Symposium Booklet

Part VII: Appendix

ABSTRACTS

A.

ABSTRACTS OF KEYNOTE LECTURES

KL1: Balancing Exploitation and Conservation in the Deep Sea: Challenges for Science

Malcolm R. Clark

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There is increasing interest in exploiting the resources of the deep sea. Commercial fisheries as well as oil and gas extraction are already common and widespread. There are emerging new pressures from potential deep-seabed mining. Science has a critical role to play in providing information to support management and policy if such activities are going to proceed in a way that can balance human needs for resources, but also ensure sustainability of the environment.

A good understanding of the environment, the structure and function of its ecosystems, and knowledge of the nature and extent of impacts is required to effectively manage exploitation. However, the complexity of deep-sea ecosystems and a lack of comprehensive data can make this task very challenging. Some of the lessons learnt the hard way in assessments of environmental impacts across several industries include insufficient baseline data, inadequate understanding of impacts, limited attention to an ecosystem approach, and poor assessment and consideration of uncertainty,

This talk is based on my experience over several decades of researching deep-sea environments, some lessons learnt the hard way, and a personal view on some of the options to consider going forward. I will focus on several of the key environmental challenges above, and discuss the role of environmental risk assessments that can ensure scientific studies are targeted at the most important ecological components and impacts, that more attention is given to describing and quantifying ecosystem functions as a basis for assessment, and that adaptive management approaches are developed to address high levels of uncertainty in our understanding of the deep-sea environment.

The focus will be on scientific issues, but I also consider some aspects of their application to, and integration with, elements of process, policy and management that can help the goal of balancing exploitation and conservation in the deep sea.

KL2: Microbial Ecosystem in Deep-Sea Hydrothermal Systems

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Over the past 40 years, researchers have explored deep-sea and subseafloor environments around the globe and studied a number of microbial ecosystems, sometime called as Dark Energy Ecosystems. Multi-omics and interdisciplinary approaches have recently provided new insights into the compositional and functional diversity of microbial life living in the dark world. It is now evident that the most fundamental driving force is chemical disequilibrium at a given habitat, which controls the outline of microbial community, in particular, the magnitude and mode of chemolithotrophic primary production and the subsequent biogeochemical energy and element cycles.

This was originally predicted by a thermodynamic calculation of energy mass balance of chemolithotrophic metabolisms in a simulated deep-sea hydrothermal vent environment. The prediction, called as McCollom and Shock's prediction, has been later justified by a number of microbiological studies in various deep-sea hydrothermal vent environments all over the world. Once the prediction could be realized as a principle, the principle can be applied not only to understanding of dark energy ecosystems other than in deep-sea hydrothermal vents but also to reconstruction of the most ancient ecosystem in the Earth and even to searching the possible extraterrestrial ecosystems in our solar system.

On the other hand, recent geoelectrochemical studies of deep-sea hydrothermal environments have revealed that the chemical disequilibrium can drive not only the chemolithotrophic primary production but also the possible electrotrophic primary production and even abiotic electrosynthesis. They represent a new aspect of Dark Energy Ecosystems and may be key processes to origin of earthly life.

KL3: Exploring Deep-sea Typical Habitats for Achieving Sustainable Development

Jiabiao Li

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The deep sea holds a wealth of unique and diverse habitats that are still largely unexplored and vulnerable. At the same time, the deep ocean poses a great potential for resources, which requires scientific understanding to achieve sustainable development. The UN Ocean Decade endorsed programme “Digital Deep-sea Typical Habitats" (Digital DEPTH) focuses on investigating the deep-sea habitats, such as seamounts, mid-ocean ridges, submarine slopes, and abyssal plains, that are vulnerable to natural and climate changes, as well as human activities. Scientific studies are jointly made over 40 countries with more than 70 institutes to develop long-term intelligent monitoring technologies for the deep ocean. The programme targets to enhance the prediction ability of typical deep-sea habitats to respond to disturbances, such as climate change and deep-sea mining, and construct a digital platform for the habitats, as well as formulating solutions for deep-sea governance. In particular, a 2024 West Pacific International Cruises was carried out over 45 days where the Jiaolong manned submersible successfully completed the 18 dives during the expedition. A total of 8 foreign scientists and 3 scientists from Hong Kong, China, took the Jiaolong to dive in this voyage, covering 6 seamounts and 1 basin in the Western Pacific. The Digital DEPTH serves as a great platform for fostering international collaboration on studying the deep-sea habitat and achieving sustainable development.

KL4: Global Subseafloor Ecosystem and Sustainability (GSES)

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The subseafloor ecosystem includes all life living in marine sediment, crust and the accompany fluids. This ecosystem is also called deep biosphere where the energy source mainly comes from geological processes, cut off from sunlight. Deep-sea hydrothermal vents and cold seeps are regarded as windows of the subsurface life. Still little is known about the subseafloor life regarding their diversity, assemblage, function, and possible services to human society which is not only the key to understand the origin of life and evolution, to explore extraterrestrial life, and also crucial to evaluate the impact of the proposed ocean-based climate interventions on Earth. Therefore, we initiate a global-scale program "Global Subseafloor Ecosystem and Sustainability" (GSES) to generate new systematic insights into subseafloor ecosystems and transform them into predictive capabilities. During this talk I will introduce the aims and goals of GSES, I will highlight findings from our group on sedimentary archaea, their roles in carbon fixation and carbon cycling, emphasizing the roles of Microbes in driving Carbon Transformation in marine Sediments (MCT-S). In the end, I'll introduce research progress and challenges in marine crustal biosphere which is potentially the largest biosphere on this planet.

KL5: Vulnerable Marine Ecosystems: Key Players for the Planet Health

Ana Colaço
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The vulnerability of deep-sea biodiversity has been recognized by the United Nations General Assembly (UNGA) that due to this fact, asked States and Regional Fisheries Management Organizations (RFMOs) to identify areas beyond national jurisdiction (ABNJ) where vulnerable marine ecosystems (VME) occur, or are likely to occur, and to prevent significant adverse impacts (UNGA, 2006). The Food and Agricultural Organization (FAO) of the United Nations were then asked to develop guidelines for the management of deep-sea fisheries in the high seas (FAO, 2009). Those guidelines included criteria for defining what constitutes a VME: (1) uniqueness or rarity; (2) functional significance of the habitat; (3) fragility; (4) life history traits of component species that make recovery difficult; and (5) structural complexity. These criteria may apply to a wide variety of habitats and ecosystems of the deep-sea (e.g., hydrothermal vents, sponge aggregations or cold-water coral reefs). The VMEs concept was developed in the framework of fisheries. However, with the crescent use of deep-sea environments, we advocate that the concept should also be framed to other industries such as deep-sea mining, oil and gas, and use in future regulations. The criteria for defining VME is activity independent, and the prevention of significant adverse impact from other industries require information based on scientific knowledge. Moreover, with the new BBNJ, we also advocate that area-based management tools could be used in the future to protect vulnerable marine ecosystems and promote their conservation for the future of humankind.

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KL6: From Magma to Microbe: The Subsurface Biosphere of Guaymas Basin

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The Guaymas Basin in the Gulf of California is a young marginal rift basin characterized by active seafloor spreading and hydrothermal venting. High plankton production in surface waters and terrigenous sedimentation from the Sonoran mainland combine to rapidly deposit organic-rich sediments, which are permeated by extensive thermal and geochemical gradients. Deeply emplaced hot volcanic sills extend across the basin and alter the surrounding sediments by transforming buried sedimentary carbon into hydrocarbons, especially methane. The rapid mobilization and re-injection of these hydrocarbons into the biosphere impact the carbon cycle of the basin and provide a model system that illuminates climate perturbations. Subsurface microbial populations potentially intercept and process these hydrothermally generated and mobilized carbon sources, but their depth extent, cell numbers and phylogenetic composition are controlled by the steep geothermal gradients that are characteristic of Guaymas Basin. Here I will provide an overview on this fascinating hydrothermal geo-ecosystem, and on IODP drilling expedition 385 to Guaymas Basin (Sept. 16 to Nov. 16, 2019) with *JOIDES Resolution*. The expedition scientists and drilling crew recovered 4 km of sediment core and >350 m of sill core from eight drilling sites across Guaymas Basin, measured geothermal gradients in diverse settings ranging from recently emplaced hot sills to cold seep sites, and probed the highly diverse biogeochemistry and microbiology of the Guaymas Basin subsurface sills and sediments. Highlights will be presented as appropriate for recently concluded and for ongoing investigations.

[Research in the lab of the PI has been supported by IODP, NSF Biological Oceanography, and NASA Exobiology.]

KL7: Cold-Seep Fauna in the South China Sea: Composition and Biogeography

Jianwen Qiu

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Determining faunal composition is a prerequisite for delineation of biogeography and defining conservation units, but many deep-sea seep- and vent-fauna remain poorly characterized. Over the last two decades, progress has been made in our understanding of the seep fauna in the South China Sea (SCS), filling a knowledge gap in the biogeography of Indo-Pacific chemosynthetic ecosystems. Roughly 40 seep areas have been identified SCS, but only three are active and distributed on the northern continental shelf. Among them, the relatively well-characterized Site F and Haima seeps illustrate different levels of seep development and faunal endemism. Site F is a small area (180 m x 180 m) located in the eastern part, with well-developed authigenic carbonate rocks harboring a community dominated by bathymodioline mussels and Shinkaia squad lobsters shared with the seep- and vent-systems of the Okinawa Trough, Ryukyu Arc and Sagami Bay. By contrast, Haima seeps located in the inner SCS show less-developed authigenic rocks and host more heterogenous epifaunal communities scattered over an area of ~ 3 km, and dominated by vesicomyid clams, siboglinid tubeworms, and bathymodioline mussels, respectively. Identifying the epifauna revealed ~30 species epibenthos from Site F and ~65 from Haima, 12 shared between the two areas, and 4 and 35 appeared endemic to Site F and Haima, respectively. Genetic studies of the bathymodioline mussel, squat lobster, and patellogastropod limpet populations revealed their different levels of connectivity with the respective vent- and seep-populations in the northwestern Pacific, but the SCS populations were always discovered as a distinct genetic group. Genus-level analyses revealed a higher similarity between SCS and North Indian Ocean seep fauna than between SCS and other western Pacific seep or vent fauna, indicating high historical connectivity between seep-fauna in the SCS and Indian Ocean. Stable isotope and genetic analyses unveiled a diversity of chemosymbioses among the epibenthos, with the symbionts being either methanotrophic bacteria or sulfur oxidizing bacteria, and associated with their hosts as endosymbionts and digested by the host cells, or epibionts with or without direct cellular integration with host cells. Overall, the diversity, genetic distinctiveness, different levels of endemism, and different modes of symbioses of in the SCS seep fauna highlight their roles in the global biogeography and the need for their conservation.

