMMOTH CAVE USING CARBON AND NITROGEN AMINO ACID-SPECIFIC ISOTOPE ANALYSIS

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Cave ecosystems are often erroneously considered less complex than those on the surface, however, many caves contain hearty detrital food webs and vibrant microbial communities whose contributions are poorly understood. We collected amino acid (AA)-specific carbon and nitrogen isotope data for a variety of macro-organism and microbial samples from Mammoth Cave—the longest mapped cave system in the world—to elucidate trophic interactions and determine the relative importance of different carbon sources (detritus, guano, surficial inputs, microbes) in this subsurface environment. AA in consumer tissues, particularly those that macro-organisms cannot synthesize (essential AA), should retain $\delta^{13}C$ signatures similar to those of their diet, but our AA_{Ess} $\delta^{13}C$ values vary extensively among samples, suggesting reliance on a variety of carbon sources. For example, AA_{Ess} $\delta^{13}C$ fingerprints in spiders and crickets reflect a traditional consumer diet relationship—corroborated by AA $\delta^{15}N$ trophic estimates—but are distinct from every other sample. Because crickets regularly feed on plant material outside the cave, this suggests other organisms are largely not reliant on surficial pant materials. Moreover, bat and cricket guano do not appear to be predominant energy sources, as anticipated. Instead, we find evidence for fungus-eating insects (e.g. beetles) and some reliance on photosynthesizing biofilms and biovermiculations growing on cave walls (flatworms). Additionally, AA_{Ess} $\delta^{13}C$ variation is high even within a single taxon, such that one isopod maps with beetles while the other looks less like the rest of the cave community than a bat that feeds outside the cave, providing some evidence for dietary specialization.

ABSTRACT 089
BOARD M001

RECONSTRUCTING LOGGERHEAD SEA TURTLE MOVEMENTS IN THE GULF OF MEXICO THROUGH SEQUENTIAL STABLE ISOTOPE ANALYSIS OF SCUTE KERATIN

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Understanding the location and timing of the movements of marine turtles throughout their life cycle is critical to conservation efforts, since anthropogenic threats to their survival cannot be accurately identified and addressed without knowledge of their geographic range, foraging sites, and movement patterns. Loggerhead turtles (*Caretta caretta*) were identified as one of the key species adversely affected by the 2010 Deepwater Horizon oil spill in the northern Gulf of Mexico (DWH NRDA Trustees, 2016), and following the spill, the comprehensive Gulf of Mexico restoration plan highlighted the need for a greater understanding of loggerhead turtle life history parameters as a critical step towards the refinement of population models and the assessment of their recovery.

Scute is a keratinous tissue that accumulates incrementally in loggerhead turtles, recording a time-series of biochemical information that can inform our understanding of their behaviour. The Gulf of Mexico exhibits baseline spatial variation in carbon and nitrogen isotopes, which provides the opportunity to identify areas of likely inhabitance through time based on the $\delta^{13}C$ and $\delta^{15}N$ values measured in each sequential layer of scute. We reconstructed the geographic histories of nine stranded loggerhead turtles in Florida and used probabilistic assignment-to-origin methods with a tissue-specific isoscape (Vander Zanden et al. 2015) to assess movement for periods of up to 20 years. Our results suggest that most individuals foraged consistently within isotopically distinct regions of the Gulf of Mexico, with one individual estimated to have left the eastern Gulf of Mexico to forage in the Caribbean before returning to the same region.

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ABSTRACT 089/BOARDM001 cont’d

ABSTRACT 090
BOARD M002

A study of anadromous and resident Brook trout (*Salvelinus fontinalis*) progeny in Coles Creek using stable isotope analysis and otolith signatures

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Salmonids exhibit a broad spectrum of life-history strategies displayed between residents to migratory anadromous. The role of anadromous and non-anadromous progeny remains poorly understood in fish science. Thus, a better understanding of the contributions of residents and migratory maternity at the inter and intra-population level has several implications, from pure ecology research to fisheries management. This research objective is to better understand the prevalence of Brook trout progeny within a sympatric population of residents and anadromous in the Coles-creek, North-River watershed, PEI. Therefore, the focus was on the early life stages. A Brook trout population was investigated, in its initial life phase, using stable isotope analysis (SIA:C13:N15) from the eggs and otolith microchemistry (Sr88:Ca44) for the young of the year. The field surveys were conducted between 2021 and 2023 during the fall, when YOY was collected in electrofishing surveys, and the eggs were collected during the following redds surveys. The surveyed sites showed an upward path through different sections of the stream, seeking a better perspective of the distribution of the potential anadromous and resident cohorts along the stream. Based on our current results from SIA and otolith analysis, there is a dominance of a resident cohort in Coles Creek and a minority of anadromous. The reason for this is still unclear, considering the lower section of the stream has free access to the sea. However, the study is still being worked on. Thus, new results are yet to come.

ABSTRACT 091
BOARD M003

Assessing the ecological drivers and consequences of partial migration in Hudson River striped bass over multiple decades

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Identifying the abiotic and biotic drivers of population stability is a fundamental concept in ecology. Intraspecific variation in life-history is an important factor promoting stability through creating asynchronous dynamics within a population. Partial migration (PM), where only some individuals from a population migrate while the rest remain resident, can mitigate population-level responses to environmental stressors as it creates diverse subpopulations that rely on a range of habitat and energetic resources. However, little is known about the underlying mechanisms driving variation in migration behavior and how these shift over time. In the Hudson River Estuary, striped bass (*Morone saxatilis*) are known to exhibit anadromous PM behavior and are a recreationally important, sentinel species. Here, we apply carbon isotope ($\delta^{13}C$) analysis of essential amino acids (AA_{ESS}) to a three-decade archive of striped bass scales collected as part of the Hudson River Biological Monitoring Program. Our primary goals are to assess annual variation in the dominant nutrient sources (e.g. freshwater, estuarine, or marine) supporting the striped bass population and determine how the degree of partial migration (i.e. life-history diversity) changes across years. By combining AA_{ESS} $\delta^{13}C$ analysis with existing records of striped bass population size, water temperature, dissolved oxygen, and freshwater flow, we will determine how variation in the proportion of migrants has influenced population stability over time and assess the relationship between migration behavior and environmental conditions.

ABSTRACT 092
BOARD M004

Isotopic insights into the migratory patterns of the painted lady butterfly *Vanessa cardui* during an outbreak year

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Each year, the Afro-Palearctic population of the painted lady butterfly, *Vanessa cardui*, undergoes a migration spanning eight to ten overlapping generations over a range that extends from Scandinavia to sub-Saharan Africa. To understand the overall migratory patterns and connectivity of this continuous movement, comprehensive spatiotemporal sampling of each segment of the annual migratory cycle is necessary. In 2019, a population outbreak occurred, likely due to an anomalous increase in larval resources within a specific region of the range, leading to a notable surge in the number of painted ladies sighted in the Middle East, Europe, and Africa. Recently, the movement of this outbreak was characterized using geolocation inferences derived from pollen metabarcoding analysis, whereby the pollen attached to butterflies is identified and movement is inferred based on the geographic distribution of the identified plant species. Building upon this analysis, we refine our understanding of the migratory patterns and connectivity of painted lady butterflies through hydrogen and strontium isotope geolocation. In total, we present isotope geolocation information for over 250 specimens collected across 19 countries. This expanded dataset allows us to achieve a more detailed characterization of the annual migratory cycle of painted ladies during the 2019 outbreak. Additionally, by combining pollen-based and isotope geolocation techniques for select individuals, we demonstrate the benefits of interdisciplinary approaches in understanding the complexities of insect migration.

ABSTRACT 093
BOARD M005

Using δ^2H to verify the latitudinal migration of *Sympetrum fonscolombii*

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Sympetrum fonscolombii, also known as the nomad dragonfly, is a widespread migratory dragonfly that is present in much of Afro-Eurasia. It is assumed that *S. fonscolombii* migrates northward in the spring and the back southward in autumn, however there has been little substantiation to this claim. Additionally, the connectivity of populations of *S. fonscolombii* appear to be disjunct is unknown (e.g. South Africa population, North Africa-Europe population, East Asian population etc.). To answer the aforementioned questions about *S. fonscolombii* migration ecology I have created a δ^2H isoscape calibrated using non-migratory damselflies from across Africa and Europe. Using this isoscape we provide isotopic evidence to confirm the latitudinal migration of a population of *S. fonscolombii*. With the creation of this isoscape we hope to also determine population connectivity of *S. fonscolombii*. Additionally, the δ^2H isoscape developed can serve as a basis for future work on migratory dragonflies and other insects.

ABSTRACT 094
BOARD A001

Isotopic Analysis of Caprine Management from Archaeological Remains at the Ancient Urban Center of Gordion, Turkey

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Agropastoral strategies at the ancient urban center of Gordion, in central Anatolia (modern Turkey), have been studied since the 1980s, with considerable progress to date in understanding the histories of farming, herding, and environmental change in the region. Less well understood, however, is the spatial patterning of agropastoral activities. By focusing on successive imperial periods, from the Late Bronze Age (1400-1200 BCE) Hittite Empire to the Medieval Seljuk Empire (13th cent. CE), this project investigates the response of farmers and herders to distinct strategies for state finance employed by different states. Using a multi-isotopic approach, this project aims to enable geographic and seasonal interpretation of past agropastoral activities, frequently at an intra-annual scale. This presentation reports carbon and oxygen isotopic results from caprine tooth enamel and provides a detailed investigation of agropastoral strategies, including an assessment of animal husbandry strategies over successive periods of distinct political authority in the region. This presentation also discusses the next steps for research and future integration with other isotopic research across Anatolia.

ABSTRACT 095
BOARD A002

Agro-Politics and the Moche: A Stable Isotope Analysis of Moche Agricultural Management During the Early Intermediate Period, Moche Valley, Peru

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Stable isotope analysis of macrobotanical remains from archaeological sites in the Americas has often been overlooked, with most analyses of this nature occurring in Eurasia. Analyzing $\delta^{13}C$ and $\delta^{15}N$ of macrobotanical remains, especially domesticated crops, provides insight into past agricultural practices and management, such as the use and application of irrigation canals and fertilization techniques. Utilizing $\delta^{13}C$ and $\delta^{15}N$ of macrobotanical remains from three Moche Valley sites spanning 200-800 CE (West Cerro León [MV-224], Cerro León [MV-225], and Ciudad de Dios [MV-83]), temporal changes in agricultural practices were examined. These sites date just prior to and during the period of Moche state formation along the north coast of Peru. The Moche are among the first archaic states in Peru, known for their construction of irrigation canals, moldmade ceramics, and expanding rule into various river valleys along the north coast. However, little is known about how Moche cities were fed and what impact agriculture had on the ability to expand influence in the region. Through the isotopic analysis of macrobotanical remains from sites dated to various periods of Moche rule, this study addresses changes in agricultural practices associated with the development of the Moche state.

ABSTRACT 096
BOARD A003

ASSESSING COUPLING OF TROPHIC POSITION AND BASELINE $\delta^{15}N$ PROXIES IN PALEOCEANOGRAPHIC ARCHIVES

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Amino acid nitrogen isotopes ($\delta^{15}N$) in paleoarchives have enormous potential to improve understanding of past biogeochemical change. A decade ago, Batista et al. (2014) published the first sedimentary amino acid $\delta^{15}N$ record and noted a puzzling observation: a strong negative correlation between proxies for trophic position (TP) and "baseline" $\delta^{15}N$ of the source amino acid phenylalanine ($\delta^{15}N_{Phe}$). They hypothesized that $\delta^{15}N$ values of the trophic and source amino acids might be inversely related in paleoarchives based on mass-balance assumptions; however, they did not identify a causal biogeochemical mechanism. Despite important implications for $\delta^{15}N$ applications, no subsequent work has directly addressed these questions.

Here we present a new ecosystem mass-balance model exploring this issue, alongside results from a compilation of ten deep-sea coral and sedimentary records. Our model simulates shifts in $\delta^{15}N$ of primary production driven by changes in the trophic structure of the planktic food web. In the model, negative relationships between TP and $\delta^{15}N_{Phe}$ arise from phytoplankton uptake of recycled nutrients.