KL8: Deep Sea Biodiversity Under Climate Change: Contributions, Vulnerabilities and Conservation

Lisa A. Levin

Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA USA

This presentation will examine deep-ocean biodiversity with a climate lens. High biodiversity in the deep sea emerges from evolutionary adaptations to a host of different environments in different ecosystems. Some deep-sea animals are pre-adapted to survive in environmental extremes - at low pH, low oxygen levels, in hot or cold water temperatures or with low food supply. This talk will examine how deep-sea environments are changing under climate change and assess both vulnerabilities and resistance potential of deep-sea species, communities and ecosystems. Deep-sea biodiversity underpins the carbon cycle, removing, transforming, transferring and sequestering carbon, and thus keeps the planet habitable. These processes will be presented alongside threats to deep-sea biodiversity and its climate functions and services, from both climate change itself, ocean-based mitigation efforts to address climate change and resource extraction activities. I will highlight what we know and the many scientific gaps in understanding that should be filled to address these climate challenges. Finally, a discussion of opportunities to promote climate resilience while conserving biodiversity will consider existing and new policy frameworks and treaties, their relation to sustainable development goals, and opportunities for deep-sea science to contribute to global policy.

KL9: Cold-Water Corals in a Changing Ocean

J Murray Roberts

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Although usually associated with shallow tropical seas, there are many species of coral in the deep ocean. These ‘cold-water corals’ form diverse seabed habitats from spectacular coral gardens growing on extinct volcanic seamounts to deep-sea coral reefs and giant coral carbonate mounds. Over the last 25 years cold-water coral research has grown exponentially showing them to be amongst the most diverse and dynamic marine ecosystems in the deep sea. It is also now clear that cold-water corals are sentinels of change in the deep ocean. The pressures of rapidly changing ocean conditions and destructive human activities imperil cold-water corals and have driven efforts at national, regional and international levels to promote sustainable use of the deep seabed. This talk will explore how cold-water coral research and deep-sea conservation policy has evolved over the last quarter century and speculate on what will drive research priorities through to the 2050s.

KL10: New Frontiers in Deep-Sea Biological Research

Roberto Danovaro

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Deep-sea ecosystems are increasingly threatened by several direct and indirect impacts. Their conservation is crucial to protect biodiversity, yet several systems have been degraded or damaged and require specific actions for their recovery. Marine ecosystem restoration is a new frontier in the deep-sea biological research and is a key challenge of the present UN decade dedicated to "Ecosystem restoration". However, appropriate tools, technologies and methodologies along with success stories are needed to incentivize society and private enterprises to build capacity and stimulate investments. Yet, we still must demonstrate that restoration efforts can effectively contribute to achieving the restoration targets. Here I will present an overview of active restoration interventions in deep-sea habitats worldwide. Available information indicates that deep-sea ecosystem restorations possible and highly successful. Restoration interventions can profit of the coupling between active and passive interventions. These results demonstrate the immediate feasibility of a global "blue restoration" plan even for deep-sea ecosystems, enabled by increasing availability of new and cost-effective technologies.

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B.

ABSTRACTS OF ORAL PRESENTATIONS

O1A-1: Deep-Sea Biodiversity in the Aleutian Trench (Aleutbio)

Brandt, A.[1,2], Di Franco, D.[1], Kaiser, S.[1], Kelch, A.[1], Knauber, H.[1], Kohlenbach, K.[1], Jazdzewska, A.[3], Gluchowska, K.[3], Gerken, S.[4], Tandberg, A.H.S.[5]

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The expedition AleutBio (Aleutian Trench Biodiversity Studies, SO293) was carried out from 24 July to 6 September 2022 on board the research vessel (FS) SONNE in the north-eastern (NE) Pacific, in the Bering Sea and the Aleutian Trench. The expedition's overall goal is to detect changes in species composition between the North Pacific, Bering Sea and Arctic Ocean in times of rapid climate change. A total area of 24,587 km^2 was mapped with the multibeam echosounder. A total of 1,765 samples were collected from 15 areas (with a total of 952 instrument deployments at the stations), sorted and labelled with 5,247 inventory numbers. To date, 55,691 organisms have been sorted from the benthic samples from the Aleutian Trench and Bering Sea. The samples came from a depth of 3498 to 7254 metres. This material contains at least 60 potential new species. A single individual of the rare giant isopod *Bathyopsurus* n. sp. was found. The individual represents the largest munnopsid specimen ever recorded worldwide. Overall, a total of 5,342 peracarid crustaceans were sampled, and among these, isopods represented the most abundant pearacarid taxon with 1948 specimens, followed by amphipods with 1936 specimens, tanaidaceans (606), cumaceans (600) and mysidaceans with only 252 specimens. The mechanisms that determine diversity and distribution of peracarid species in the deep sea are still unclear. However, it is thought that spatial distance, the presence of biogeographical barriers and the dispersal ability of adults are likely to be important factors. For AleutBio, we study deep-sea isopod communities from abyssal and hadal areas of the North Pacific, where topographic and hydrographic discontinuities represent dispersal barriers that likely influence species distribution. The current state of investigation will be presented. The study will contribute to our understanding of the origin of deep-sea diversity, but will also provide estimates of biodiversity in a region undergoing significant environmental change.

O1A-2: Meiofauna Patterns in Three Contrasting Habitats at the Lucky Strike Vent Field: Focus on Nematode Diversity

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The diversity of deep-sea ecosystems significantly contributes to global biodiversity and various ecosystem functions. Hydrothermal vents, such as those at the Lucky Strike vent field (LS) on the Mid-Atlantic Ridge, support large endemic biological communities of specialized fauna. While a number of ecological studies described benthic communities associated to active areas, biodiversity associated with neighboring periphery and inactive structures remains poorly to un-known. This study investigates meiofaunal biodiversity from samples collected in three habitats at LS: an active hydrothermal mound (Montségur, samples A1-A4), a peripheral region 30 meters away (P1-P2), and an inactive structure 400 meters north (I1-I2). Six meiofaunal groups were identified: Nematoda, Copepoda, Polychaeta, Ostracoda, Acari, and Gastropoda. Nematoda dominated all samples, followed by Copepoda and Polychaeta. The most abundant nematode genera were Cephalochaetosoma, Oncholaimus, Microlaimus, and Epsilonema. The PCA with abundance data (Hellinger transformed) reveals the clearly difference between the faunal composition across the tree habitats. Our data show high Nematoda dominance in the active habitat while Copepoda dominated in non active ones. While 14 genera of Nematoda were found in the active and inactive habitats, this number doubled in the peripheral region. Surprisingly, common hydrothermal genera like Halomonhystera and Monhystrella were found in very low abundances or were absent in several samples. Consistent with recent studies, vent physico-chemical conditions constitute a strong environmental filter for Nematoda and the whole meiofaunal distribution, indicating that few species possess traits to tolerate extreme conditions near the vents (Cephalochaetosoma, Oncholaimus, and others). Future research will focus on the functional analysis of nematodes to better understand their traits and how these influence the distribution patterns in hydrothermal regions.

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O1A-3: Senckenberg Ocean Species Alliance (SOSA) — Novel Solutions Combining Discovery, Conservation and Fascination of Marine Invertebrates

Julia D. Sigwart, Julia Silva Beneti, Anchita Casaubon, Henry Knauber, Carlos Alberto Martínez Muñoz, Yumi Nakadera, Jan Steger, Anne Helene Tandberg, Alica Torkov, Carly Rospert, Bianca Trautwein, Katarzyna Vončina, Ruth Wasmund, Torben Riehl

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Invertebrates are the dominant components of marine biodiversity. However, most of these species are unknown, unprotected and under-appreciated by both science and society, especially in the deep sea. These three problems are normally treated separately, by research on biodiversity, or conservation projects, or outreach efforts that may or may not be connected to research. The Senckenberg Ocean Species Alliance (SOSA) is a new initiative dedicated to species-based marine research with three goals: (1) speeding up high-quality species descriptions by providing new support services for data and publication of pure taxonomic work; (2) improving conservation through the IUCN global Red List of Threatened species and establishing a Marine Invertebrate Red List Authority (MIRLA); (3) stimulating societal engagement with and appreciation of marine biodiversity and taxonomy, through creative public outreach. These three components have important synergies: For decades, taxonomists have feared the lack of recognition and support for the process of describing and naming species. The IUCN Red List is a globally recognized conservation tool, and it is fundamentally a communication tool, which provides a powerful connection to public outreach. As a species-based approach, this depends on taxonomic identification of species – if a species does not have a name, it cannot be protected. Our Germany-based team has made significant progress in developing new tools to support these efforts at global levels, and we look forward to expanding the alliance with your collaboration. In the Deep Sea Biodiversity Symposium 2025, we are excited to share our progress to date and discuss future collaborations.

[This project is funded by a generous philanthropic donation that supports the Senckenberg Ocean Species Alliance (SOSA) with additional support from the International Union for Conservation of Nature (IUCN).]

O1A-4: Diversity across the Philippine Sea: Benthic Megafauna Community Composition across Four Ridges in Southern Japan

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Examining drivers behind diversity are crucial in understanding life history, dispersal, and ecology. In the Kuroshio Current region, latitude and longitude are critical in determining fish and coral communities because this relates to the direction of current flow around the Philippine Islands and Japan. However, similar drivers of diversity outside of this region, including across the wider Philippine Sea, have not yet been explored. We examined the community composition between 300–800 m depth at four ridges within the Philippine Sea in southern Japan, including the Daito Ridge, the Kyushu-Palau Ridge, and the Central and Western Mariana Ridges. We conducted remotely operated vehicle (ROV) surveys at five sites within these ridges; Minamidaito and Kitadaito islands (Daito Ridge), Kita-Koho Seamount (Kyushu-Palau Ridge), Nikko Seamount (Central Mariana Ridge), and Ritto Seamount (West Mariana Ridge). Sites were selected due to their similarity in latitude (between 20–26° N) and surface primary productivity. We excluded megafauna which possessed a shell or test (including gastropods, hermit crabs, and feather worms), as it was difficult to determine whether these animals were alive from video. To compare the diversity across regions, we created generalized linear models and determined the beta-diversity for each site. Few black coral (order Antipatharia) were observed in the Daito Ridge, yet this group was abundant between 300–600 m in Kyushu-Palau Ridge and the Central and Western Mariana Ridge. In contrast, brisingid sea stars (family Brisingidae) were abundant at the Daito Islands yet few were observed elsewhere. The Daito Islands have lower diversity overall, but have a community composition not seen elsewhere. While seamounts in the Kyushu-Palau Ridge and the Central and Western Mariana Ridges were formed volcanically, the Daito Ridge was formed by coral buildup, which may be responsible for the distinct community at the Daito Islands.

[This work is supported by the Ocean Shot Research Grant Project of the Sasakawa Peace Foundation (OPRI-SPF), which is supported by the Nippon Foundation.]

O1A-5: Exploring Deep-Sea Ecosystems in Palau with Baited Cameras and ROVs

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The archipelago of Palau is a hotspot for coral reef biodiversity. However, its varied deep-sea environments (e.g., seamounts, slopes, abyssal plains, and trenches) remain largely unexplored. In 2024, National Geographic Pristine Seas and the Ocean Exploration Trust explored Palau’s deep ocean using baited cameras and remotely operated vehicles (ROVs). We conducted 56 baited camera deployments on seamounts and island slopes along the west coast of the islands of Palau and in the Southwest Islands at depths ranging from 214 to 2370 meters. We observed 115 bait-attracted taxa, as well as 63 non-attracted taxa. Of the bait-attracted invertebrates, the most commonly observed taxa were Acanthephyridae, Pandalidae, and *Chaceon micronesicus*. Of the bait-attracted fishes, the most commonly observed were Synaphobranchidae, and the Macrourid genera *Coryphaenoides* and *Coelorinchus*. Communities differed across depths and between the Southwest and main islands. We examine potential drivers of community structure including depth, temperature, oxygen, substrate, and geographic location. 24 dives were conducted with a small ROV at depths ranging from 77 to 557 meters. 192 taxa were observed, including large corals, sponges, and fishes, including several taxa of sharks. We also present highlights from Ocean Exploration Trust cruises NA167 and NA168, including mapping and ROV dives at greater depths to explore more of Palau’s deep ocean, particularly in areas thought to harbor diverse communities of deep-sea corals and sponges.

[This work was supported by the National Geographic Pristine Seas Program, NOAA Ocean Exploration, and the Ocean Exploration Trust. Thanks to the Pristine Seas Palau team and the NA167 and NA168 expedition teams.]

O1A-6: Faunal Communities of Deep Arctic Methane Seeps are Specialized with Links to Hydrothermal Vents

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Cold seeps are common seafloor features on the Arctic continental margin, but most of the cold seep sites where faunal communities have been characterized are in shallow waters (<1000 m). The presence of specialized fauna in chemosynthesis-based ecosystems such as cold seeps and hydrothermal vents is strongly correlated to depth. Shallower sites typically have a low proportion of specialized fauna, probably due to the prevalence of photosynthesis-based organic material, and this pattern is reflected in what is known of Arctic cold seep faunas to date. In this study we characterized the fauna of two deep cold seeps on the Vestnesa (1300 m) and Svyatogor Ridges (1900 m) based on morphological analyses and DNA barcoding. We found a clearly specialized fauna at both seeps and document several shared species between the Arctic deep seeps and the sediment-influenced hydrothermal vent Loki's Castle, with several species identified that were previously only recorded from vents. The dataset presented illustrates a close connection between vent and seep faunas in the Arctic, probably driven by the geographic proximity of vents and seeps in the region and the presence of intermediate habitats such as sedimented vents.

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O1A-7: Biodiversity of Abyssal Polymetallic Nodule Fields in the Easternmost Region of the Clarion-Clipperton Fracture Zone, Pacific Ocean

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The Clarion-Clipperton Fracture Zone (CCFZ) is a vast area in the Pacific Ocean, spanning approximately 5,000 km across from the east of the Hawaiian Islands to the west of Mexico. The abyssal plains of CCFZ harbour one of the world's highest densities of polymetallic nodules that contain economically important metals such as nickel, copper and cobalt. This area currently consists of 16 exploration areas, and 13 areas of particular environmental interest (APEIs) that are gazetted for conservation. We assessed the biodiversity at the easternmost region of CCFZ, specifically in the Ocean Marine Singapore (OMS) exploration area and APEI-6, primarily based on samples collected from depths of about 4,000 m using multiple corers, box corers, epibenthic sleds, and autonomous underwater vehicles (AUVs). More than 1,000 species and morphospecies were identified from about 180,000 specimens and 30,000 images. Most of these taxa are new to science, including at least 22 species of foraminiferans, sponges, polychaetes, isopods and tanaids that were recently described. The three size classes of benthic communities were dominated by different animal groups: meiofauna by nematodes, crustacean nauplii and copepods; macrofauna by polychaetes, tanaids and isopods; and megafauna by sponges, echinoderms and cnidarians. There was substantial variation in the diversity and distribution of fauna within the OMS area, providing further evidence that the abyssal plains of CCFZ is a heterogenous environment. There was no significant correlation between meiofaunal diversity and environmental parameters but macrofaunal diversity was positively and significantly correlated with nodule abundance. Comparison of our species inventory with that of other study areas showed that most taxa exhibited a restricted distribution, but this result could be an artifact of poor effort in sampling and species identification in the entire region. Meiofaunal and macrofaunal abundances were found to be relatively high in the OMS area, confirming the westward decrease in faunal abundance across the CCFZ.

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O1A-8: Revealing Intra- and Inter- Trenches Biodiversity of Hadal Meiofauna Using Molecular Approaches

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Hadal trenches are characterized by great depth (>6000m), extremely high hydrostatic pressure, and are one of the least explored marine habitats on Earth. While environmental factors such as temperature, salinity, dissolved oxygen, and bottom currents are similar to what is encountered in the abyss hadal trenches act as depocenter for organic material, with intensified biological activity as compared to adjacent abyssal settings. The elevated food availability appears to result in higher density and biomass of meiofauna, but the community composition, diversity, and ecological role of hadal meiofauna remains unclear. To address this knowledge gap, we employed metabarcoding approach to investigate the composition and diversity of nematodes in Aleutian Trench and South Sandwich Trench. In addition, we also adopted whole genome sequencing from individual hadal nematodes specimen to consolidate the current database for a better molecular resolution. We hypothesed that certain environmental condition, such as depths and organic carbon, are the primary driver for shaping the meiofaunal diversity in hadal realm. In all, this study demonstrates an alternative approach to study meiofauna biodiversity in extreme environment and also provide the baseline information for future environmental monitoring using meiofauna as bioindication species.

O1B-1: Diversity, Ecology and Utilization of Deep-Sea Fungi from the Eastern Pacific and Gulf of Mexico

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Since the first fungus documented from an oceanic sample in Mexico in 1984, the formal exploration of deep-sea biomes developed until the early XXI. These exploration efforts have reached deep-sea plains, hydrothermal vents, and oxygen minimum zones, revealing an extraordinary taxonomic and functional diversity characterized by the occurrence of abundant, widely distributed, uncultured phylotypes that remain to be described. In addition, fungal isolates obtained from deep-sea samples across the Gulf of Mexico have been proposed as valuable elements for the bioremediation of marine oil spills, as they have demonstrated the ability to metabolize aliphatic hydrocarbons and extra-heavy crude oil. In this sense, metabolomic data has revealed the chemical and antimicrobial potential of deep-sea derived isolates, highlighting that culture temperature is the primary factor modeling metabolite features. Despite incipient advances, a lot of work remains to be done to conclude on fungal diversity figures and ecological roles in the deep-sea.

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O1B-2：Deep-Sea Fish Biodiversity on A Seamount Protected Area

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Marine Protected Areas (MPAs) have largely been advocated as tools for biodiversity conservation. Benefits of MPAs on species are well documented, especially on coastal areas; nonetheless, the effects on biodiversity are not unequivocally positive, and have not been extensively studied in deep-sea ecosystems. Long-term research and monitoring represent an important tool for tracking and understanding temporal changes and patterns of biological communities, and for assessing effects of MPAs on biodiversity. The Condor seamount in the Azores (NE Atlantic), located at depths between 185-2000 m, hosts vulnerable marine ecosystems and important fish commercial species. Condor was closed to bottom fisheries in 2010 and declared MPA for resource management in 2016. Since 2009, it has been regularly monitored by fish scientific survey, using two types of bottom longline gear, one shallower (200-1100m depth, mainly targeting the commercial fish *Pagellus bogaraveo*) than the other (1100-1350m depth, targeting *Aphanopus* spp. and deep-sea sharks). Analysis on longline data on deep-sea fish richness, diversity and community structure between 2009 and 2020 show different responses along time, depending on the depth zone. Among them, there was significant decrease of diversity indexes after MPA implementation in the seamount upper-slope (200-500m depth), dominated by *P. bogaraveo*, the species with the highest increase in abundance after MPA. On the contrary, in the deep-slope (750-1100m depth) there was an increase in fish diversity, although not significant. In the seamount flanks areas sampled by the deeper longline (1100-1350m depth), the lowest value of species richness was recorded in 2009, before full MPA implementation, although no significant temporal trend was detected. Complementary monitoring data from several bottom longline types provide a comprehensive picture of fish diversity and the effects of a seamount MPA on the deep-sea fish community.

O1B-3: Diverse and Self-Sustaining Benthos of an Arctic Oil Seep

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Petroleum is well known to be highly prevalent in the Arctic, and arguably governs much of the commercial and political dynamics of the region. Though petroleum reserves tend to be located deep below the seafloor, recently the benthos in the Hopen Deep region south of Svalbard was observed to be saturated with petroleum; with oil even escaping into the water column and forming slicks on the sea surface. We used a highly interdisciplinary approach to characterize the ecology of the Hopen oil seep benthos and how the physical and chemical environment drives ecosystem function. Despite the presence of potentially toxic oil and gas, communities were diverse with high abundances of taxa. The local physico-chemical environment was measurably varied and heterogeneous, which drives site specific communities and species turnover, thereby increasing overall diversity. Chemosynthetically fixed carbon appears to be a major part of the food web, with contributions to higher level trophic levels surpassing what has been seen at Arctic gas seeps. The Hopen ecosystem appears thus to not be highly linked to photosynthesis which could suggest that oil seeps could affect pelagic benthic coupling (known to traditionally be tight in many regions of the Arctic). Since the Hopen seep covers a large area of the seafloor, and there is potential for similar systems to exist across the Arctic, the presence of such ecosystems should be considered in key processes within the Arctic marine ecosystem.