Consistent with model predictions, we observe statistically significant inverse relationships between TP and $\delta^{15}N_{Phe}$ in archives from across the Pacific Basin. Our results indicate ecosystem trophic structure is likely an important driver of $\delta^{15}N_{Phe}$, in addition to typically considered factors like $\delta^{15}N$ of source nitrate and nutrient utilization. These findings challenge common assumptions about independence of baseline and trophic structure information from amino acid $\delta^{15}N$ approaches. We propose that our new mass-balance modeling framework will be useful for future interpretations of paleoceanographic amino acid $\delta^{15}N$ data.

ABSTRACT 097
BOARD A004

Impacts of industrialization on arctic fox (*Vulpes lagopus*) foraging ecology during the 20th century

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During the 20th century, the landscape and land management practices of the Canadian Arctic/Inuit Nunangat [the Inuit homeland] changed from pre-contact times. Traditional Inuit subsistence practices were transformed by the fur trade and introduction of European food items, Euro-Canadian settlements were built, and burning of fossil fuels warmed the climate. We evaluated how these environmental changes affected the foraging ecology of arctic fox (*Vulpes lagopus*). Arctic fox are opportunistic omnivores that may forage for human food remains. We analyzed carbon ($\delta^{13}C$), nitrogen ($\delta^{15}N$), and sulfur ($\delta^{34}S$) isotopes of bone collagen from 92 arctic fox that were trapped between 1914 and 1976. We discuss whether our results indicate that arctic fox diets changed with industrialization, and if they scavenged food remains from human settlements to bolster against population decline when natural prey were scarce. Our study has important implications for ensuring the health of arctic fox populations, which are threatened by northward expanding red fox (*Vulpes vulpes*) range in response to warming of the arctic.

ABSTRACT 098
BOARD A005

Stable Isotope Ecology of Thule and Birnirk Canids at Cape Espenberg, Alaska

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Since the twilight of the Pleistocene, dogs have been important to human societies. In Arctic hunter-fisher-gatherer communities, the ecology of the two was especially intertwined, with dogs serving as hunting aids and/or transportation, often resulting in divergent subsistence strategies for domestic dogs and their wild canid counterparts. We present the $\delta^{13}C$ and $\delta^{15}N$ of 20 individual canids from the Rising Whale site of Cape Espenberg, Alaska, represented by a total of 56 bone and dentin collagen samples. Both canid species (dogs and wolves) were recovered from two structures, associated with the Thule and Birnirk cultures respectively. The $\delta^{13}C$ and $\delta^{15}N$ values of all canids were strongly correlated, suggesting a range in diets of exclusively terrestrial to exclusively marine for both dogs and wolves. A significantly higher portion of the dog diet was from marine foods relative to wolves. Sequential sampling of dentin indicates relative dietary stability through the period of tooth formation. Surprisingly, some wolves (identified by mtDNA) possessed strongly marine diets, possibly suggesting the presence of hybrid animals living amongst these human communities.

ABSTRACT 099
BOARD A006

LATE PLEISTOCENE COMMUNITY STRUCTURE AND TROPHIC DIVERSITY AT THE RANCHO LA BREA AND MCKITTRICK ASPHALT SEEPS

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Investigating fossil assemblages found in asphaltum through isotopic analysis provides insights into late Pleistocene ecosystem dynamics. While the La Brea Tar Pits (LA Basin), representing a coastal ecosystem, have been extensively studied, the McKittrick asphalt seeps are understudied and offer insight into a distinct ecosystem in inland central California. We collected stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope values of collagen from a variety of taxa including felids, canids, artiodactyls, perissodactyls, and proboscideans housed in the University of California Museum of Paleontology. We incorporated newly obtained isotopic data from McKittrick (n = 30) with previously published data from both McKittrick (n = 13) and Rancho La Brea (n = 164), allowing for a comparison of late Pleistocene ecosystems in California. We calculated six community-wide metrics (Layman metrics) to assess trophic diversity and community structure within isotopic space of each locality: convex hull area, $\delta^{15}N$ range, $\delta^{13}C$ range, mean distance to $\delta^{13}C$ - $\delta^{15}N$ centroid, density of species, and the evenness of species density. Our results show that McKittrick exhibits greater trophic diversity and a broader spacing of ecological roles compared to Rancho La Brea. Moreover, McKittrick's food web demonstrates higher trophic redundancy and a more even distribution of trophic niches. While the localities share many of the same animals, variation in metric values suggests different ecosystem structures, likely reflecting higher habitat heterogeneity at McKittrick relative to Rancho La Brea.

ABSTRACT 100
BOARD A007

Palaeoecological evidence of increasingly pelagic resource use by modern Alaskan pinnipeds in the face of Arctic warming

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Stable carbon and nitrogen isotope compositions of ancient pinniped bone collagen (n=130) from three archaeological sites (A.D. 1170-1813) and modern bone collagen and muscle tissue (n=73) from pinnipeds harvested in northwestern Alaska were determined to investigate trends in the long-term foraging ecology of six pinniped species. Substantial changes in ringed seal stable isotope values were observed between archaeological and modern seals, with dramatic decreases in modern seal $\delta^{13}C$ values. Modern ringed seals showed continuing declines in $\delta^{13}C$ values post 2008, which marked a period of major decline in Arctic sea ice extent in the Chukchi and Bering Seas. These results reflect increased use of pelagic resources yet stable trophic positions in modern Alaskan ringed seals. The observed increase in pelagic resource use corresponds with recent and unprecedented environmental changes in the Arctic due to anthropogenic activities, including rapidly increasing temperatures, large-scale reductions in sea ice extent, and decreasing benthic productivity. The results of this study emphasize the value of the archaeological record and the use of palaeoecological data in providing context for current environmental changes.

ABSTRACT 101
BOARD A008

Variation in amino acid $\delta^{13}C$ isotopic fractionation during harmful algae *Pseudonitzschia* spp. event

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Amino acid (AA) metabolic pathways are central during photosynthesis, carbon fixation, growth and cellular N cycling in phytoplankton. In this study, $\delta^{13}C$ from individual AA were used to investigate the metabolic state of the phytoplankton community during a phytoplankton bloom in a hot spot for domoic acid (DA) outbreaks in Baja California. Temperature, nutrients, phytoplankton pigments, and $Chla_{tot}$ were obtained. The $\delta^{13}C$ bulk and AA $\delta^{13}C$ values from particulate organic material (POM) collected ≤ 30 m from the sea surface were quantified; some POM samples correspond to toxigenic *Pseudonitzschia* spp. blooms with DA (an AA analog) production. Toxigenic blooms exhibited a unique pattern of $\delta^{13}C$ isotopic fractionation with the highest $\delta^{13}C$ values for serine, glycine and threonine, while glutamic acid (a precursor of DA) had moderate values. The variability in AA $\delta^{13}C$ isotopic fractionation among POM samples reveals different patterns of regulation possibly associated to the phytoplankton community, size and growth. The preliminary results of this study show the strong potential of AA $\delta^{13}C$ analysis for investigating HABs metabolism.

ABSTRACT 102
BOARD A009

11 500 Years of Camelid Diet and Mobility in the Northern Chilean Highlands

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Since the initial occupation of South America, camelids (vicunas, guanacos, llamas and alpacas) have been critical to the development of human populations. As the relationship between northern Chile's past human and camelid populations is relatively unknown, this study aims to decipher differences in camelid mobility and foraging ecology from two archaeological sites through the application of stable isotope analysis. Altitudinal zones of the Andes have vastly different ecological niches, resulting in unique lifeways for those inhabiting them. The archaeological site of Hakenasa is located in the altiplano at 4100 meters above sea level (masl). Within the *altiplano*, the camelids have access to unique resources provided by *bofedales* (high-altitude wetlands) that occur above ~3800 masl. Furthermore, the South American Monsoon causes higher humidity in this region, allowing for year-round occupation. The archaeological site of Patapatane is located in the *precordillera* region at 3800 masl, and despite being 50 km from Hakenasa the site is surrounded by a vastly different environment. Bone and dentin collagen (bulk and sequentially sampled) demonstrate significant differences in foraging ecology and mobility across altitudinal zones between the two sites. Most notably, Hakenasa demonstrates a diet restricted to the *altiplano*, with exclusive consumption of C3 plants, possibly from *bofedales*. Patapatane demonstrates a wide range in C3 and C4 plants consumed, and therefore a large mobility circuit with individuals from a variety of geographical locations. These results support past studies suggesting the sedentary lifestyle of those in the *altiplano* versus seasonal mobility in the *precordillera*.

ABSTRACT 103
BOARD A010

Quantifying Isotopic Variation within Bones

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Bone collagen is a common material used for stable isotope analysis in archaeology, palaeontology, and ecology to generate insights about an individual's life history. The extent of intra-bone isotopic variation has generally been considered to be small, and sample sizes are minimized to preserve bone integrity. In this study, we extracted hundreds of sequential samples from various regions of the midshaft of two kangaroo tibiae and two cow radii to assess the extent of isotopic variation ($\delta^{13}C$ and $\delta^{15}N$) in bone collagen within a single skeletal element. We found that within a single bone, $\delta^{13}C$ varied by up to 10.6 ‰ and $\delta^{15}N$ by up to 3.6 ‰. Isotopic variation within a bone likely reflects the range of isotopic compositions of foods that were regularly consumed throughout life. The pericortical section of mammalian long bones likely presents a longer-term averaged isotope profile, while inner regions (perimedullary) may be biased towards later in life. As bone sample size decreases, the probability of obtaining an isotopic composition that dicers significantly from the lifetime average increases. Rather than conceptualizing stable isotope measurements from bone collagen as being akin to those derived from tissues such as muscle, liver, or skin, they may be better understood as being similar to sequentially sampled hair or tooth samples that have lost their specific temporal information.

ABSTRACT 104
BOARD S001

Geochemical and isotopic characteristics of the Algerian geothermal waters

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This research deals with the results of a geochemical and isotopic characteristics of the Algerian geothermal waters. Eleven samples were collected to identify the origin of the thermal groundwater and for the evaluation of the reservoir temperature in the geothermal systems, the following data were used: concentrations of major chemical constituents, stable isotope ratios (δD and $\delta^{18}O$), saturation indices and chemical geothermometer temperatures. The physicochemical parameters (temperature, pH, and electric conductivity) were measured in-situ; the temperature of the thermal water samples varied from 38 to 96 °C, the pH value of these springs is slightly acid to neutral, with high electrical conductivities up to 4500 µS/Cm. Piper diagrams highlighted two major hydrochemical facies namely sodium chloride (Na-Cl) and sodium sulfate ($Na\text{-}SO_4$). The mineral composition of the thermal waters reflects the geological formations found in the deep origin reservoir and chemical changes in the fluids were highly influenced by water-rock interaction. The thermal waters from the study area are depleted in ^{18}O and D and plot on the global meteoric water line (GMWL), their deep-circulating meteoric origin shows that most thermal waters plot on or near the meteoric water line, with some exceptions due to Mediterranean precipitation, probable water-rock isotope exchange or mixing takes place between the ascending geothermal water and shallow colder groundwater. The subsurface reservoir temperatures were calculated using different solute geothermometers and computation of saturation indices for different solid phases. The highest estimated reservoir temperatures are indicated by the cation composition geothermometer (CCG) and the Na–K–Ca geothermometer, while slightly lower estimates are obtained using silica geothermometers, with local geothermal gradients ranging from 25 to 45 °C/km.

ABSTRACT 105
BOARD S002

Testing the usefulness of carbon and nitrogen stable isotopes to understand organic carbon source partitioning within marine sediments

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Marine sediments are one of the largest reservoirs of organic carbon (OC) in the planet; biochemical processes happening therein, such as organic matter degradation, are thus a vital part of the global carbon cycle. Many studies have focused on how degradation occurs and what are the parameters relevant to the process; fewer have characterised how proxies for OC source, such as stable isotopes (SI) and fatty acids, change in relation to burial duration (and degradation), or how can such information be used to quantify source-specific contribution of OC to marine sediments. Our study tests whether known combinations of organic matter inputs can be successfully reconstructed after periods of incubation extending up to two years using quantitative measurements of SI composition combined with mixing models. We are conducting a long-term laboratory experiment in which known quantities of sediment and three macrophytes (red and brown macroalgae and seagrass) are incubated for various durations (4, 10, 21, 45, 90, 180, 365, and 730 days) under different treatments (control, single species, and multi-species) and without additional input of organic matter. We will present preliminary data on the total OC content and carbon and nitrogen contents and SI signals of experimental samples and discuss how proxies are affected by degradation and how they can be used to predict/validate macrophyte contribution to sedimentary OC.

ABSTRACT 106
BOARD S003

The role of farm drains in attenuating nitrogen from agricultural farms

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Agricultural activities are widely acknowledged as significant contributors to eutrophication and consequent algal blooms in waterways, especially in nutrient-limited systems. Previous studies have primarily focused on nutrient dynamics and fate at the catchment scale, while research at the farm scale remains scarce, despite the potential role of farm drains in mitigating the availability of nitrogen and phosphorus in receiving waters. In this study, we delved into the mechanisms driving the export of excess nutrients from agricultural farms, utilizing both nutrient concentrations (nitrate, ammonium, phosphorus) and isotopes ($\delta^{15}N\text{-}NO_3^-$, $\delta^{18}O\text{-}NO_3^-$, $\delta^{15}N\text{-}NH_4^+$). Farm drains were classified based on irrigation method (Sprinkler versus Flood irrigation) and waste management practices (re-use dam application versus non reuse dam application). Runoff water samples were collected from farm drains during rainfall and irrigation events. Across all sampled drains, mean concentrations of (nitrate, ammonium, phosphorus) were significantly higher in runoff from the sprinkler irrigation drains compared to the flood irrigation drains during rainfall events. While phosphorus concentrations were significantly higher in the flood irrigation drain than the sprinkler irrigation drains during irrigation events. The $\delta^{15}N\text{-}NO_3^-$ and $\delta^{18}O\text{-}NO_3^-$ clustering indicated majority of the farm drains had high contributions of manure-derived NO_3^- in the runoff. We observed a positive correlation in the relationship between $\delta^{15}N\text{-}NO_3^-$, and $\delta^{18}O\text{-}NO_3^-$, during both events, with more enriched signatures observed during rainfall events indicating potential occurrence of denitrification. Combined $\delta^{15}N\text{-}NO_3^-$ and NO_3^- concentration data from all the drains showed little evidence of denitrification and potential nitrification/denitrification signals, particularly, during rainfall events which potentially overprinted signals for denitrification in the drains. The predominance of nitrification/denitrification in the drains was substantiated based on the trajectory between $\delta^{15}N\text{-}NO_3^-$ and $\delta^{15}N\text{-} NH_4^+$ which showed concomitant enrichment of both isotopes in majority of the drains. Overall, our findings provided evidence that irrigation systems create conditions for NO_3^- and DRP accumulation and runoff from dairy farms respectively.

ABSTRACT 107
BOARD S004

Individual specialization on marine resources facilitated by physiological adaptations predicts growth in a freshwater piscivore (*Esox lucius*) inhabiting brackish lagoons

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Individual diet specializations, often accompanied by behavioral, physiological and morphological adaptations, contribute to intrapopulation divergence and speciation. Coupling of food webs, e.g., marine and freshwater food webs in brackish environments, where pulses of marine prey are available to freshwater predators, can facilitate individual specialization on these novel resources. Our objective was to study the role of marine energy pulses through, e.g., migrating herring (*Clupea harengus*) for individual specialization and population differentiation of a freshwater piscivore (northern pike, *Esox lucius*) in brackish habitats. Dietary contributions from freshwater, lagoon, and offshore marine food webs were characterized using stomach content data of 171 pike, and stable isotope mixing models in 302 pike. We assessed lifelong individual specialization from consecutive eye lens lamina isotope values in 82 individuals, and estimated lifelong growth benefits of a putative marine diet. Body length and habitat use behavior were major predictors of diet contributions, with larger, more saline-adapted individuals relying more on marine resources. Individual specialization was strongest in brackish-adapted individuals, whereas migratory and freshwater-resident individuals appeared more generalist. Marine prey had a higher energy content and benefitted growth of pike in our study. We suggest the evolution of physiological adaptations enabled part of the population to access marine resources, facilitating individual specialization. Given current declines of coastal pike and the strong link of lagoon and marine food webs, the management of pike needs to be considered as part of a holistic ecosystem management of the Baltic Sea fishes.

ABSTRACT 108
BOARD S005

Variation in marine mammal sulfur stable isotope compositions ($\delta^{34}S$) is driven by sources of primary production not trophic position

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The homogenous isotopic composition of marine sulfate ($\delta^{34}S \cong +21$ ‰) leads to the expectation of an oceanic isoscape exhibiting little variation in $\delta^{34}S$. Nevertheless, instances of variation in $\delta^{34}S$ have been identified in Arctic marine ecosystems that require clarification to explain the mechanisms driving unexpectedly low values. Walruses are frequently characterized by low $\delta^{34}S$ compared to other marine mammals, but it is unclear if these values are a function of the low trophic position of walruses or of a specialized foraging niche. This study examines the two potential drivers of differences in sulfur isotopes at the species level: trophic position and foraging ecology. By analysing archaeological samples of walrus, ringed seal and polar bear from archaeological sites at three discrete locations in the Canadian Arctic (Ellesmere Island, Devon Island and northwest Hudson Bay), we have clarified and confirmed that in collagen-to-collagen comparisons, differences in $\delta^{34}S$ are not driven by trophic discrimination factors. Bacterial influences on the sulfur cycle, particularly symbiotic relationships between chemosynthetic bacteria and invertebrates in the benthos may be a cause of the low $\delta^{34}S$ values in walrus and likely represent an often overlooked element of primary production to the shelf food web.

ABSTRACT 109
BOARD S006

How do mixotrophic plankton stabilize food webs in the face of climate change? A model aquatic ecosystem in Antarctica

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Earth's most productive marine ecosystems rely on mixotrophic microplankton, which can both photosynthesize and consume bacteria, to support biogeochemical cycles and diversity in higher-level consumers. While studies have suggested that mixotrophs are essential in stabilizing complex food webs by increasing the efficiency of energy flow, their physiologies and trophic dynamics are poorly resolved. Further study of these organisms is an important step in understanding how aquatic ecosystems will shift in response to climate change. Lake Fryxell, an entirely microbial aquatic ecosystem in the McMurdo Dry Valleys of Antarctica, is an ideal model ecosystem to study mixotrophy due to its bimodal sun pattern and lack of higher-level consumers. We will present metagenomic and essential amino acid (AA_{ESS}) stable isotope data that further delineates the role of mixotrophic cryptophytes (*Geminigera cryophila*) in Lake Fryxell with direct implications for regional marine food webs and biogeochemical cycling. Our preliminary AA_{ESS} $\delta^{13}C$ results show that cryptophytes are isotopically distinct from their food source (bacteria), suggesting this approach can distinguish between cryptophytes that rely on photosynthesis versus those that engage in phagotrophy. Our goal is to perform a cultured feeding experiment to further determine if their AA_{ESS} $\delta^{13}C$ values reflect their nutritional mode along with analysis of wild samples. We are also utilizing metagenomic analysis to identify the biosynthetic pathways that cryptophytes use to synthesize AA_{ESS}. By combining AA_{ESS} isotope and genetic analysis, we showcase a novel method to evaluate how mixotrophy influences biogeochemical cycles and may stabilize food web structure in highly seasonal ecosystems.

ABSTRACT 110
BOARD S007

The population identity and foraging ecology of South Atlantic Humpback Whales

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Anthropogenic exploitation can impact multiple aspects of species and populations, from their demographic composition, life-history strategies, and evolutionary potential to patterns of population connectivity and structure. An in-depth understanding of population structure and animal life history is essential for informing conservation and management efforts. One population which was heavily exploited was the southwest Atlantic humpback whale (*Megaptera novaeangliae*), which breeds off Brazil. Approximately 27,000 humpbacks were killed in the southwest Atlantic during the whaling period (1904-1965). This population is now estimated to be nearly recovered, however the precise range, demography and foraging ecology of this breeding population are not known, as its population structuring on offshore feeding grounds in the South Atlantic has not been characterised. In this study we have used biopsy samples from the Falkland Islands and South Georgia to take a holistic approach utilising genetic, hormonal, epigenetic and stable isotopic methods to better understand this population. Our results show the population is highly diverse with a complex age and hormonal structure. The stable isotope results shed light on the foraging ecology, showing trophic levels consistent with previous studies on baleen whales, and variation in foraging strategies between the Falkland Islands and South Georgia, helping to inform the stock management of economically important fisheries in the South Atlantic. Comparison with larger datasets from higher latitude breeding grounds allows us to understand our findings in the global context of this highly migratory species.

ABSTRACT 111
BOARD S008

Compound specific nitrogen isotope analysis of amino acids in marine mammal bone collagen

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The analysis of stable carbon and nitrogen isotopes of amino acids is routinely applied in ecology to assess trophic relationships and isotopic baselines. More recently the method is now also used in archaeological science, where amino acids are analyzed in ancient bone collagen to attempt reconstruction of past diet and food webs. Previous studies have attempted to infer trophic positions of marine mammals using the nitrogen isotopic signatures of the trophic amino acid glutamic acid/glutamine (glx) and the source amino acid phenylalanine (phe). Trophic formulas, relying on trophic discrimination factors (TDF) that have proven useful for fish and invertebrates, have yielded confounding results when applied to marine mammals. This has led to discussion in the field and the realization that our understanding of higher marine mammal isotopic fractionation remains limited (see Matthews et al. 2015). Here, we present new amino acid data of ancient bone collagen from Steller sea lions and Northern fur seals from Unangax̂ ancestral middens in the Aleutian Islands. We explore the potential causes of high phenylalanine nitrogen values (range = 11-20 $\delta^{15}N$) in these ancient *Otariid* samples and compare our results to other published marine mammal studies.

ABSTRACT 112
BOARD S009

The viability of mucus for providing isotopic insights into the trophic ecology of manta rays

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Manta rays are iconic and enigmatic species with poorly understood life histories. Gaps in knowledge surrounding their trophic ecology can be partly attributed to tissue sampling restrictions in aggregation areas often located in less economically developed countries, which can have a heavy reliance on income from manta tourism and regularly reject applications to perform tagging and tissue biopsies on the grounds of visual impairment to manta rays and negative tourism impacts. The non-invasive collection of mucus from manta skins may thus provide a solution for many knowledge gaps. Mucus has been used successfully in multiple DNA studies and a preliminary study explored mucus fatty acids and isotopes in mantas. Such isotope analyses can revel important life history traits, specifically in terms of diets and movement ecology. However, interpreting isotopes measured in manta mucus depends on validated methodology and better understanding of the isotopic relationships between mucus and diets, especially in terms of isotopic offsets and turnover times. Here we explore the viability of manta mucus in isotope studies based on preliminary data from the first controlled feeding study of a manta ray.

ABSTRACT 113
BOARD S010

IMPORTANCE OF ACCOUNTING FOR THE INFECTION STATUS OF HOST ORGANISMS IN ISOTOPE ECOLOGY STUDIES: WHAT CAN WE LEARN FROM FEEDING EXPERIMENTS?

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Wild organisms are usually infected with a variety of parasites, functionally forming an ecosystem by themselves. Parasites are therefore integral part of all ecosystems and play an important role in food webs, thereby often altering food web properties. However, the infection status of organisms is rarely taken into consideration in ecological and food web studies. Parasites can impact host organisms in two ways, affecting (i) the resource intake, by causing behavioral, morphological or physiological changes that can lead to alterations in the quantity or quality of the food consumed, or (ii) internal resource use, e.g. by affecting the physiology, metabolism, reproduction, growth or immune response of their hosts. These changes can lead to changes in the isotopic composition or niche, potentially causing differences between infected and uninfected organisms that can lead to erroneous conclusions in isotope ecology studies. We conducted laboratory feeding experiments on two common coastal parasite-host systems to test our conceptual model. For this, we applied both stable isotope analysis of whole tissues (bulk SIA, ^{13}C and ^{15}N) and compound-specific stable isotope analysis of amino acids (CSIA-AA), which allows for comparison of source vs trophic amino acids to infer the trophic level of individual animals. This way, we aim to determine isotopic changes caused by dietary shifts or parasitic infections, making a significant contribution to our understanding of parasitic trophic interactions and their potential to affect the isotopic composition of infected hosts.
Acknowledgments: Horizon 2020 - Research and Innovation Framework Programme (MSCA -IF, project number 101027941).