O1B-4: From Bubbles to Biology: Macrobenthos Abundance, Diversity, and Assemblage Structure at South Georgia's Methane Seeps

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A quarter of all marine methane, a potent greenhouse gas, is estimated to be in Southern Ocean sediments. Climate change induced ocean warming and ice shelf melting risk the stability of gas hydrates, resulting in subsequent degassing and establishment of marine methane seeps. The impact of these seeps and their risks to the diverse sub-Antarctic and Antarctic benthic shelf fauna is uncertain. As a sentinel for change in Antarctica, this study explores South Georgia's continental shelf macroben-thic methane seep assemblages, for their diversity, richness, and abundance, and their environmental drivers. Six of South Georgia's shelf troughs hosting methane seepage were investigated during RV Meteor's M134 expedition in 2017. Species richness at eleven stations ranged from 19-51 species from a total of 103 species discovered across all sites, while abundance ranged from 3,303-30,326 m^{-2} with higher diversity at stations with raised methane in the upper sediment layers. Abundance and species richness drop markedly at the only station with gas hydrates present. Assemblages were characterized by the presence of Southern Ocean species and by the absence of chemosynthetic and distinct methane seep taxa such as erect siboglinid worms, vesicomyid and solemyid bivalves. Arthropods, mostly crustacean, and annelid species made up three quarters of overall species richness, while molluscan and echinoderm species were depauperate with only 15 species. Compared with Southern Ocean macrobenthic assemblages, the South Georgia seep assemblages from sediments with gas hydrates present in the near-surface (~250 m) showed a decrease in species richness and change in taxon composition, with a decline in calcium-carbonate shell bearing taxa. The current diverse benthic Antarctic biodiversity, especially the diversity of calcifiers, is likely at risk when methane seeps become established on Southern Ocean continental shelves.

O1B-5: Serpentinite-Hosted Alkaline Seep Communities on the Mariana Forearc Show Lasting Impacts from Scientific Drilling

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Deep-sea chemosynthetic ecosystems are ‘oases’ of life powered by reducing geofluids, among which serpentinite-hosted seeps supported by alkaline geofluid are particularly understudied. Mariana Forearc hosts the world’s only series of active serpentinite mud volcanoes and here we report faunal characteristics of seeps found on Asùt Tesoru (‘Big Blue’) and South Chamorro seamounts, plus preliminary data for Conical Seamount. Newly discovered Asùt Tesoru and Conical seeps lack large-bodied species such as bathymodioline mussels, likely the reason why these assemblages eluded previous expeditions. Similar seep communities probably exist on other active serpentinite mud volcanoes on the Mariana Forearc like Quaker, warranting future explorations. Animals such as *Provanna* snails and *Bathyacmaea* limpets are shared with nearby Mariana Arc and Mariana Trough hydrothermal vents, indicating these seeps may be important stepping-stones for dispersal. The Asùt Tesoru seep was adjacent to three drill holes made by the International Ocean Discovery Program expedition 366 in 2017, impacting seepage and assemblages. More strikingly, a mussel bed on South Chamorro was drilled by the Ocean Drilling Program in 2001 resulting in six holes, the deepest being 266 m. Cuttings ~50 cm deep still covers a 60 m radius even 22 years later, showing no sign of recovery. Low geofluid supply in serpentinite-hosted seamounts may not allow decadal recovery of animal colonies. We recommend scientific drilling programs to consider these unique seafloor assemblages when making decisions on drilling target points, and also conduct more detailed pre-drilling surveys in the future.

O1B-6: Biogeography and Biodiversity of Hydrothermal Vent Fauna along the Central Indian Ridge

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The Central Indian Ridge (CIR) is located between the Carlsberg Ridge and the Rodrigues Triple Junction. Its central location makes the CIR optimal for studying the biogeographic connectivity of hydrothermal vent fauna across the Mid-Indian Ridge (MIR). In this study, we analyzed the biogeography and biodiversity of hydrothermal vent communities using imagery from seven active vent fields along the CIR: Onbada, Onnare, Onnuri, and Saero (northern CIR; nCIR), Cheoeum, Mirae-2, and Maru (southern CIR; sCIR). Video and still images were acquired using the Remotely Operated Vehicle (ROV) ROPOS from 2021 to 2024. The megafauna observed in the images were analyzed to the lowest possible level by comparing them with the morphological and genetic analysis results of the collected specimens. Our findings revealed notable differences in vent fauna between the nCIR and sCIR. The sCIR demonstrated relatively lower diversity, with a prevalence of *Rimicaris* shrimps. Additionally, the sCIR exhibited a total absence or scarcity of *Bathymodiolus* mussels and *Alviniconcha* snails. In the sCIR, mussels and juvenile snails were observed at Cheoeum, only juvenile snails at Mirae-2, and neither at Maru. This suggests that the hydrothermal vents in the nCIR could be more mature and well-established environments in comparison to those in the sCIR. Alternatively, dispersal barriers between the nCIR and the sCIR may result in the distinct biogeography and biodiversity of vent fauna along the CIR. These findings emphasize the necessity for continued and detailed exploration of the hydrothermal vent fauna in the CIR to enhance our understanding of the biogeography and biodiversity of hydrothermal vent fauna along the MIR.

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O1B-7: Faunal Novelty and Dynamic Controls on the YBW Vent Field, East Pacific Rise

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The structure of space-limited hydrothermal vent faunal communities has been explained by the influence of geological setting, fluid chemistry, larval availability, microbial associations, disturbance, and stages of habitat development. Discovered in 2021, the YBW-Sentry hydrothermal field is ~750 m east of the East Pacific Rise axis, associated with an off-axis fault scarp. To identify faunal community assemblages and their habitats within this novel off-axis field and infer controls on their community structure, we examined the faunal diversity, composition, distribution, and habitat types. Using 25 cm-resolution bathymetric maps collected by autonomous underwater vehicle *Sentry*, ROV *Jason* and HOV *Alvin* navigation and imaging surveys (covering >12,800 m^2), coordinated faunal and fluid samples, and QGIS geo-reference mapping techniques, we identified and mapped biological and hydrothermal characteristics to reveal: 1) the field extent to be 152 m long by 68 m wide, an area of approximately 4500 m^2; 2) ~97 black smokers (<1 to 13m tall) and >700 inactive smokers (<1-12 m tall); 3) widespread (>1200 m^2) areas of diffuse fluid venting; 4) hydrothermally-active (>128°C) white cracks in basalt with nascent (<5 cm tall) sulfide structures hosting alvinellid communities; 5) at least 42 faunal morpho-taxa; 6) the greatest biomass of vent fauna is associated with black smokers; 7) YBW fauna appear to be a subset (30%) of those in the trough and include species not known to be from the trough; 8) the absence of vent-endemic fauna in areas of diffuse flow; and 9) a notable absence of endosymbiont-bearing, regionally-abundant foundation species, particularly *Riftia* and *Tevnia* tubeworms as well as clams and mussels. In addition to habitat availability, fluid chemistry, and physical isolation, we also present temporal changes across three years and a baseline for future testing of presented hypotheses and for future biological studies of disturbance along the EPR trough and fault systems.

O1C-1: Time-Calibrated Phylogenomic Analyses Reveal New Insights into the Evolution of Modern and Deep-Sea Asteroidea

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Asteroidea, one of the most diverse groups within the phylum Echinodermata with over 1900 extant species, occur at all depths and are present throughout the world's oceans. All living asteroids are considered descendants from a single post-Paleozoic diversification event approximately 250 million years ago. Historically, comprehensive asteroid phylogenetic reconstruction has been based primarily on morphology data. Although recent molecular phylogeny studies have aimed to resolve fine-scale or familial relationships, a comprehensive analysis of the entire class using multiple genetic markers and with adequate sampling efforts is yet to be seen. Deep phylogenetic divergences among some major lineages remain controversial. Early molecular studies tested Paxillosida as "primitive" hypotheses, while other recent studies showed members of Velatida as part of the basal dichotomy. Additionally, the placement of some diverse clades remains a difficult question. Using genome skimming data, we derived more than 150 new complete or near-complete Asteroidea mitochondrial genomes, emphasizing species inhabiting the deep sea, previously undescribed, or with enigmatic relationships. We conducted phylogenetic and phylogenomic analyses of more than 300 species, representing as diverse taxon sampling as possible. Here, we present the most comprehensive phylogenetic hypothesis for Asteroidea to date, representing all major lineages with many species sequenced for the first time. Divergence times were also estimated and calibrated using the largest fossil occurrence dataset to date. Results indicate that some deep-sea groups, such as Cribellina and Zorocallida, diversified early during the Jurassic period, while other groups like Brisingida and Ophidiasteridae appear to represent ghost lineages with no fossil record for the past 200 million years. The phylogeny also supports Caymanostellidae as members of the Velatida along with Pterasteridae and Myxasteridae, which further supports the monophyly of Forcipulatacea. Our analyses provide new insights into the diversification of modern Asteroidea and highlight questions for future systematic research.

O1C-2: Clue to the Maze: A History of Phylogenetic Relationships in Deep-Sea Typhlotanaidae (Crustacea: Tanaidacea)

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Typhlotanaidae Sieg, 1984 (Tanaidacea) is a phylogenetically young and morphologically diverse family represented by small-sized, and mainly deep-sea, benthic detritivores. They are characterised by the presence of a three-articulated antennule, the absence of eyes, and a unique structure on the last three pairs of pereopods, often known as the 'clinging apparatus'. This consists of various hooks, spines, tubercles, and thorns, and represents a morphological adaptation that facilitates movement within the self-constructed tube in which most typhlotanaids probably live. The absence of eyes in Typhlotanaidae (from which their name is derived) is considered a consequence of their radiation in the deep-sea. Indeed, most typhlotanaids are deep sea forms, although some species are found on the continental shelf in medium or high latitudes. The low mobility and high taxonomic diversity of typhlotanaids make them model organisms for studies of biodiversity and evolutionary processes of the benthic macrofauna in the deep-sea, but the life history strategies of the Typhlotanaidae have never been studied and their monophyly has been questioned several times. The present study is the first attempt to investigate the historical radiation processes of this deep-sea family and the first for the suborder Tanaidomorpha using molecular markers.