ABSTRACT 114
BOARD S011

LONG-TERM REPRODUCIBILITY OF CSIA-AA DATA IN BIOLOGICAL MATERIALS

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Application of compound-specific stable isotope analysis of nitrogen ($\delta^{15}N$) and carbon ($\delta^{13}C$) in amino acids (CSIA-AA) has expanded rapidly in recent decades, particularly in the fields of modern and paleoecology. The comparability of ecological or paleo literature data, in particular from different labs, fundamentally depends on how accurate and reproducible CSIA-AA data can be over long time frames, with varied users, protocols, and instrumentation. However, to date there are no established CSIA-AA reference materials, no common data validation protocols, and no large multi-lab intercalibrations. Instead, labs employ a variety of individual approaches, typically based on internal or external standards, while long-term reproducibly is essentially never reported. We report here a unique >10-year record of $\delta^{15}N$ and $\delta^{13}C$ values generated for an internal biological reference material (*Spirulina sp.*), using TFA derivatization and GC-IRMS analysis. This data set represents the output of many users, variations in wet chemistry, and multiple GC-C-IRMS instruments, so likely represents an excellent proxy for reproducibility of a single material between labs. The overall record demonstrates remarkable robustness in both $\delta^{15}N$ and $\delta^{13}C$ data, while at the same time revealing substantial differences for specific AA. The degree of long-term CSI-AA variably for standard materials likely reveals the “real” limit that can be assumed regarding CSI-AA data comparability. The goal, ultimately, is to use the information provided by this long-term record as a tool for assessing CSI-AA data quality, for better differentiation of natural sample variation from method variability, and for informing the ongoing refinement of best lab practices.

ABSTRACT 115
BOARD S012

Standardising reference materials for amino acid carbon stable isotope analyses to determine analytical biases between labs

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Stable isotope analysis of specific compounds is rapidly expanding across ecology and archaeology, addressing many of the limitations associated with bulk approaches such as variable environmental baselines and limited numbers of tracers. Carbon stable isotope ratios in amino acids (AA) have shown considerable promise in tracing the origins of basal resources in diverse food webs, due to consistent offsets in $\delta^{13}C$ values among the essential AAs across taxa and spatiotemporal scales (i.e. $\delta^{13}C$-EAA patterns), with limited modifications during trophic transfer. Despite these advances, the method's increased logistical efforts and expense, especially for analysing microbial organisms, means many studies do not analyse all basal organisms associated with their ecosystem of interest. Instead, studies often rely on previously published data to characterise their basal organism groups. However, the direct comparison of data from across studies and labs is problematic due to the absence of internationally agreed standard reference materials coupled with biases associated with different analytical protocols. For example, for GC-IRMS analyses, comparisons of N-trifluoroacetyl isopropyl esters (TFA/IP) and N-acetyl methyl ester (NACME) AA derivative $\delta^{13}C$ values show molecular weight-dependent biases. To address these challenges, we invite researchers to an inter-lab comparison study encompassing different analytical protocols to identify and quantify protocol-specific biases. By freely distributing sets of standard reference materials at IsoEcol for practitioners, we aim to facilitate direct data comparisons across labs and the establishment of reference libraries of $\delta^{13}C$-AA values in basal organisms to augment future studies.

ABSTRACT 116
BOARD S013

A COMMON ONTOLOGY FOR STABLE ISOTOPE DATA

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Australian government science agencies are developing a public-good national asset for environmental stable isotope data. The aim of the national asset is to repurpose existing publicly available environmental stable isotope data into a federated data platform, allowing single point access to the data collections. The challenge is to bring siloed data, which is stored in different formats with differing levels of accessibility, together while maintaining the data integrity. Each organisation has different systems in place for the unique identification of their samples and resulting data. These systems, however, are focused to meet the specific scope of the organisation and are not easily adapted outside of the organisation. To connect the disparate data from each organisation into a usable whole, a common ontology has been co-designed between the collaborating agencies. The development of a common ontology is a foundational step in enabling data to be unified for reuse. It has been designed to be easily adopted by future users, while maintaining data integrity. The common ontology describes the different concepts present in the data, giving meaning to the stable isotope 'observations' or measurements of (isotopic) properties of physical samples of the environment. It coordinates this description of samples with standardised metadata and vocabularies, which facilitate machine-readability and semantic cross-linking of resources for interoperability between multiple systems. We will present the first iteration of the common ontology, as well as how it is operationalized across different datasets and the logistical challenges faced in dealing with different data partners and stakeholders.

ABSTRACT 117
BOARD S014

UNRAVELING DIETARY INTERACTIONS AND ASSESSING ECOSYSTEM HEALTH: A FOCUS ON ATLANTIC SALMON *SALMO SALAR* IN THE MEDWAY RIVER, NOVA SCOTIA

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The Medway River supports Southern Upland Atlantic salmon that are assessed as endangered by COSEWIC. In partnership with the Medway River Salmon Association (MRSA), this study aims to determine the relative habitat health and give insight on habitat suitability to sustain an Atlantic salmon population. Despite limited stable isotope analysis (SIA) studies in Atlantic Canada pertaining to salmon habitats, this methodology offers unique advantages and should be further explored. Notably, the availability of various standards for individual isotopes allows cross-experimental comparisons. Carbon and nitrogen signatures derived from SIA provide invaluable insights into food web dynamics and trophic relationships within complex ecosystems. Hence, this study aims to assess habitat quality by examining food web dynamics within the Medway River watershed. Using a model integrating physical and chemical habitat conditions alongside SIA, findings are compared with other common indices, trends, and SIA datasets. This study demonstrates the use of SIA for assessing habitat quality via food web dynamics in rivers with declining Atlantic salmon populations. The outcomes of this study not only contribute to comparative analyses with existing community data but also serve as a reference for future river monitoring initiatives within the Medway River watershed. Ultimately, our project offers a broadly applicable methodology for watershed assessment, complementing other comparison methods such as indices and the CABIN (Canadian Aquatic Biomonitoring Network) ARM (Atlantic Reference Model).

ABSTRACT 119
BOARD S016

Do fish fertilize trees? An analysis of marine-derived nutrient subsidies to riparian ecosystems in New Brunswick, Canada

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Marine-derived nutrients (MDNs) are important subsidies brought to river ecosystems by anadromous fish on their return from the marine environment. MDNs are released into the freshwater environment via excretory products, gamete deposition, and mortalities. While there is an ever-growing body of research demonstrating the benefits of MDNs to Atlantic river ecosystems, there has been significantly less research on their benefits to surrounding terrestrial ecosystems. Research has found that it is possible to use stable isotope analysis to identify the marine signature of ^{15}N from these anadromous fish in riparian trees. Using tree growth rings as an index of time, researchers have been able to reconstruct historic population levels of Pacific salmon based on the annual marine-terrestrial transfer of MDNs. However, this phenomenon has yet to be identified on the East Coast of North America. Therefore, the goal of this project is to identify MDNs (specifically nitrogen: ^{15}N) from anadromous fish including: Atlantic salmon (*Salmo salar*), alewife (*Alosa pseudoharengus*), blueback herring (*Alosa aestivalis*), and sea lamprey (*Petromyzon marinus*) in tree rings from rivers in New Brunswick, Canada. Tree rings will be analyzed from selected hardwood (red maple (*Acer rubrum*)) and softwood (Eastern white pine (*Pinus strobus*)) trees along riverbanks. This is a novel study, primarily due to the iteroparous nature of Atlantic anadromous fish (fewer MDNs) and the relatively young (in comparison to the West Coast) age of the forests. This project will yield great insight into the occurrence of this phenomenon on the East Coast of Canada.

ABSTRACT 120
BOARD S017

ISOTOPIC VARIABILITY OF BONE COLLAGEN AMINO ACIDS IN MAMMALS WITHIN A TEMPERATE FOREST ECOSYSTEM – ACTUALISTIC APPROACH WITH IMPLICATIONS FOR PALEOECOLOGICAL RECONSTRUCTIONS

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Carbon and nitrogen stable isotope analysis of animal tissues is a common tool for investigating animal and human populations' dietary ecology and paleoecology. Though a powerful method, bulk collagen analysis has important limitations, resulting from averaging isotopic signals of individual amino acids (AA) that come from variable sources and undergo different metabolic pathways. This limitation led to seeking more advanced methods, including stable isotope composition of individual AAs in bone collagen, a method progressively implemented in paleoecology in recent years. However, studies focused on fossil mammals showed that the isotopic composition of bone collagen AAs varies among animals within one assemblage, even within ecological guilds (such as herbivores or carnivores). This calls for more studies of AA isotopic variability and trophic relationships within representative ecosystems. Our study focuses on Bialowieża Primeval Forest (BPF, Poland), a model of European temperate natural forest ecosystems. We analyze AAs $\delta^{15}N$ and $\delta^{13}C$ values in a collection of BPF modern mammals. We track the variability of the isotopic composition of bone collagen AAs among large herbivores and carnivores and use this data to indicate general intra-ecosystem variability and quantify the prey-to-predator flux of isotopes within a single forest ecosystem. The results may serve as a model of AAs isotopic diversity in paleoecological reconstructions.

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ABSTRACT 121
BOARD S018

DEALING WITH BIASES INTRODUCED BY LIPIDS IN STABLE CARBON AND NITROGEN ISOTOPE ANALYSES: A SOLUTION BASED ON 28 MARINE INVERTEBRATE, FISH AND MAMMAL SPECIES

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Lipids are naturally depleted in ^{13}C relative to proteins, causing a bias in $\delta^{13}C$ of bulk samples that varies with lipid content. Failure to account for this issue results in inaccurate conclusions in marine food web and habitat use studies. This issue can be resolved by 1) extracting lipids from samples prior to measurement, a resource-intensive process that can also alter $\delta^{15}N$, or 2) estimating a lipid-free $\delta^{13}C$ using one of several equations that differ in degree of sophistication and generalization across taxa. Here, $\delta^{13}C$ and $\delta^{15}N$ were measured on bulk and lipid-extracted muscle samples of a large dataset of over 2000 specimens of 28 species of marine invertebrates, fishes, and mammals. Our objectives were to compare the effect of lipid extraction on $\delta^{13}C$ and $\delta^{15}N$ across taxa and the performance of five normalization models, overall and on subsets of species, to propose a model to revert lipid-extracted $\delta^{15}N$ back to their bulk values, and to identify the best approach for dealing with lipid-related biases. Lipid extraction caused an uneven enrichment in $\delta^{13}C$ and $\delta^{15}N$ across species. Model taxonomic specificity increased estimation accuracy for both isotopes. While models from Logan et al. (2008) and McConnaughey and McRoy (1979) were the best at predicting $\delta^{13}C_{\text{lipid-free}}$, a linear model reliably estimates $\delta^{15}N_{\text{bulk}}$ from $\delta^{15}N_{\text{lipid-free}}$ values. This study provides a way forward for obtaining reliable $\delta^{13}C$ and $\delta^{15}N$ values for muscle tissue without the costs of duplicate analyses, representing a major step toward the harmonization of datasets generated using bulk and lipid-extracted samples.

ABSTRACT 122
BOARD S019

Impacts of Decomposition on the Stable Isotope Compositions ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$) of Human Skin

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In forensic investigations, estimation of the post-mortem interval, the time since death, is essential to the legal process. The timeline of decomposition can be estimated through the use of certain methods; however, these methods are less accurate or unapplicable in later stages. In this study, changes to the stable isotope compositions of human skin samples ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$) from donors placed at body farms were examined over the course of decomposition. While the primary purpose of this study was to determine the suitability of using soft tissue stable isotope compositions for estimating time since death, the results also have implications for interpreting isotopic data collected from ancient, naturally mummified skin samples.

ABSTRACT 123
BOARD S020

HYDROGEN AND OXYGEN ISOTOPES IN VERTEBRATE TISSUE ORGANIC SUBSTRATES VARY BY DIET TYPE

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Hydrogen and oxygen isotope ratios in hard and soft tissues are useful tracers in migratory, ecological, and archaeological studies. Controlled feeding experiments have been used to determine the isotopic contribution of food and water to tissues. Here we report the results of a feeding experiment where the diet type was varied, from plant-based, insect-based, and meat-based pelleted diets, all of which were fed to three different vertebrate taxa. We determined the diet to tissue offsets for δ^2H ($\Delta\delta^2H$) and $\delta^{18}O$ ($\Delta\delta^{18}O$) of tissue-bound organic matter in rats, guinea pigs, and quails in two tissue types: muscle and dentine.
The diet to tissue offset varies by diet type by up to ~20 ‰ ($\Delta\delta^2H$) and ~2 ‰ ($\Delta\delta^{18}O$) in lipid-extracted muscle tissue and dentine collagen. We also observe variation in $\Delta\delta^2H$ and $\Delta\delta^{18}O$ by species and tissue type. The effect of diet type on consumer tissue $\Delta\delta^2H$ and $\Delta\delta^{18}O$ is important to consider as a source of isotopic variability for some studies such as diet or drinking water reconstructions and (palaeo-)climate inferences drawn from them, particularly in species that may vary their dietary habits.

ABSTRACT 124
BOARD S021

Assessment of δ^2H values of non-exchangeable hydrogen in organic Reference Materials: Progress and challenges towards robust procedures to ensure comparable isotopic data for aquatic and terrestrial ecology and environmental forensics

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The hydrogen stable-isotope (δ^2H) composition of complex organics (flora, fauna) is widely used in environmental and forensics studies. Non-exchangeable, carbon-bound H, is mainly derived from environmental water used by organisms and plants and correlates to provenance via predictable global patterns in precipitation. However, a significant fraction of the H in complex organics can exchange H atoms (O-H, N-H groups) with ambient laboratory vapor. The exchangeable H can range from ca. 2-60 % of the total H, depending on the type of organic sample. Uncontrolled H isotope exchange alters the environmental signal of the H isotope content of bulk organic matter in the laboratory, depending on location and season. Moreover, inconsistent analytical approaches or incomplete drying (contamination) can additionally compromise the comparability of data produced by laboratories. Recently, new organic reference materials (RMs) were introduced which do not have reproducible δ^2H values for their non-exchangeable H. Organic H isotope RMs are vital to ensure data are fully traceable and comparable among laboratories. Advances in understanding aquatic and terrestrial biochemical processes are only possible if H isotope data generated by laboratories can be replicated using these properly calibrated materials.

In this ongoing international project (2023-2025) funded by the Austrian Science Foundation (FwF), we aim to establish standardized procedures in multiple laboratories with the goal to establish consensus δ^2H values for non-exchangeable H for the current suite of complex organic reference materials (RMs) that contain exchangeable H. These international RMs are wood: (USGS54, USGS55, USGS56, IAEA-613, IAEA 614); L-valine: (USGS73, USGS74, USGS75); glycine: (USGS64, USGS65, USGS66); honey: (USGS82, USGS83); collagen (USGS88, USGS89); keratin: (CBS, KHS), hair: (USGS42, USGS43) and flour: (USGS90, USGS91), among others. Ultimately, the consensus values can be used to normalize data for matrix equivalent samples using, for example, high sample-throughput approaches like comparative equilibration to ensure all laboratories can produce comparable results.

We aim to establish non-exchangeable $\delta^{2}H$ values by developing standardized equilibration and drying procedures that enable scientists to normalize measurements of organic samples to the VSMOW-SLAP scale thereby leading to widespread adoption of these RMs by the global scientific community. A team of scientists in 10 laboratories (Austria, Belgium, Czechia, Germany, Canada, USA, Taiwan, IAEA) will cooperate to develop a suite of optimized identical treatment (IT) approaches for online heated drying, dual-vapor isothermal equilibrations, QA/QC checks, and thermochemical reduction of samples using chromium or carbon reactors, and two-point delta-scale calibration using primary δ-scale defining reference materials (VSMOW2, SLAP2). The presentation summarizes the issues, current progress, and challenges we have encountered in various laboratories to underscore the difficultly of obtaining reproducible organic H isotope analyses.

ABSTRACT 124
BOARD S021
cont’d

ABSTRACT 125
BOARD T001

FEDERATING STABLE ISOTOPE DATA TO CREATE A NATIONAL ASSET IN AUSTRALIA

Nina Welti[1], Jagoda Crawford[2], Geoff Fraser[3], Lian Flick[1], Christoph Gerber[1], Steph Hawkins[3], Cath Hughes[2], Mark Lewin[4], Alex Leslie[2], Fong Liu[4], Alex Mustakov[1], Abhijit Paul[4], Athina Puccini[1], Tim Stobaus[4], Axel Suckow[1], Steve Szarvas[1], Kathryn Waltenberg[3]

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Australia's agriculture and food system is highly trusted and reputable, both domestically and internationally, due to a responsive and effective assurance system. However, rising consumer demands for detailed information on food production practices alongside multiple and conflicting regulatory objectives, is increasing the cost and complexity of compliance across Australia. To strike a balance between the needs and interests across the food industry, consumers and government agencies, a pilot project involving Australian government science agencies is developing a public-good national asset for environmental stable isotope data. Australian government science agencies regularly include stable isotope measurements in their environmental monitoring and research activities, but the utility of the existing data is limited. The challenge is that the data are often siloed within organisations, stored in different formats and with differing levels of accessibility. This has been a barrier to developing technology that addresses the growing expectations for information and data. By federating significant, yet disconnected, public-good data resources of environmental stable isotopes, the Australian government agencies can make foundational data available and realise the full value of these national assets and support key industries. Repurposing these data collections creates a return on investment for the research organisations and incentive for continued research. This talk will discuss the challenges and solutions faced in this pilot, balancing economic competitiveness with social inclusiveness, environmental sustainability, open participation, highlighting data management, governance, and stewardship of environmental stable isotope data.

ABSTRACT 126
BOARD T002

Assessing the Ecological Services of Urban Wetlands: Exploring Contamination, Food Web Dynamics, and Wildlife Habitat Quality

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Urban wetlands play a crucial role in providing ecosystem services, yet their proximity to harmful industries raises concerns about contamination and its impact on quality of these services. These wetlands offer a crucial source of nutrition enriched with highly unsaturated fatty acids, primarily in the form of emerging aquatic insects (secondary production), which support the dietary needs of aerial insectivores (birds and bats). It is plausible that these species rely on habitat cues provided by these wetlands when selecting breeding areas in spring irrespective of the quality of habitat. Central to our inquiry is the examination of whether these wetlands serve as beneficial habitats for wildlife or function as ecological traps.

To address this question, we selected seven urban floodplain wetlands in the Wolastoq|Saint John River located within the Fredericton city limits. Our preliminary research focused on assessing baseline condition within these wetlands with respect to contamination levels, the quantity of emerging aquatic insect biomass, their fatty acid profiles, adjacent bird and bat richness and the isotopic signature of the benthic macroinvertebrate community. However, to answer our major research question we are expecting to identify food sources of riparian birds using stable isotope analysis. Through a multidisciplinary approach encompassing ecological, chemical, and isotopic analyses, we aim to provide insights into the quality of ecosystem services provided by urban wetlands and their implications for wildlife conservation and management in urban environments.

ABSTRACT 127
BOARD T003

Synchronous partial diel vertical migration and niche partitioning in *Mysis* revealed by stable isotopes

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Diel Vertical Migration (DVM) plays a critical role in aquatic food webs by linking benthic and pelagic habitats. *Mysis* spp. are vital in this process because they consume and are consumed in both habitats, moving energy and matter through DVM. Recent observations show that *Mysis* exhibits partial DVM (pDVM) with some individuals migrating and some remaining benthic, being unclear whether pDVM results from synchronous or asynchronous behavior in individual *Mysis*. To evaluate these behaviors, *Mysis diluviana* was collected from benthic and pelagic habitats day and night across bathymetric depths ranging from 50 to 250 m in Lake Superior. We evaluated isotopic niche size (Standard Ellipse Area - SEA$_b$) and overlap between different size classes in both habitats and periods (day vs. night). Large *Mysis* (>15 mm length) presented larger SEA$_b$ ($1.8 \pm 0.4‰^2$) compared to small (<10 mm; $0.3 \pm 0.1‰^2$) and medium (10-15 mm; $0.7 \pm 0.2‰^2$) individuals, with no isotopic niche overlap between large and other size classes, indicating differential usage of available resources. Stable isotopic values and niche overlap among habitats and periods indicated the population has a synchronous pDVM, where small individuals migrate, and large *Mysis* stay at the bottom. Within size groups, we found asynchronous pDVM for medium and large individuals. *Mysis* presents a complex ecological behavior, shifting migration and foraging habits depending on the life stage, likely due to different environmental pressures, such as predation, light, depth, and food availability. Our work successfully revealed the synchronization patterns in pDVM, contributing a step further to understanding pelagic-benthic coupling in deep lakes.

ABSTRACT 128
BOARD T004

Baleen as a biological testimonial of trophic ecology individual variation on a southern humpback whale (*Megaptera novaeangliae*)

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The stable isotope analysis in the baleen plates is a tool to access individual variation of fine-scale trophic ecology. During baleen synthesis, it incorporates the isotopic values related to the recent diet and, over its growth, becomes an inert tissue. The present study aimed to bring new information about stock A humpback whale trophic ecology. The baleen plate was obtained from an adult female humpback whale carcass found stranding in southeastern Brazil, in 2014. It was washed with chloroform:methanol (2:1, v/v), and subsamples were taken from each centimeter (n=60). The $\delta^{15}N$ and $\delta^{13}C$ values were determined by an isotope-ratio mass spectrometer. The $\delta^{15}N$ ranged from 5.4‰ to 7.2‰ ($\bar{X} = 6.45 \pm 0.4$‰); the $\delta^{13}C$ varied from -26.0‰ to -22.9‰ ($\bar{X} = -24.5 \pm 0.6$‰). The newer baleen segments (0 to 11 cm) were ^{15}N enriched ($\bar{X} = 6.8 \pm 0.2$‰), indicating a fasting response due to their large migration. The $\delta^{15}N$ shifts perform three and a half cycles of reproductive and feed seasons with different durations. The fluctuation along the plate can be explained by migration patterns and variations on the food web baseline values. Nevertheless, between 24 cm and 28 cm occurs a slight ^{13}C enrichment ($\bar{X} = -23.8 \pm 0.6$‰) and ^{15}N depletion ($\bar{X} = 6.2 \pm 0.1$‰) during a feeding season, which may suggest foraging in different areas within their feeding ground. This sign of diversity in the feeding strategy of humpback whales deserves more investigation once it can amplify our ecological knowledge and improve the conservation efforts over this species.

ABSTRACT 129
BOARD T005

CEREAL CO-FEEDING IN FISHPONDS. DO WE NEED IT? OR IT IS JUST WASTE OF OUR SOURCES

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Fishponds are an important part of the middle Europe countryside. In this region, thousands of ponds are used for fish production, focusing on common carp production (*Cyprinus carpio*, L.1758). During the last century, an intensification of fish production (adding manure and cereal co-feeding into ponds) connected with overpopulated fish stock in ponds led to eutrophication and disbalance of whole pond ecosystems. In this study, we aim to 1/reduce the amount of cereal co-feeding and maintain the net carp production per hectare, like with a traditional concept; 2/Reduce nutrients loading of the pond ecosystem. To do so, we combine stable isotopes and fatty acid analysis together with physicochemical water parameters and abundance and biomass of all important biota inhabiting ponds. In the first step, we monitored chosen fishponds one year before our manipulative experiment began to have a comparison with the traditional approach. In the following years, we divided ponds into two groups: with and without cereal co-feeding. Also, we adjusted fish stock in ponds to maximize natural food source utilization and improve physicochemical water parameters at given ponds. Sampling (biota, physicochemical water parameters) was carried out monthly. Our results show that common carp food source utilization varies across the season, and cereals seem to be the last option to be eaten - only when natural food sources are depleted. Also, we maintain the same production per hectare and improve water quality at a given pond. We prove our concept is valid, and now we must increase awareness among fishermen.