For this research we studied over 11,000 typhlotanaid individuals collected from depths of 200–6000 m during several deep-sea expeditions completed over six decades (1960–2021). We applied an integrative taxonomic approach that included a combination of morphological, morphometric, environmental, and genetic data that included the three molecular markers COI, H3 and 18S rDNA. Our results support the polyphyletic nature of the Typhlotanaidae as currently understood and reveal a significant underestimation of its taxonomic diversity. Cheliped and pereopod morphology were key foci in interpreting and identifying three new families, new13 genera and 24 species and our study significantly expands information about tanaid diversity and distribution generally, increasing the number of deep-sea typhlotanaid species and genera by 42% and 40% in the Northwest Pacific, and by 67% and 130% in the North Atlantic. The molecular-clock calibration suggests that the Typhlotanaidae probably evolved between 10.6 and 4.9 million years ago, and it confirms previous hypotheses about the relatively young age of the deep-sea fauna, at least for this group of peracarid crustaceans.

O1C-3: Phylogeography and Systematics of the Mesosignidae Schultz, 1969: Survey of Isopod Diversity in North Pacific Trenches

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Isopods are diverse components of deep-sea ecosystems and occur at depths down to the hadal zone. Similar to other peracarid orders, they lack free-swimming larval stages, a characteristic believed to restrict their dispersal ability and lead to more confined geographic distributions. In this study, we investigate the distribution of the deep-sea isopod family Mesosignidae within two trench areas: the Aleutian Trench (AT) and the Kuril-Kamchatka Trench (KKT). These areas were sampled during the AleutBio (SO293), KuramBio II (SO250), and KuramBio (SO223) expeditions in the North Pacific. With 17 species described across 5 genera, Mesosignidae constitute a relatively small taxonomic group, typically comprising a minor portion of the total isopod populations. However, studies examining phylogeographic patterns within this family are scarce. We combined morphological studies with molecular (mtDNA and proteomic) analyses to increase robustness in species delimitation through an integrative taxonomic approach. Morphologically, we distinguished two species within the family, one of which is newly discovered and found in both the KKT and AT regions. Given their poor swimming abilities, we anticipated pronounced molecular differentiation or even the presence of distinct species between the KKT and AT. Furthermore, we hypothesized divergence across a depth gradient exceeding 1500 meters, alongside significant environmental variations associated with depth. Genetic results revealed that the newly discovered species is actually a species complex, consisting of two closely resembling species. One of these seems to be distributed across the Northern Pacific continental plate, while the other one occurs only near the trench system itself. Alongside the description of the new species, this study adds a vital piece to the puzzle, enhancing our understanding of isopod diversity and their origins in the region.

O1C-4: Analysis of Vesicomyids Clam Shed Light on the Updated Taxonomy and Evolution

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Vesicomyid clams in the subfamily Pliocardiinae are chemosymbiotic and specific to deep-sea chemosynthetic ecosystems with wide bathymetric and geographic ranges, making them a good model to study molecular adaptation and biogeography. The phylogeny of Pliocardiinae, however, still remains highly contentious due to limited molecular markers. Here, we elucidate the evolutionary relationships among pliocardiine species through a combination of mitogenome-based and genomics-based reconstructions. By testing a wide range of methods including maximum likelihood, maximum parsimony, Bayesian interference, and coalescent approach, we present a robust phylogenetic tree supported by the AU-test and GLS analyses. We revise the genus-level taxonomy of pliocardiines based on this tree, merging a number of genera in the '*gigas*-group' into *Archivesica*. Our fossil-calibrated tree reveals that Pliocardiinae originated around 42.33 Ma in the middle Eocene, similar to other chemosynthetic bivalves such as bathymodioline mussels. Diversifications of this subfamily appears to be concurrent with global climatic cooling events, though the reason remains unclear. Ancestral state reconstruction analyses found two independent invasions into the abyssal zone, a shift from lineages harboring the *Ca.* Ruthia symbionts to *Ca.* Vesicomyosocius symbionts, and a likely Western Pacific Ocean origin. Our results present a solid backbone for the future investigations into molecular adaptation, biogeography, and symbiosis in this fascinating group of molluscs.

O1C-5: The Distribution of Hadal Snailfishes from the Trenches in the Northwestern Pacific

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The hadal snailfish (family Liparidae) are deep-sea fishes found at depths exceeding 6,500 meters. In the sea around Japan, *Pseudoliparis amblystomopsis* has distributed in the Japan Trench and Kuril-Kamchatka Trench, while *P. belyaevi* has been reported only from the Japan Trench. During the KH-22-6 and KH-23-5 expeditions conducted by the research vessel *Hakuho Maru* in 2022 and 2023, we collected *P. belyaevi* and *P. amblystomopsis* from the Japan Trench and Kuril-Kamchatka Trench. Molecular phylogenetic analysis based on the 16S rRNA gene and species identification based on vertebral counts and pectoral fin morphology showed *P. belyaevi* is also distributed in the Kuril-Kamchatka Trench and this species is more closely related to *P. swirei*, which is endemic to the Mariana Trench.

Furthermore, the genetic diversity of the *P. amblystomopsis* distributed in the Japan Trench and the Kuril-Kamchatka Trench is likely to be significantly higher compared to the other two species. In this presentation, we will discuss the evolution process of *Pseudoliparis* in the trench regions of the Western Pacific, including more detailed morphological observations and additional phylogenetic analysis.

O1D-1: Ecology of Deep-Sea Protistan and Metazoan Meiofauna: Experimental Approaches

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Meiofauna, organisms that pass through a 1 mm (500 μm) mesh sieve but retained on 20 to 63 μm mesh sieve, are important components of deep-sea benthic ecosystems in terms of biodiversity, ecosystem functioning, and biogeochemical cycles. Meiofauna are also useful organisms for biomonitoring because they are sensitive for environmental changes and small volume of sediment contains sufficient numbers of meiofauna for quantification. However, many biological and chemical analyses were difficult to apply due to their small body sizes and hence their ecology and biology are not well understood so far. We have developed small scale analyses of isotopic compositions and applied them to investigate feeding habits of major meiofaunal taxa. We further performed series of in situ experiments on the deep-sea floor to evaluate roles of meiofauna in ecosystem functioning. Another challenging theme of meiofauna is a taxonomy; their small size and high species diversity requires expertized but wide-ranges of taxonomical knowledges/techniques using microscopy, and there is only limited gene sequence data for meiofauna. We will shortly introduce a new project for meiofaunal taxonomy based on recent microscope imaging and pattern recognition with the aid of artificial intelligence, together with new genomics technologies.

O1D-2: A Deep-Sea Isopod That Consumes *Sargassum* Sinking from the Ocean's Surface

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Most deep-ocean life relies on organic carbon from the surface ocean. While settling primary production rapidly attenuates in the water column, pulses of organic material can be quickly transported to depth in the form of food falls. One example of fresh material that can reach great depths across the tropical Atlantic Ocean and Caribbean Sea is the pelagic macroalgae *Sargassum*. However, little is known about the deep-ocean organisms able to use this food source. Here, we encountered the isopod *Bathyopsurus nybelini* at depths 5,002–6,288 m in the Puerto Rico Trench and Mid-Cayman Spreading Center using the Deep Submergence Vehicle *Alvin*. In most of the 32 observations, the isopods carried fronds of *Sargassum*. Through an integrative suite of morphological, DNA sequencing, and microbiological approaches, we show that this species is adapted to feed on *Sargassum* by using a specialized swimming stroke, having serrated and grinding mouthparts, and containing a gut microbiome that provides a dietary contribution through the degradation of macroalgal polysaccharides and fixing nitrogen. The isopod's physiological, morphological, and ecological adaptations demonstrate that vertical deposition of *Sargassum* is a direct trophic link between the surface and deep ocean and that some deep-sea organisms are poised to use this material.

O1D-3: Rocky Seafloor — Underestimated Driver for Habitat Heterogeneity and Benthic Biodiversity (RUBBLE)

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Recent seafloor exploration has revealed significant heterogeneity in the abyssal seafloor, particularly in the Vema Fracture Zone (VFZ), where exposed bedrock patches are more common than previously thought. High-resolution hydroacoustic maps indicate that over 5% of the ~95,000 km² studied area likely consists of bare rock. This challenges the long-held view of the abyssal seafloor as featureless and suggests that ~264,000 km² of Atlantic fracture zones may have high hard-rock exposure. This discovery has important implications for understanding abyssal biodiversity, as rocky substrates in soft-sediment ecosystems often enhance biodiversity. Additionally, these ecosystems face increasing threats from climate change, seafloor mining, and pollution.

The RUBBLE project aims to explore the relationship between habitat heterogeneity and abyssal benthic biodiversity across space and time in the VFZ. Between October 22 and November 28, 2024, we conducted fine-scale benthos and sediment sampling in the eastern VFZ, considering geological, ecological, and evolutionary perspectives. We look forward to presenting our initial findings at the Deep-Sea Biology Symposium 2025.

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O1D-4: Illuminating the Diversity of Deep-Sea Anthozoans Found in Selected Sites of the Northwestern Pacific

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The deep sea is the world's largest ecosystem and supports high levels of diversity. The communities making up the deep-sea benthic environments are often composed of diverse forms of cold-water sponges and anthozoans. However, we know only little about the identity and distribution of these deep-sea communities. To help address this data gap, we have collated information on deep-water anthozoans encountered from selected seamounts and limestone caves of the Northwestern Pacific between 2020 and 2024. Specimens were collected by remotely operated vehicles and manned submersibles from Shotoku, Ritto, Nikko, Kita-Koho, and Enshunada-Oki Seamounts, Shima Spur, and the Daito Islands, at depths between 200 and 3200 m. Morphological-based identifications were made with the use of light and scanning electron microscopy and were supplemented by multi-locus DNA barcoding (i.e. ITS1, cox, igrW, igrN, msh1). This integrated taxonomic approach revealed specimens belonging to at least four octocoral families (Chrysogorgiidae, Primnoidae, Ellisellidae, Coralliidae), five antipatharian families (Antipathidae, Aphanipathidae, Cladopathidae, Leiopathidae, Schizopathidae), and two zoantharian families (Epizoanthidae, Parazoanthidae). Among the antipatharians, we documented the occurrence of the genera *Leiopathes* and *Acanthopathes*, which are thought to be ancestral deep-sea lineages. The study extends the current geographic and bathymetric distribution of many of these anthozoans, and includes putatively undescribed species. Taken together, these findings have important conservation implications that support the establishment of marine protected area networks to ensure the long-term protection of these deep-water anthozoans and their ecosystems.

O1D-5: Calcareous Tubeworms (Serpulidae, Annelida) of the Abyss Revisited: Mystery of Elusive and Mysterious Mollusk-Like Worms Solved

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Annelida evolved into 10,000 species over 500 million years, which gave them enough time to adapt to every marine habitat. Among annelids, members of the family Serpulidae are unique in inhabiting self-secreted calcareous tubes attached to hard substrates. They are found from intertidal flats to abyssal plains and deep-sea trenches. But because hard substrates are rare in the deep ocean covered with soft sediments, some serpulids of the abyss pre-adapted to living in unattached tubes which allows them to avoid being buried. The free-lying tubes of such serpulids resemble tusk-shaped shells of scaphopod molluscs. The resemblance is so striking that it resulted in a long-standing mystery of the deep-sea. Empty tiny tusk-shaped tubes with eight edges were first collected in 1872 from the abyss of the Labrador Sea and named *Ditrupa groenlandica*. But whether the owner of the tube was an annelid or a scaphopod remained unknown for over 130 years. In 1909 another unattached serpulid, *Spirodiscus grimaldii,* was described from lower bathyal depths off the Azores. The name referred to the tube, quadrangular in cross-section and coiled into a flat spiral. In 1993 a serpulid with quadrangular but tusk-shaped tubes was described as *Bathyditrupa hovei* from the Kuril-Kamchatka Trench. But only in 2015 deep-sea serpulids inhabiting free-lying polygonal tubes collected in the 20th century were unearthed from the museum collections and re-described as *Bathyditrupa hovei, Spirodiscus grimaldii,* and *S. groenlandicus*. Most recently these animals were collected from the abyss off eastern Australia and Clarion-Clipperton Fracture Zone of the Pacific Ocean. For the first time we have molecular-grade material which allowed testing whether these abyssal animals form a monophyletic group (genus *Spirodiscus*) using DNA sequence data. This material also allowed us to study evolutionary transitions to secondary free-living in sedentary serpulids and genetic connectivity across the Pacific Ocean.

O1D-6: A Pioneering Long-Term Experiment: Mesophotic Macrofouling Communities in the North Atlantic

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The mesophotic zone, a vast and underexplored marine biome, plays a crucial role in the functioning of ocean ecosystems. The factors influencing the structure of macrofouling communities at these depths, however, remain poorly understood. This knowledge gap limits our ability to predict anthropogenic impacts and develop effective restoration strategies. We conducted a 24-month experiment in the North Atlantic, specifically in Madeira's deep waters, utilizing a manned submersible to examine how depth, substrate orientation, and material type influence the composition of mesophotic macrobenthic communities. We deployed recruitment panels of basalt and PVC at 100, 200, and 400 meters, positioned both vertically and horizontally. Results revealed a clear decrease in biodiversity and species abundance with increasing depth, corroborating the significant role of depth in structuring these communities. Depth-related environmental factors such as light attenuation, temperature, and pressure likely drive these patterns by influencing food availability and other resources. Substrate orientation also played a role, particularly at shallower depths. Species-specific preferences observed in this work suggest that substrate orientation effects are complex and vary across taxa. The influence of substrate orientation diminished with depth, likely due to factors like sedimentation, which had a more pronounced impact at deeper sites. The type of material had a relatively minor influence, though certain taxa showed a preference for artificial (PVC) over natural (basalt) substrates. This finding raises concerns about the ecological impacts of increasing plastic pollution in the ocean, potentially facilitating the spread of non-indigenous species. Our study highlights the importance of depth and substrate orientation in shaping mesophotic macrofouling communities in Madeira's deeper waters. As one of the first experiments at these depths around Madeira this work represents a valuable contribution for future restoration and conservation efforts in the region's mesophotic environments but also demonstrates the feasibility of conducting long-term, deep-sea monitoring experiments around Madeira.

O1E-1: Biogeography of Arctic Vents and Seeps: How and Why does it Differ as a Province?

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The Arctic remains one of the least explored provinces of vent and seep biogeography, with only six active deep-sea hydrothermal vent fields currently confirmed beyond latitude 70ºN. An overlap between vent and seep fauna may be a distinctive feature of the region, however, as indicated by the recent discovery of a methane hydrate seep at 3640 m on the Molløy Ridge. This cold seep site, named the Freya mounds, hosts taxa including siboglinid and maldanid polychaetes, rissoid and skeneid gastropods, and melitid amphipods, which are also present at the newly discovered Jøtul vent field at 3020 m on the Knipovich Ridge. Another distinctive feature suggested by recent exploration is that species known from non-chemosynthetic habitats, such as carnivorous sponges, sometimes occur in niches that are usually occupied by vent-endemic taxa. These features of Arctic vent and seep biogeography may be consequences of basin geomorphology and recent glaciological history, when ice-sheet cover during the Last Glacial Maximum interrupted phytodetrital flux to the Arctic deep sea and potentially restricted its fauna to chemosynthetic habitats. That recent climatic event (~20 kya) is also likely to have filtered out vent and seep taxa with planktotrophic larval development such as bathymodiolin mussels and alvinocaridid shrimps, while favouring taxa with non-planktotrophic development such as melitid amphipods and siboglinid polychaetes, and possibly created empty niche space now colonised by non-chemosynthetic species. Furthermore, as taxa with non-planktotrophic development may have lower dispersal capability, the greater spacing of vent fields on ultraslow-spreading Arctic ridges may favour chemosynthetic-dependent species that can occupy both vents and seeps, which occur in proximity in this region.

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O1E-2: Across Trenches, Plains and Ridges – Distribution and Differentiation Patterns of Deep-Sea Isopods in the North Pacific Ocean

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The role of geomorphological features as drivers for benthic deep-sea biodiversity remains poorly understood. This research focused on isopod species of the families Haploniscidae Hansen, 1916, and Macrostylidae Hansen, 1916, from the North Pacific Ocean to elucidate deep-sea differentiation and distribution patterns. By integrating molecular data (16S, COI, 18S) with biogeographical distribution data, the differentiating effects of bathymetric barriers such as trenches (Japan, Kurile-Kamchatka, Aleutian) and ridges (Kurile-Island, Aleutian-Island), as well as large geographical distances and depth ranges were investigated. Species delimitation and population genetic analyses were used to assess the effects of Isolation by Distance and the Depth-Differentiation-Hypothesis in abyssohadal environments. Our findings reveal a diverse picture of distribution and differentiation patterns, even amongst congeneric species, highlighting the importance of species-level analysis to comprehend these processes. Multiple examples demonstrated a strong molecular distinction between abyssal and hadal populations, while distances of several thousand kilometers exhibited comparably lesser effects on differentiation patterns.

O1E-3：Global Evolutionary Biogeography of the Ophiuroidea

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The compilation of a global phylogenomic and distributional dataset of brittle-stars has the potential to vastly improve our knowledge of the distribution and evolution of deep-sea life and our ability to identify priority areas for conservation. Our team has produced a 2800-sample robust, comprehensive, fossil-calibrated phylogeny of the group based on 275 kb of exonic nDNA and 1.4 kb mtDNA COI sequences. Here I present a global marine biogeography from this data, showing the evolutionary relationships between 37 biomes, across 3 depth strata (shelf, bathyal, abyssal) and all oceans, analyzed using multivariate statistics on a novel phylodiversity index, and Markov-k models of discrete character (biome) evolution. The shelf has the greatest range of phylodiversity, with tropical, temperate, and polar biomes forming distinct clusters. The temperate shelf faunas have evolved independently from tropical faunas over the past 50 my, whereas polar shelf faunas are more closely related to bathyal faunas. The bathyal and abyssal faunas have reduced variability and are much more connected over evolutionary time. In particular, many temperate bathyal species or lineages have achieved widespread distributions, crossing the tropics on the eastern side of the Atlantic and Pacific Oceans. The overall impression is one of historical and ongoing interchange of biodiversity across the entire marine realm.

O1E-4：Exploring the Unknown: NOAA Okeanos Expeditions Reveal Alaska's Hidden Deep-Sea Sponge and Coral Communities

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Alaska hosts highly diverse and abundant cold-water coral and sponge and communities. While previous research has focused on shallower regions along the Aleutian Islands and Gulf of Alaska's shelf, depths below 900 meters remain largely unexplored. Two recent NOAA Okeanos Explorer expeditions (EX2304 - EX2306, July - September 2023) visited some unmapped regions, including the continental shelf, seamounts, and canyons, and produced high-resolution maps and imagery. In this study, we: 1) describe and characterize 15 dive sites at depths ranging from 400 to 3,300 meters across a variety of geographic features, substrates, and environmental conditions; 2) assess coral and sponge diversity and community composition; 3) identify areas of high density; and 4) explore environmental drivers and spatial patterns of the observed communities. Our findings reveal 73 coral and 91 sponge taxa (or morphospecies), with 14,650 observations recorded over 75 hours of dive time. Each site displayed a nearly unique community composition with minimal overlap. Biodiversity and density were highest above 2,000 meters, with a non-gradual decline in diversity and abundance with increasing depth. The only soft-bottom habitat surveyed, Umnak Canyon (1,450m), showed the lowest diversity, with only 3 morphotypes observed, whereas harder substrates supported greater diversity and abundance. Aside from substrate type, multivariate analyses suggest that depth and local oceanographic conditions most influence the observed community compositions. Eight high-density areas were identified, with densities ranging from 3 to 22 individuals per m^2, including two exceptionally dense cladorhizid sponge habitats and several mixed coral and sponge gardens. These findings not only reveal the yet unexplored biodiversity of Alaska's deep-sea but also provide crucial baseline data for future research and conservation efforts for these valuable ecosystems.