ABSTRACT 130
BOARD T006

Assessing heterotrophy in mixotrophic corals using multiple isotope metrics

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Scleractinian corals are the foundation of coral reefs, which are among the most diverse ecosystems on Earth and provide valuable resources to millions of people living nearby. Corals are highly productive in nutrient-poor waters due to efficient nutrient recycling between the coral host, its endosymbiotic Symbiodiniaceae dinoflagellates, and other associated microbes. Symbiodiniaceae play a significant role in corals' autotrophic nutrition by providing their host with carbon-rich molecules called photosynthates, which can cover up to 90% of the coral's energetic requirements in optimal conditions. Corals are also heterotrophic organisms that can consume a variety of particles, ranging from bacteria to macrozooplankton. Therefore, corals have evolved different feeding strategies based on both autotrophic and heterotrophic nutrient acquisition, also called mixotrophy. Laboratory experiments have shown that corals change their diet under stress conditions, and corals with a higher rate of zooplankton predation (heterotrophic diet), evident through a compound-specific stable isotope analysis of amino acids (CSIA-AA), have better survival rates. In this study, we investigate whether these isotopic changes are observed in the field, in addition to the lab. We sampled four coral species at two sites in the Ulithi Atoll Micronesia, where one site is considered pristine and the other is considered deteriorated. We examined changes in the sources and cycling of carbon and nitrogen within the coral holobiont using CSIA-AA. These data can serve as a proxy for coral health to provide early warnings and science-based management to local communities while there is still time to protect the corals.

ABSTRACT 131
BOARD T007

ISOTOPIC ECOLOGY APPLIED TO CONCEPTS IN RIVER FUNCTION UNVEIL NATURAL GRADIENTS IN THE PAMPAS BIOME, SOUTH AMERICA.

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Theoretical frameworks in fluvial ecology aim to identify global patterns of river ecosystem function. Over the past 50 years, the basal evidence to support these theories is largely derived from temperate ecosystems or tropical regions with flood seasonality, potentially biasing the global reach of these fundamental concepts. We apply these concepts to subtropical river ecosystems with irregular flow regimes in South America to broaden our general understanding of fluvial system function. Using bulk C and N stable isotope analysis combined with standardized fish community monitoring and gut content analysis, we tested the applicability of different theoretical frameworks along a longitudinal gradient in one of the less impacted rivers of the Pampa biome in Uruguay. The isotopic niche of fish communities was used as a proxy for ecological niche metrics, such as trophic diversity and food web length, while Bayesian isotopic mixing models unveiled the origin of biomass in metazoan assemblages along spatial and temporal gradients. Moreover, by analyzing tissues with differing turnover rates in local fish, we explored changes in energetic subsidies with varying river hydrology in time. Trophic diversity and food web length did not increase along the longitudinal gradient as many theories predict, but rather were associated with geomorphological features that influence community composition and body size of the dominant predator, *Hoplias lacerdae* (wolf fish). Fish biomass was largely supported by allochthonous detritus, except in the headwaters, contrasting most theories. Our results demonstrate how isotopic ecology is crucial to characterizing river function and testing global fluvial ecological theory.

ABSTRACT 132
BOARD T008

Combining biochemical tracers and stomach content data to resolve interspecific competition among oceanic meso-predators from the North Pacific

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Competition for resources may have strong impacts on species’ survival, potentially playing an important role in defining species’ distribution patterns and abundances. Competing species might co-occur in large spatial scales (e.g., within the Gulf of Alaska), but avoid each other at finer spatial scales by consuming resources at different water depths, or through sub-regional differences in distribution along environmental gradients. Characterizing the resource utilization by sympatric species helps to identify interspecific competition and its potential effects when resources are limited or competitor abundance increases. This is particularly relevant under current scenarios of climate changes and shifting species distributions. Resolving competitive interactions requires knowledge of species’ trophic level and prey consumption. The 2022 *International Year of the Salmon* Pan-Pacific expeditions provided a unique opportunity to obtain samples of meso-predator species in the eastern North Pacific Ocean, including salmon and other nektonic and micronekton species (e.g., cephalopods, myctophids). The analysis of $\delta^{13}C$ and $\delta^{15}N$ in bulk-tissue has revealed substantial isotopic niche overlap among North Pacific meso-predator species. Here, we combine dietary analysis from stomach content data, bulk-tissue, and compound-specific stable isotopes to empirically resolve 1) the feeding habits of open ocean North Pacific meso-predators; 2) interspecific competition for food; and 3) assess whether competition varies spatially in relation to local oceanographic conditions. Our results will inform the development of food web models to investigate how interspecific interactions may be affected by climate-driven shifts in prey availability and species distribution.

ABSTRACT 133
BOARD T009

Application of stable isotopes analysis ^{13}C and ^{15}N to unravel the trophic dynamics of the charismatic marine fauna in Malaysia: opportunities and challenges

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Understanding the complex trophic dynamics of marine food webs, particularly interactions involving threatened or endangered species, has become more practical and reliable with the help of advanced ecological tools such as stable isotope analysis of $\delta^{13}C$ and $\delta^{15}N$ (SIA). It offers higher levels of accuracy and precision, greater insights and a deeper understanding of marine systems and processes, and greater accessibility compared to conventional research methods such as gut content analysis, allowing researchers to confidently draw conclusions from the data obtained. In this presentation, several unique cases from ecological studies to unravel the trophic dynamics of charismatic marine species, such as the predator prey relationships between the blacktip reef shark *Carcharhinus melanopterus* and hatchlings of the globally endangered green sea turtle *Chelonia mydas*, and the Irrawaddy dolphins *Orcaella brevirostris* in Malaysian marine ecosystems, will be shared. Additionally, research opportunities, including the exceptional findings and their challenges, will be discussed.

ABSTRACT 134
BOARD T010

ATMOSPHERIC NITROGEN FIXATION IN FUNGUS-GROWING TERMITES CHALLENGES TROPHIC POSITION ESTIMATION USING δ^{15}N VALUES OF AMINO ACIDS

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Fungus-growing termites and their symbiotic fungi (*Termitomyces* spp.) are ecological keystone organisms of dry savanna ecosystems. *Termitomyces* breaks down plant matter and improves termite nutrition by serving as a proteinaceous food source for the termite hosts. A significant imbalance was discovered some years ago in nitrogen isotope systematics of Kenyan *Macrotermes michaelseni* termite colonies, suggesting that either the baseline dietary plant inputs were insufficiently constrained, or that there was a sizeable contribution of atmospheric nitrogen (δ^{15}N ~0‰) entering the system. Here we report δ^{15}N analysis of individual amino acids (AA), with the aim of gaining a clearer understanding of the nitrogen sources and trophic hierarchies within this symbiotic system. The trophic position estimates (TP_{CSIA}) for the termite castes ranged from <1 to 4 and were inconsistent between the different source-trophic AA combinations. The δ$^{15}N_{Phe}$ (source AA) values for the *Termitomyces* fungus (expected 1st consumer) and all termite castes (1st-2nd consumers) were below those of the vegetation sources, and the δ$^{15}N_{Glx}$ (trophic AA) values were only slightly higher in consumers than in plants, with termite queens showing lower δ$^{15}N_{Glx}$ than the vegetation. The observed patterns support the hypothesis of atmospheric N_2 fixation within the nests, and suggest that the fixation takes place at several locations within the symbiotic system. The obtained inconsistent TP_{CSIA} estimates also challenge the reliability of the AA-CSIA approach in assessing trophic relationships in terrestrial systems that have the potential to obtain nitrogen also from sources other than the vegetation.

ABSTRACT 135
BOARD T011

High-resolution description of insular and fjordic benthic food webs along the West Antarctic Peninsula

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The West Antarctic Peninsula (WAP) is one of the most rapidly warming region on Earth. In this context, it is crucial to improve our understanding of the consequences of future changes in the local biotic and abiotic environments on marine ecosystem functioning. Here, we focused on food web structure of shallow-water benthic communities. In February 2023, the TANGO1 expedition, using a sailboat, brought nine Belgian scientists to the WAP. To assess the importance of environmental changes on local food web dynamics, five benthic communities were investigated, focusing on macroalgae forests (n=2) and sedimentary soft bottoms (n=3). These stations were distributed between two contrasted environments, Dodman Island (Grandidier Channel, 66°S) & Blaiklock Island (Bigourdan Fjord, 67.5°S). These two locations differed markedly in terms of sea-ice cover, and in terms of general hydrography (small island exposed to the Grandidier Channel's currents VS fjord system surrounded by active glaciers). Ateach station, basal food sources (i.e. sediment-associated POM, water-column POM, macroalgae, microphytobenthos) as well as benthic invertebrates (435 individuals, 64 morphospecies) were sampled quantitatively to assess their biomass, and for later stable isotope analysis. Using stable isotope ratios of carbon, nitrogen and sulphur, and Bayesian tools, we aim to formally represent the communities in isotopic space, and to compare their topologies along the environmental gradient studied. These representations will then be used to test whether differences in food web structure reflect general community characteristics, such as the higher biomass of organisms measured in macroalgae forests, which also display the greatest species diversity.

ABSTRACT 136
BOARD T012

STABLE ISOTOPE METRICS DESCRIBING LAKE FOOD WEBS – HOW CONSISTENT ARE THEY DURING FOUR SEASONS IN A BOREAL HUMIC LAKE?

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Stable isotopes are commonly used in food web ecology; however, few studies have revealed food web metrics in seasonally ice-covered lakes. In this study, we tested seasonal variation in boreal humic lake by revealing change in 1) bulk stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotope range, 2) convex hull area of dual isotope food web and 3) food chain length (FCL) by using four trophic level stable isotope nitrogen data from algae to top predators. Monthly sampling of all trophic levels was conducted in three main habitats for one year in 2020-2021. 13 fish species were caught, as well as ten invertebrate taxa and one benthic algae. The $\delta^{13}C$ range was highest in summer and lowest in winter. Highest enrichment of $\delta^{13}C$ was measured in benthic algae in summer and roach in winter. In both seasons, calanoids were most depleted in $\delta^{13}C$. The $\delta^{15}N$ range was highest in summer and lowest in spring. In both seasons, burbot (*Lota lota*) was the species at the top of the food web, while the lowest organism was water louse (*Asellus aquaticus*) in summer and benthic algae in spring. Convex hull area of the food web was largest in summer and smallest in winter. The FCL did not vary significantly, however, it was longest in spring and shortest in autumn. While the FCL appeared relatively stable, varying energy sources of organisms between seasons suggest a need to standardize sampling time to compare stable isotope ratio-based food webs collected in different years and lakes.

ABSTRACT 137
BOARD T013

LAND USE DRIVES TERRESTRIAL SUPPORT OF BOREAL LAKE FOOD WEBS

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There is a growing awareness of the importance of cross-boundary transfers between adjacent ecosystems. Lake ecosystems can receive high inputs of terrestrial organic matter (t-OM) that microbes make available to higher trophic level consumers. However, how environmental drivers influence t-OM support of benthic and pelagic consumers at multiple trophic levels remains underexplored. Using hydrogen stable isotopes as a tracer of t-OM, we found large variation in the contribution of t-OM to biomass of aquatic consumers (i.e., consumer allochthony) among 35 boreal lakes, with benthic consumers being particularly supported by t-OM. Consumer allochthony decreased along the environmental gradient from forested to agricultural catchments, likely due to alteration in the origin of lake organic matter. Our results demonstrate how cross-system transfer of organic matter can influence community dynamics in recipient ecosystems, with anthropogenic management of donor terrestrial ecosystems affecting the structure and function of food webs in recipient aquatic ecosystems.

ABSTRACT 138
BOARD T014

PRELIMINARY ANALYSIS ON FISH TROPHIC DYNAMICS IN MEGATIDAL AND MICROTIDAL SALT MARSHES IN MARITIME CANADA

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The frequency and extent of tidal flooding are driving factors in providing fish access to salt marsh ecosystems. Two distinct biophysical regions exist in Maritime Canada with contrasting tidal regimes. Bay of Fundy salt marshes experience a high energy megatidal (> 8 m tidal range) system, while those in the Northumberland Strait are exposed to a lower energy microtidal (< 2 m tidal range) system. We compared the trophic dynamics in replicate salt marshes (3 sites per region) using 13C and 15N isotope signatures of primary producers and dorsal muscle from three fish species. Mummichogs (*Fundulus heteroclitus*) were the focal species as they can spend their entire lives within a salt marsh and are ubiquitous in both regions. Atlantic tomcods (*Microgadus tomcod*) and striped bass (*Morone saxatilis*) are larger-bodied fishes visiting the marshes, likely feeding at a higher trophic level. All fishes were captured during spring, summer, or fall month in 2022–2023 using fyke or seine nets. For both regions, mummichogs used a range of carbon sources, but individuals reflected specific sources representing salt marsh grasses or microalgal biofilm. Tomcods appeared to use different carbon sources between the two regions, and as expected were at a higher trophic level than mummichogs. Striped bass isotope signatures overlapped those of tomcods in the Northumberland Strait (no bass were caught in the Bay of Fundy for comparison). Understanding the trophic dynamics of salt marshes in both regions will improve our ability to protect and restore these ecosystems in Maritime Canada.