O1E-5: Inventory of Bathyal Holothurian Species in New Caledonia EEZ Over Half a Century

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This work inventories holothurians collected in the New-Caledonian bathyal zone by the Tropical Deep-Sea Benthos (TDSB) program. TDSB encompasses more than 75 research cruises (44 in New-Caledonia), with over 7800 dredging and trawling operations. Over the past 40 years, the study of collected specimens, deposited at the Muséum National d'Histoire Naturelle, has led to more than 1500 scientific papers and more than 3600 deep-sea species descriptions (mainly Crustacea and Molluscs). However, only five papers have been published on holothurians despite their significant ecological role as deposit feeders in deep-sea ecosystems, with high bioturbation and sediment filtration rates. The first step of the study was to seek the specimens from New-Caledonia and nearby areas. As no study was available, we used an integrative taxonomic strategy. Approximately 1,600 specimens have been inventoried. Each specimen has been photographed, and samples for DNA (COI) analysis and ossicle examination have been taken. A three-step approach has been followed. First, specimens were molecularly identified (MOTUs) to the lowest possible taxonomic level using the available genetic data. Then, the MOTUs identified as new are being described using a turbo-taxonomy approach, (i.e., molecular species delineation complemented by documentation of standard holothurian morphological characteristics). Finally, the remaining MOTUs, which were not molecularly identifiable, will be studied more thoroughly in collaboration with taxonomists and through the acquisition of additional data. This work is still ongoing but the first results have led to the identification of 135 MOTUs. In particular, two species have a high spatial and temporal coverage. This is of particular interest as this work is the taxonomic side of the BackPlast project, which retrospectively investigates microplastic pollution of the deep-sea benthic fauna (100-2500 m) from the Indo-Pacific using holothurian as model organisms,(see XXX abstract).This allowed selecting two candidate species for the BackPlast project.

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O1E-6：Spatial and Bathymetric Diversity of Tanaidacea (Crustacea) Assemblages in the Bering Sea and Aleutian Trench

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Tanaidacea is an order of small crustaceans that inhabit various ecosystems on the ocean floor. They are considered one of the least studied benthic animals, with currently 1,500 known species classified in 42 families. According to estimations, the total number of Tanaidacea species worldwide is much higher, and could be as high as 40,000 species. These crustaceans are often the dominant component of the benthic fauna and are used as bioindicators and model organisms in studies of population genetic connectivity.The eastern North Pacific is the least studied oceanic region in terms of marine biodiversity. The goal of the German AleutBio expedition (Aleutian Trench Biodiversity Studies, RV Sonne: 24.07.2022-6.09.2022) was to study biologically unexplored areas of the Bering Sea and Aleutian Trench. Samples were taken at 14 research stations located along the Aleutian Trench and in the Bering Sea in a wide depth gradient from 3,504 to 7,242 meters.The study aimed to determine the biodiversity of Tanaidacea in the Bering Sea and Aleutian Trench and to investigate environmental factors affecting their distribution. The study also aimed to compare Tanaidacea assemblages between different study areas: Bering Sea, northern and southern slopes of the Aleutian Trench, and its floor.Tanaidacea collected during the AleutBio expedition was represented by 730 specimens, classified into 15 families, 36 genera and 63 morphogroups, the vast majority of which are new to science. Taxonomic identification was carried out based on both morphological and molecular characteristics. Statistical analyses included assessment of species richness, diversity and spatial distribution patterns of species.The study showed that Tanaidacea assemblages in the Bering Sea and Aleutian Trench are both morphologically and molecularly diverse. Depth, temperature, salinity,and nutrient availability are key factors affecting the distribution of Tanaidacea. The differences in species composition between the areas studied suggest that each environment has unique ecological conditions that shape Tanaidacea assemblages.The study provides new information on the biodiversity of the deep-sea ecosystems of the Bering Sea and Aleutian Trench. The research contributes to a better understanding of one of the least studied ecosystems on Earth and underscores the importance of continuing research in this area.

O1E-7: The Phylogeography of the Cumacean *Eudorella Emarginata*

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The Sea of Japan, surrounded by the Asian continent and the Japanese archipelago, is characterized by the anoxic events in the glacial periods (Tada et al., 1999) and the topography connecting to neighboring seas via shallow straits (less than 140 m depth). The biogeographical insights on both features have been understudied, particularly regarding benthic invertebrates (Fujita et al., 2021). In this context, *Eudorella emarginata* (Cumacea, Peracarida) is a noteworthy species. As this species is expected to have limited dispersal capability due to a lack of planktonic larval stage (Sanders and Grassle, 1971) and reported from the Sea of Japan and the Pacific Ocean. Thus, this species might provide insights into the formation processes of the biogeographical structures around Japan. Phylogenetic analyses based on mitochondrial and nuclear DNAs showed three distinct clades within Japanese *E. emarginata*, suggesting the existence of sibling species. Only a single clade included individuals from both the Sea of Japan (depth: 519–1,024 m) and the Pacific Ocean (490–1,504 m). Further analysis focusing on this clade explored the relationship between population dynamics and climate change. While local populations in two regions are isolated from each other, our results suggested dispersal events during the Pleistocene. This population history might be linked to their shallower bathymetric distribution and/or colder environments around a strait in glacial periods. Despite the assumed bottleneck effect due to the past anoxic events in the Sea of Japan, a local population nearby the strait in the Sea of Japan showed as high haplotype diversity as those of the Pacific Ocean. The inflow of oxygen-rich seawater from the strait might have maintained suitable conditions during the glacial periods. Our results emphasize the importance of local populations nearby the strait for considering population dynamics of deep-sea benthic organisms in the Sea of Japan.

O2-1: What Are the Prevalent Clades Involved in Marine Biogeochemical Processes at Extreme Energy Limitation?

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https://cordis.europa.eu/project/id/899667

The deep biosphere is an essential component of marine ecosystems extensively populating seabed sediments and regulating key nutrient cycling. Its distribution and density in the global ocean mainly derive from primary organic matter production while sedimentation rates control the depth of O_2 penetration in the subsurface.

Focusing on organic-poor oxic and anoxic clays from the North Atlantic abyssal plain, we targeted both environmental DNA and RNA using quantitative PCR and high-throughput sequencing of 16S rRNA genes, metagenomes, and metatranscriptomes. In the oxic sediment, 16S rRNA gene copies decreased from 10^7 at the surface to 10^3 at 16 meters below seafloor (mbsf), with an assemblage dominated by benthic ammonia-oxidizing Nitrososphaeria. Their metabolism is characterized by ammonia oxidation, mixotrophic utilization of organic nitrogen via deamination, and the 3-hydroxypropionate/4-hydroxybutyrate carbon fixation cycle. In the anoxic sediment, 16S rRNA gene copies increased by an order of magnitude from the seafloor to 10^6 at 5 mbsf, decreasing to 10^4 at the core bottom. A single Atribacteria JS1 taxon dominated the entire assemblage throughout the core. This taxon displayed metabolic potential for sugar and peptide fermentation, a partial tricarboxylic acid cycle and the Wood-Ljungdahl pathway. Transcriptomes demonstrated active cell division down to 10 mbsf with energy production sustained via acetogenic fermentation and recycling of alcohols, ketoacids and volatile fatty acids made possible by a microcompartment in the cell. Various Dehaloccocoidia reached cell division at similar depths, persisting via homoacetogenic fermentation of proteinaceous material and β-oxidation of fatty acids. The deep biosphere metabolisms are designed to reduce energy loss and make use of bacterial necromass for cellular survival, enabling reproduction over millions of years in the Atlantic abyssal subseafloor. Comparing these omics results with those from Barents Sea epicontinental sediments, we observe that homoacetogenesis systematically outcompetes sulfate reduction under organic-poor energy-limited conditions.

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O2-2: Distribution and Genomic Variation of Ammonia-Oxidizing Archaea in Abyssal and Hadal Surface Sediments

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Ammonia oxidizing archaea of the phylum Thaumarchaeota play a central role in the biogeochemical cycling of nitrogen in benthic sediments, at the interface between pelagic and subsurface ecosystems. However, our understanding of their niche separation and of the processes controlling their population structure in hadal and abyssal surface sediments is still limited. Here, we reconstructed 47 AOA metagenome-assembled genomes (MAGs) from surface sediments of the Atacama and Kermadec trench systems. They formed deep-sea specific groups within the family *Nitrosopumilaceae* and were assigned to six *amo*A gene-based clades. MAGs from different clades had distinct distribution patterns along oxygen-ammonium countergradients in surface sediments. At the species level, MAGs thus seemed to form different ecotypes and follow deterministic niche-based distributions. In contrast, intraspecific population structure, defined by patterns of Single Nucleotide Variants (SNV), seemed to reflect more complex contributions of both deterministic and stochastic processes. Firstly, the bathymetric range had a strong effect on population structure, with distinct populations in abyssal plains and hadal trenches. Then, hadal populations were clearly separated by trench system, suggesting a strong isolation-by-topography effect, whereas abyssal populations were rather controlled by sediment depth or geographic distances, depending on the clade considered. Interestingly, genetic variability between samples was lowest in sediment layers where the mean MAG coverage was highest, highlighting the importance of selective pressure linked with each AOA clade's ecological niche. Overall, our results show that deep-sea AOA genome distributions seem to follow both deterministic and stochastic processes, depending on the genomic variability scale considered.

O2-3: Death in the Deep: Microeukaryotes in Hydrothermal Vent Food Webs

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Deep-sea hydrothermal vents are oases of microbial and animal biological diversity that is made possible by primary production sourced by chemolithoautotrophic microorganisms. Yet, the rate and route of how this energy is transferred to higher trophic levels to sustain the local hydrothermal vent community remains understudied. This research addresses the ecological contributions that single-celled microbial eukaryotes (protists or microeukaryotes) make to deep-sea food webs, with a particular focus on microbial mortality (e.g., grazing, parasitism). Centered at two vent fields at the Mid-Cayman Rise, Von Damm and Piccard, we quantified protistan predation pressure (grazing on bacteria and archaea) and biomass (derived from cell abundance) to more clearly understand the flow of carbon through the hydrothermal vent food web. Protists were found to exert predation pressure on the local hydrothermal vent bacteria and archaea, which may account for the trophic transfer of a substantial amount of carbon. We also used genetic methods to link transcript profiles to microeukaryotic activities, specifically identifying metabolic pathways associated with heterotrophic modes of nutrition. Results from meta-omic analyses highlight how trends in expressed transcripts clustered similarly to taxonomic diversity across the vent sites and provide new insight into generalist vs. specialist lifestyles among vent-associated protists. Altogether, our study contributes to a clearer understanding of how microeukaryotic species mediate linkages between the hydrothermal vent food web to the broader deep-sea carbon budget.