ABSTRACT 139
BOARD T015

Stable isotope analyses of eye lens layers reveal ontogenetic shifts in the trophic ecology of Atlantic halibut (*Hippoglossus hippoglossus*) and compliment results from other tissue types

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Stable isotope analysis has become a cornerstone in understanding trophic ecology of ecosystems, spanning from individuals to the community level and multiple temporal scales. Despite their large size, longevity and high fisheries value, little is known about the trophic ecology of Atlantic halibut (*Hippoglossus hippoglossus*), a species that has shown remarkable recovery in the northwest Atlantic after a period of heavy exploitation. Here, we used carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope analysis of eye lenses, muscle and stomach tissue from 49 halibuts sampled on the Eastern Scotian Shelf to characterize ontogenetic shifts in trophic history and quantify similarities in isotopic signatures among tissue types to evaluate their consistencies as potential sources of isotopic information. Preliminary results show a strong correlation in the number of layers in eye lenses and fish size ($R^2 = 0.75$) contrasting a lower correlation ($R^2 = 0.52$) between number of layers and age, suggesting that formation of layers in eye lenses are growth rather than strictly age dependent. Nitrogen ratios in muscles tissue showed a clear linear trend with fish size, indicating ontogenetic shift in trophic positioning with growth, corroborated by similar trends in individual eye lens layers. Carbon ratios in eye lens layers indicated that halibut utilizes mainly benthic components of the food web, and individual foraging specialization occurs. This information is some of the first to shed light on the trophic ecology of this commercial important top predator species that has recovered to record high abundances in the last three decades.

ABSTRACT 140
BOARD T016

More than one fish in the lake? Unexpected isotopic diversity in the endemic fish species *Orestias chungarensis* from Lake Chungará (4520 m asl), northern Chile

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Orestias chungarensis is a small-bodied fish whose global distribution is limited to a single high-altitude (4520 m) Andean lake (Chungará) located in the Altiplano of northern Chile. Until the late 20th century *O. chungarensis* was the only fish species inhabiting the lake. The introduction of rainbow trout at this time led to the loss of *Orestias* from the River Chungará. Although of elevated conservation concern, little is known regarding *Orestias* ecology: the few studies conducted have relied on individuals captured from the shallow littoral. Here we analysed multi-tissue stable isotopes ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$) and stomach contents to study the trophic ecology of *Orestias* captured in different lake habitats.

Stable isotope values showed the existence of two putative groups of *Orestias*. A discriminant function analysis function supports to separation of two groups with a classification success of 98%. The *Orestias* included individuals belonging to a putative pelagic group (^{13}C-depleted, ^{15}N-enriched, ^{34}S-depleted) and a benthic/littoral group (^{13}C-enriched, ^{15}N-depleted and ^{34}S-enriched). Mixing models analysis showed the main contribution to the assimilated diet of the pelagic group *Orestias* in a short and longer time was pelagic zooplankton and benthic/littoral group amphipods and zooplankton from littoral indicating different foraging habitats.

Our stomach contents results showed that *Orestias* feed mainly on benthic macroinvertebrates (amphipods, chironomids, and gastropods.). However, the isotopic variation shown by *O. chungarensis* in Lake Chungará suggests that individuals forage across different habitats over time. Given the remarkable plasticity found in the genus, may reflect the existence of a previously unrecognized ecotype.

ABSTRACT 141
BOARD T017

King of the Jungle No More: Compound Specific Isotope Analysis Reveals Lions May Not Be the Top of the Savanna Food Web

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African savannas have historically been some of the most diverse terrestrial mammalian ecosystems on the globe. In recent history, anthropogenic influences have altered resource availability, predator-prey interactions, and forced many meat-eaters (carnivores and omnivores) into competition. Dietary categorizations of animals in these systems are based on observational data, stomach content, scat analysis, and recently, bulk tissue stable isotope analysis of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$). However, variability in baseline $\delta^{15}N$ values of these food webs (e.g., plants) can obscure trophic assignment or dietary categorization of higher-order consumers when using bulk tissues alone. Evaluating individual amino acids through compound-specific isotope analysis (CSIA-AA) allows us to define primary producer baselines and trophic offsets within each individual.

Our study pairs traditional bulk tissue $\delta^{15}N$ and $\delta^{13}C$ with CSIA-AA from bone collagen of 54 historic large-bodied (>5 kg) African mammals from the greater Masai Mara/Serengeti ecosystem to examine trophic dynamics between 11 species (4 herbivores, 4 carnivores, 2 omnivores, 1 insectivore). Cortical bone samples were taken from the Roosevelt (1909–11) and Rainey (1911–12) collections at the Smithsonian Institution's National Museum of Natural History. Our results suggest that traditional trophic classifications for these species may not tell the entire story. Bulk analyses comparing omnivores and carnivores indicate that these groups have nearly indistinguishable trophic positions. CSIA-AA resolves these ambiguities, yielding more reasonable trophic estimates for carnivores and omnivores. Interestingly, CSIA-AA reveals that the highest trophic level belongs to bat-eared foxes (insectivores), rather than lions.

ABSTRACT 142
BOARD T018

Trophic position and niche width of both anchovy and sardine larvae in Canary Islands archipelago (Spain)

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Anchovy (*Engraulis encrasicolus*) and European sardine (*Sardina pilchardus*) comprises the most important small pelagic fishery in the Iberian and Canary Upwelling Ecosystems. These short-lived species are subject to natural fluctuations of productivity and heavily exploited, and thus its recruitment variability quickly translates to variability in population size. The trophic ecology of anchovy and sardine larvae from Canary Islands archipelago (Spain) were studied by analyzing nitrogen and carbon stable isotopes. Larvae were collected during the RAPROCAN2103 survey in 2021 early spring. Larval isotopic niche widths were estimated using stable isotope Bayesian ellipses in R (SIBER package) and by Kernel utilization density (rKIN package) from N and C isotopes values analyzed in post-flexion larvae. Trophic position value was estimated by means of both frequentist model and *tRophicPosition* package Bayesian models at the individual and population level, using microzooplankton (55-200 μm) and mesozooplankton (200-2000 μm) size fractions as isotopic baseline for primary consumers. Species isotopic niche widths are discussed considering differences in food resources utilization and repartitioning together with feeding strategies. Ontogenetic differences in the isotopic signatures between pre- and post-flexion stages were assessed providing a solid understanding of small pelagic trophic ecology at these critical early life stages with direct implications on larval survival and consequent recruitment processes and management strategies repercussion, even more challenging in the current climate change scenario. This study has been carried out as part of the RAPROCAN Project, the Canary Islands component of the core observational program of the Instituto Español de Oceanografía.

ABSTRACT 143
BOARD T019

STABLE ISOTOPE ASSESSMENT OF ATLANTIC SALMON (*SALMO SALAR*) SMOLTS ACROSS REGIONAL POPULATIONS IN EASTERN CANADA

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Atlantic salmon are a significant species environmentally, economically, and culturally in many Indigenous communities, used as a diet staple and symbolic species in social and cultural ceremonies. They play a vital role environmentally by connecting freshwater and marine ecosystems through facilitating nutrient transport and trophic interactions. However, Atlantic salmon are at risk, listed as endangered, threatened, or of special concern in multiple populations across Eastern Canada. Exploring Atlantic salmon's energy source and food webs can provide information about how they are gaining their nutrients and the overall function of the ecosystem. This collaborative project will examine the stable isotope composition of Atlantic salmon smolts collected from various rivers with genetically distinct populations in Eastern Canada. Isotopic data includes carbon ($\delta^{13}C$), nitrogen ($\delta^{15}N$), and C: N ratios from archived data and new smolts samples collected from smolts wheel mortalities. Initial results on changes over time in smolts niche and trophic diversity as well as differences between the rivers and populations will be presented. In addition, biological measurements such as length, weight, sex, age, and lipid content will be assessed to examine differences in the physiology and variability of carbon ($\delta^{13}C$), and nitrogen ($\delta^{15}N$) among Atlantic salmon smolts. This study aims to examine changes in the trophic ecology of Atlantic salmon smolts over time and between populations to give us insight on their resource use and pre-oceanic state, which will help implement future management protocols.

ABSTRACT 144
BOARD T020

Stable isotopes analyses reveal maternal and trophodynamic effects on larval growth of Atlantic bluefin tuna (Thunnus thynnus) from the Gulf of Mexico

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Stable isotope analysis (SIA) has proven useful in evaluating the diet and trophic relationships in marine ecosystems. The current study uses bulk nitrogen and carbon SIA to investigate trophodynamics and growth variability of Atlantic bluefin tuna (ABFT, *Thunnus thynnus*) of two larval cohorts (2017 and 2018) in the Gulf of Mexico (GoM) under both inter and intra-population analysis. We consider two segregated groups of pre-flexion (PRE) and post-flexion (POST) larvae, which respectively reflect maternal and larval trophodynamic influences. Maternal isotopic trophic widths have been estimated using SIBER package (Stable isotope Bayesian ellipses in R) of SIAR (Stable Isotope Analysis in R). Our results corroborate that there is a direct relationship between growth potential and δ^{15}N signatures for ABFT pre-flexion stages due to feeding behavior of the breeders and maternal heritance. ABFT post-flexion larval trophic behavior adapts to availability and diversity of prey is reflected in their isotopic niche widths and overlaps, influencing growth potential. TPs estimates are influenced by food web length/efficiency, which can lead to substantial range in these estimates with temporal and spatial variability in trophic conditions. This research opens new research horizons that can begin to estimate the maternal trophic characteristics that influence larval survival, growth and condition with a direct effect on recruitment. This study was funded by ECOLATUN project (CTM-2015-68473-R MINECO/FEDER) and BLOOFINZ-GOM projects NOAA-NOS-NCCOS-2017-2004875 and NA15OAR4320 071 of the NOAA RESTORE Science Program and US National Science Foundation grants OCE-1851558 and – 1851395

ABSTRACT 145
BOARD T021

ROBUST TROPHIC PATHWAYS IN CARNIVOROUS REEF FISHES ACROSS A MAJOR HUMAN DISTURBANCE GRADIENT

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Myriad human stressors threaten the persistence and functioning of coral reefs. Negative effects of overexploitation on fish community structure and of thermal stress on coral cover and community composition are well-documented. However, how coral reef food webs may reorganize in response to these, and other stressors is poorly understood. Using an ecosystem-scale natural experiment and novel integrations of bulk and molecular stable isotope approaches, we investigated how chronic local human disturbance reshapes carbon flow pathways and trophic niches of predatory coral reef fish communities across the world's largest atoll (Kiritimati, central equatorial Pacific Ocean). Kiritimati has a well-documented human disturbance gradient spanning very high disturbance sites affected by coastal development and subsistence fishing to very low disturbance sites containing near-pristine reefs spatially isolated from most human activities. We found that the broad energy channels connecting basal resources to 'nominally generalist' upper trophic level reef fish are highly conserved across this chronic local human disturbance gradient despite human disturbance-mediated variation in macroalgal abundance, coral cover, habitat complexity, and fish community structure. Specifically, carnivorous reef fishes foraged in highly siloed food chains supported by consistent baseline carbon sources, with energy disproportionately originating from planktonic production. This consistency was mirrored in reef fish trophic ecology, with species maintaining uniform isotopic niches and trophic positions across the disturbance gradient. Together, our findings suggest robust planktonic energy channels may buffer nominally generalist carnivorous reef fish from negative effects of chronic local human disturbance, promoting the maintenance of dominant energy fluxes to upper trophic level consumers on human-disturbed coral reefs.

ABSTRACT 146
BOARD T022

Estimating bulk $\delta^{13}C$ and $\delta^{15}N$ trophic enrichment factors and equilibration rates for mysids consuming different prey types at two experimental temperatures

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Mysids are small, shrimp-like crustaceans that form an important part of the Chesapeake Bay food web. They serve as prey for a variety of predators; however, less is known about mysids' feeding ecology although their diets often include a wide variety of prey resources. As part of a broader study on the role of mysid omnivory, we are applying both bulk and compound-specific stable isotope analyses of carbon and nitrogen on field-caught mysids. To effectively use stable isotope techniques to answer questions of trophic ecology, two central unknowns must be accounted for: the amount that stable isotope values differ between consumers and their food (trophic enrichment factor [TEF]) and the rate at which consumers equilibrate to their prey's isotope composition. In this present study, we describe experiments done to quantify bulk $\delta^{13}C$ and $\delta^{15}N$ TEFs for mysids feeding on both a zooplankton and a phytoplankton prey. Additionally, we have quantified the equilibration rate for each prey type at three different temperature treatments (15 °C, 22 °C, and 28 °C). Following the capture of our target mysid genera (*Americamysis* spp.), mysids were allowed to acclimate to the given experimental temperature. Then, mysids were provided either zooplankton or phytoplankton prey daily, with regular water changes and removal of dead mysids. Every week, three mysids were sacrificed and both bulk $\delta^{13}C$ and $\delta^{15}N$ were measured, with the longest experiment lasting 8 weeks.

ABSTRACT 147
BOARD T023

Using carbon isotope ratios of amino acids to estimate contribution of protein sources in herbivorous mammals

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Because herbivores cannot degrade plant fiber, they have evolved mutualisms with microbes that break down fiber and provide energy to the animal. Microbes are also used as a protein source to differing extents: foregut fermenters (ruminants) digest rumen microbes in addition to plant proteins, whereas hindgut fermenters cannot; however, some hindgut fermenters digest microbial protein by consuming cecal pellets (coprophagy). Isotopic fingerprinting is a recently refined approach that uses characteristic differences in patterns of carbon isotope ratios (CIRs) among essential amino acids (EAAs) synthesized by major lineages of life (e.g., bacteria, fungi, and terrestrial plants) to identify protein sources to consumers. Here we use isotopic fingerprinting to examine the extent to which mammalian herbivores rely on microbes as a source of protein, in two ruminants (moose, *Alces alces* and muskoxen, *Ovibos moschatus*), a hindgut fermenter (horse, *Equus ferus caballus*) and a coprophagic hindgut fermenter (snowshoe hare, *Lepus americanus*). We also measured EAA CIR from rumen microbial samples and rumen microbes grown anaerobically. We estimated the contribution of gut microbiota to herbivore dietary protein by examining the CIRs of EAAs from archived blood samples of each species. From Bayesian mixing models, we found moose, muskox, and hares relied heavily on protein derived from bacteria, whereas horses relied primarily on protein derived from plants. We also observed that anaerobically grown rumen bacteria had a distinct fingerprint from aerobic bacteria. Isotopic fingerprinting can provide a biologically relevant measure for understanding microbial contribution to protein nutrition in herbivores with different digestive strategies.

ABSTRACT 148
BOARD T024

SALT MARSH-MUDFLAT LINKAGE INFERRED FROM STABLE ISOTOPE ANALYSIS IN MEGA- AND MICROTIDAL SYSTEMS

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Neighbouring ecosystems are not typically isolated from each other, rather they interact and exchange matter, nutrients, and energy. In Maritime Canada, salt marshes and mudflats are neighbouring soft-sediment ecosystems that are highly productive and provide a myriad of ecosystem services. We investigated linkages between salt marsh and mudflat ecosystems in megatidal (> 12m amplitudes; Bay of Fundy) and microtidal (< 2m; Northumberland Strait) regions in Maritime Canada, using ^{13}C and ^{15}N isotope signatures of primary producers and invertebrate consumers. Over 2 years (3 sampling rounds throughout the growing season), we observed consistent stable isotope values. Certain mudflat infauna appear to be feeding on exported salt marsh grass detritus. The trophic relationships showed regional differences, including elevated ^{15}N isotope values in the megatidal region and a wider ^{13}C isotopic range in the microtidal region, the latter partly reflecting linkage with subtidal eelgrass beds. Overall, the degree of linkage and the number of ecosystem types that are linked varied with hydrodynamic regime. Salt marshes and mudflats elsewhere in the world have been reported to supplement adjacent coastal systems and we are starting to find evidence of this at north temperate latitudes. This is important, as fully understanding how energy and matter move in and out of salt marshes could help to conserve and restore these environments, and the important ecosystems services they provide.

ABSTRACT 149
BOARD T025

TEMPORAL TRENDS IN RESOURCE USE OF GREEN TURTLES IN THE NORTH ATLANTIC

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The degree to which individuals in a population specialize in resource use over time and across life stages has important implications for characterizing the ecological niche requirements and conservation plans for imperiled species. Stable isotope analysis of single samples that offer a chronological record can be used to quantify resource-use history within and among individuals. Green turtles (*Chelonia mydas*) in coastal areas are primarily herbivorous, though some populations may feed on invertebrates. This species is listed as endangered on the IUCN Red List, though nest counts on Florida Index Nesting Beaches have increased dramatically since monitoring was initiated in 1989. To assess resource use in multiple life stages of green turtles (juveniles, adults) utilizing waters in the northern extent of this growing North Atlantic population, we examined $\delta^{13}C$ and $\delta^{15}N$ values in successive layers of scute (keratin sampled from the carapace) of 20 green turtles that were stranded, cold stunned, or died in rehabilitation facilities across a range of sites in Gulf of Mexico states. We quantified the degree of individual specialization (proportion of the isotopic niche used by an average individual) and temporal consistency (variance in individual resource use) for periods up to nine years. We observed differences in isotopic patterns among life stages, supporting previous observations in the Caribbean that adult green turtles fill a more consistent ecological role as herbivores than juveniles. Our results highlight the necessity of considering multiple life stages to inform our understanding of the ecological niche use and conservation plans for this species.

ABSTRACT 150
BOARD T026

The shifting trophodynamics in four southern Nova Scotia lakes after the introduction of Chain Pickerel (*Esox niger*)

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The invasive fish species Chain pickerel (*Esox niger*) was first reported in the Kejimkujik National Park and Historical Site (KNPHS) in 2018. As *E. niger* and other invasive *Esox* spp. (e.g. Northern pike) have been documented to have significant food web impacts, our immediate concern was to assess whether there might be risks to the protected lakes of KNPHS. We used stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) ratios to assess food web structure and trophodynamics in four four lakes ranging over a spectrum of invasion timelines from 2018 to 2021: Loon Lake (first chain pickerel report in 2018), Grafton Lake (2019), Big Dam West Lake (2020) and Cobrielle Lake (2021). The presence of two distinct feeding classes of *E. niger* were very apparent through K-mean cluster analysis in δ-space. Average linkage clustering was used top determine the transitional point in δ-space between the two clusters (-29.6834 ± 1.8422‰, 7.0859 ± 0.8735‰). A dietary shift occurs between clusters, this shift occurs at the centroid between clusters one and two when *E. niger* reach a total length of 21.4 ± 2.2 cm. Next, a three-source mixing model was used to determine the proportion of native fish, Anisoptera, and zooplankton sources for each grouping. Chain pickerel assigned to cluster one feed primarily on the Anisoptera family Libellulidae with an average total length of 5.6 cm and a mean dietary contribution of 0.736 ± 0.079. Those assigned to cluster two have an average total length of 36.4 ± 11.6 cm and feed predominantly on native fish with a mean dietary contribution of 0.724 ± 0.032. Our stable isotope data indicate that chain pickerel are impacting the trophodynamics within each lake. At least 3-5 years after first introductions, there is a consistent formation of two distinct size classes of chain pickerel within each food web, with the smaller fish (4 – 21cm) focusing on benthic invertebrates and larger fish (22 – 58 cm) on other fish respectively.

ABSTRACT 151
BOARD T027

CSIA-AA reveals tightly coupled, bidirectional metabolite exchange between a temperate coral and its symbionts

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Compound-specific stable isotope analysis of amino acids (CSIA-AA) has provided a novel method for investigating trophic dynamics in complex symbiotic systems like corals. We used CSIA-AA to test differences in resource use between ecotypes of the temperate coral, *Astrangia poculata*, which is classically separated into “hetereotrophic” aposymbiotic (low symbionts) or “mixotrophic” eusymbiotic (high symbionts) ecotypes. We conducted an *in situ* shading experiment in Narragansett Bay, RI, USA where colonies of aposymbiotic and eusymbiotic *A. poculata* (n = 190) were acclimated to control (unshaded, 7.5m), shaded (shaded, 7.5m) and deep (unshaded, 14m) conditions for four months. While low light conditions caused eusymbiotic corals to lose symbionts and chlorophyl and change metabolite production, their symbiont state did not affect their dietary resource use. Carbon fingerprints of essential amino acids, indicating the relative contribution of endosymbiont vs external plankton contribution, did not differ across treatments or ecotype classification. Similarly, trophic position, internally indexed to variations in baseline nitrogen isotope dynamics, were 2.4±0.2 for symbionts and 2.5±0.2 for the coral host, regardless of symbiont density, indicating a marked heterotrophy signal and high degree of sharing of organic molecules between host and symbionts. Together, these data suggest that our classic understanding of *A. poculata* metabolism and symbiosis is inaccurate. While light availability modulates symbiont density and physiology, trophic ecology does not exhibit strong plasticity under different light conditions. Our evidence suggests that the temperate coral *A. poculata* relies predominantly on heterotrophy and strongly shares metabolites with its symbionts, regardless of symbiont state or light conditions.

ABSTRACT 152
BOARD T028

Isotopic Tracing of Variable Biofilm Consumption by Migrating Western Sandpipers (*Calidris mauri*) at Fraser River Delta Mudflats and Another Highly Used Stopover Site

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Migrating Western Sandpipers (*Calidris mauri*) stop to refuel at mudflats along the Pacific Flyway where surface biofilm is thought to be a major component of their diet. Omega-3 (n3) long-chain polyunsaturated fatty acids (LC-PUFAs) within biofilm diatoms have been hypothesized to improve the physiological condition and migration performance of marine associated birds. At mudflats in the Fraser River Delta (FRD) of British Columbia, Canada, outflowing freshwater from the spring snowmelt is suspected to induce n3 LC-PUFA proliferation in biofilm diatoms responding to lowered salinity, potentially making this refueling site a distinctly important source of biofilm-derived n3 LC-PUFAs. However, while past studies have estimated biofilm as a significant portion of Western Sandpiper diet in the FRD, the assumption that this refueling area provides a distinct advantage has never been tested by comparing estimates to other stopover mudflat systems. Using updated Bayesian mixing model methods, we provide, for the first time, a comparison of Western Sandpiper biofilm consumption at FRD areas to another highly frequented stopover site, the relatively marine-influenced Wah-nah-jus Hilth-hoo-is mudflat system in Tofino, BC. Our results confirm assumptions that biofilm consumption in the FRD is significantly greater than other commonly used refueling locations. Seasonal effects were also measured for the first time, revealing that biofilm consumption is higher during spring migration. These findings can inform land use decisions that may impact essential shorebird habitat, particularly at the Roberts Bank mudflat area of the FRD, where a planned major port expansion will eliminate a significant portion of the biofilm foraging space.

ABSTRACT 153
BOARD T029

BALANCING THE SCALES: THE ECOLOGY AND CONSERVATION OF PANGOLIN USING STABLE ISOTOPE FORENSICS

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We detail two interrelated projects looking at the stable isotope (H, C, N, S) composition of pangolin scales.

The first uses stable isotopes to investigate the ecology and life history of giant pangolin (*Smutsia gigantea*), a poorly understood species due to its predominantly nocturnal lifestyle and use of deep inaccessible burrows. In collaboration with the ANPN in Gabon, we have collected samples from live and deceased giant pangolins across the country. From a preliminary study of ant and termite samples from Lope National Park, we have shown that species and even nests can be distinguished from combined carbon, nitrogen and sulfur isotope composition. We present data from a *S. gigantea* scale that has been subsampled in the direction of growth to elucidate seasonal dietary changes, and we compare/contrast with subsampled scales of museum pangolin specimens. Results potentially will directly impact the ANPN's conservation management, as currently the lack of knowledge hinders their efforts to protect this species.

A further objective centres on the urgent need for new forensic solutions to the poaching crisis that faces *all nine* species of pangolin. While progress has been made in identifying trafficking points, seizures generally contain mixed pangolin scales without location data. Current forensic tools lack the ability to pinpoint poaching origins, hindering strategic policing efforts. We discuss our developing database of pangolin scale stable isotope composition which will result in a robust multi-isotope provenance map, enabling the identification of species and poached areas. This advancement could revolutionize conservation by directing resources more effectively.