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O2-4: Prevalent and Active Dehalogenation Metabolism in Microorganisms of the Deepest Oceanic Trench

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The hadal trenches are the deepest parts of the Earth's oceans, serving as the end for the sinking of marine particles and as a "tunnel" for the exchange of materials between the ocean and the deep Earth. Despite extreme conditions such as high pressure, the hadal trenches harbor high content of organic carbon (OC) and active microbial carbon turnover, are "hotspots" for deep-sea OC degradation and extreme microbial processes. However, little is known regarding the components of trench OCs and the major microbial processes driving the OC degradation in the hadal trenches. In this study, we show unexpectedly high concentration of halogenated organic compounds (HOCs) in the sediments of hadal trenches, averagely 1 halogen per 58 carbon atoms in the OC pool. We further show the prevalence of dehalogenation metabolisms in the hadal trench microbial communities, based on systematic analysis on 27 deep sequenced metagenomes and 2517 metagenome assembled genomes from the Mariana Trench. Diverse dehalogenases with different dehalogenation mechanisms present in all of the metagenomes from the trench, and dehalogenase showed significantly higher relative abundance than those in non-trench environments. More than 50% of the MAGs retrieved from the trench metagenomes showed potential of dehalogenation. The identified dehalogenation microorganisms belong to 16 phyla and 52 orders, majority of which were reported to be potential dehalogenation microorganisms for the first time. High-pressure and low temperature microcosms simulating the *in-situ* trench environments showed rapid degradation of typical anthropogenic organohalides and transcription of enzymes related with metabolisms of HOCs, demonstrating the active HOCs degradation by the trench microorganisms. The findings suggest the dehalogenation metabolism as an important process in the remineralization of organic matter in the hadal trenches, which greatly advanced the understanding on deep-sea carbon cycling mechanisms and survival strategies of deep-sea microorganisms.

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O2-5: Crude-Oil Degradation Capabilities by Microscopic Fungi of Deep-Sea Hydrothermal Vents of the Gulf of California

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Some microscopic fungi from extreme marine ecosystems possess unique capacities to degrade complex oil molecules, which confers them a growing interest in bioremediation. However, fungi from deep-sea hydrothermal vents and their metabolic strategies have been poorly assessed. This study evaluated the oil-degrading capabilities of six fungal isolates from deep-sea vents of the Gulf of California (*Aspergillus terreus*, *Aspergillus sydowii*, *Aspergillus* sp., *Penicillium miczynskii*, *Penicillium miczynskii* (F), and *Penicillium dodgei*). The response of the isolates to the presence of light LCO and heavy crude oil HCO was assessed through a tolerance bioassay, while their capabilities to degrade crude oil as the sole carbon source were tested in a biodegradation bioassay. The assimilation of oil derivatives into fungal tissues was determined by comparing the carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotopic signatures of the isolates and oils. Additionally, the composition of the HCO before and after exposure to *A. terreus* and *P. miczynskii* (F) was assessed by gas chromatography. All the isolates grew in the presence of both oils in the tolerance bioassay: *P. miczynskii* (F) and *A. sydowi* had enhanced growth in LCO and HCO, respectively. In the biodegradation bioassay, *A. terreus*, *A. sydowi*, *P. miczynskii* (F), and *P. miczynskii* showed enhanced growth concerning the controls when using crude oil as the sole carbon source. The $\delta^{13}C$ values were more enriched in the isolates than in the oil, suggesting they used it as a carbon source. The fungal $\delta^{15}N$ values were more heterogeneous, suggesting the assimilation of various nitrogen sources. The analysis of the oil exposed to fungal activity showed that fungi degraded both medium and long-chain hydrocarbons, thus causing an increase in short-chain hydrocarbons. Due to its remarkable growth and capacity to degrade complex hydrocarbons, *P. miczynskii* (F) represents a promising bioremediation agent. Further studies are needed to explore its potential.

O2-6: The Far-Reaching Impacts of Hydrothermal Plumes on Microbial Communities and Biogeochemistry Significance in the Okinawa Trough

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Deep-sea hydrothermal vents, known as chemosynthetic ecosystems, spew out high-temperature (~400°C), oxygen-free fluids that rapidly mix with the surrounding cold, oxygenated seawater to form hydrothermal plumes. These plumes significantly affect the microbial communities and their metabolic activities. However, due to the difficulty of sampling, the range and extent of hydrothermal plumes' influence on microbial communities and their characteristics have not been fully understood. Here, the structure and activities of microbial communities and their potential functions in water columns near the Yokosuka hydrothermal vent, which has the highest fluid temperature (383.3°C) in the Okinawa Trough, were investigated. The SUP05 cluster (*Thioglobaceae*) and *Methylococcales* were the dominant and active sulfur-oxidizing bacteria (SOB) and methane-oxidizing bacteria (MOB) in the hydrothermal plumes, respectively, showing significant differences compared to non-hydrothermal environments. The co-occurrence network analyses showed that these SOB and MOB mainly had positive associations, indicating their cooperative relationships. Sulfide oxidation (*sqr*), thiosulfate oxidation (Sox system) and aerobic methane oxidation were the dominant biogeochemical processes found in the bottom water layers of the Yokosuka hydrothermal vent. Based on the Bray-Curtis dissimilarity analyses, the hydrothermal plume affected the surrounding microorganisms within a range of 1200 m vertically and at least 3378 m horizontally. The MOB and aerobic methane oxidation were particularly sensitive to the physical and chemical changes of plume environments. Furthermore, bacteria with quorum sensing activities were also investigated to reveal their cooperation in hydrothermal vents of Okinawa Trough. Our study provides comprehensive evidence revealing the influence of hydrothermal plumes on the microbial communities and their biogeochemical roles in the Okinawa Trough.

O2-7: Novel Insight into Microbiosphere and Metabolisms in the Subseafloor Sediments of the Challenge Deep

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The Mariana Trench is the deepest known site in the earth's oceans, reaching a depth of ~11,000 m at the Challenger Deep. Recent studies revealed that hadal waters and surface sediments harbor distinctive microbial communities, which play key biogeochemical roles. However, the microbial community structures and their metabolisms in the subseafloor of the Challenger Deep are largely unknown. Here, a ~750 cm long sediment core was sampled from the Challenger Deep and a detailed biochemical and microbial properties were subsequently investigated. Analyses of carbon isotope composition in the sediment core revealed noncontinuous deposition, with anomalous ^{14}C ages likely caused by seismically driven mass transport and the funneling effect of trench geomorphology. Evidence is provided of a unique role for high-rate episodic sedimentation events in controlling the subsurface microbiosphere in Earth's deepest ocean floor. In addition, the hydrocarbon degradation bacterium in the core were found to be significantly different from those in seawater, and phylum *Chloroflexi*, *Proteobacteria*, *Planctomycetota* and *Actinobacteriota* may play significant role in hydrocarbon degradation in the core. Moreover, novel insights were provided on the hadal *Thaumarchaeota* evolution and intraspecies-level genomic variation in *Thaumarchaeota* was revealed to be linked to the benthic-*versus*-pelagic niche partitioning in the deep ocean. Finally, novel dimethylsulfoniopropionate (DMSP) metabolic genes/pathways in deep sediment of the Mariana Trench were revealed. Our study extends the current understanding of subsurface microbiosphere and metabolisms in Earth's deepest ocean floor and highlight the need to perform thorough analysis over more samples to characterize hadal benthic populations and their biogeochemical roles.

O2-8: Nitrous Oxide Reduction by Model Deep-Sea Isolates and Susceptibility to Metal Exposure

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Nitrous oxide (N_2O) is a potent greenhouse gas and predicted to be the dominant ozone-depleting gas of the 21st century. Microbial processes, such as nitrification, denitrification, or dissimilatory reduction of nitrate to ammonium often control net N_2O emissions in different environments. Particularly, bacteria and archaea carrying the *nosZ* gene, encoding the N_2O reductase enzyme, are the only known biological sink of this important greenhouse gas and may be crucial to maintaining low levels of dissolved N_2O in the deep ocean. However, N_2O reduction by deep-sea microorganisms is vastly unexplored. Moreover, its susceptibility to metal exposure, a potential consequence from emerging deep-sea mining activities, is currently unknown and may represent a harmful consequence for environmental health. In this research, we evaluated the effects of cadmium (Cd) and copper (Cu) exposure on two deep-sea isolates carrying the *nosZ* gene, *Shewanella loihica* PV-4 and *Thalassospira indica* PB8B. The two strains also represent distinct N_2O metabolic phenotypes, with S. *loihica* PV-4 being able to produce and reduce N_2O, while *T. indica* PB8B only able to reduce it. We performed a series of metal exposure experiments in semi-closed bioreactors and evaluated the Cd and Cu impacts on growth, net N_2O production, *nosZ* gene expression, and the overall transcriptome. In *S. loihica* PV-4, Cd and Cu had opposite effects on the N_2O metabolism, with the former inhibiting net N_2O production and the latter enhancing it, causing an accumulation of headspace N_2O. Gene expression patterns partially explained this observation, but post-transcriptional effects may also be relevant. In *T. indica* PB8B, Cu also caused an accumulation of headspace N_2O due to delayed N_2O reduction. We believe that the observations and findings from this research will contribute to start unveiling the dynamics of N_2O metabolism by deep-sea microorganisms as well as the potential consequences of metal exposure.

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O3-1: The Ins and Outs of Associations Between Beneficial and Pathogenic Bacteria of Deep-Sea Mussels

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The manner in which the microbiome is acquired and persists over the lifetime of hosts shapes the ecology and evolution of both beneficial and pathogenic associations. However, our understanding of microbial acquisition and persistence is still rudimentary, particularly in the vast diversity of life that is not genetically tractable, so-called non-model organisms. *Bathymodiolus* mussels have fascinated biologists since their discovery in the early 1980s at deep-sea hydrothermal vents. These mussels thrive in the deep sea, far away from the photosynthetic primary production at the ocean surface, thanks to their intimate symbiosis with bacteria that provide them with nutrition. In addition to their beneficial symbionts, bathymodioline mussels also host a pathogen, *Ca.* Endonucleobacter, that infects their nuclei. A single pathogen invades the mussel's nuclei, replicates there, generating up to 80,000 cells and causing the nuclei to swell to 50 times their original size, and eventually escapes when the infected mussel cell bursts.

In my talk, I will describe the combined molecular and imaging approaches we are using to gain insights into how the beneficial and pathogenic microbiota of deep-sea mussels enter and persist in their hosts, and how these processes affect the ecology and evolution of these associations.

O3-2: Exploring the Depths: Insights into Symbiosis-Driven Biodiversity in Cold Seeps

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Deep-sea chemosynthetic ecosystems, such as cold seeps and hydrothermal vents, have significantly advanced our understanding of life in extreme environments. However, new methodological paradigms are needed to elucidate life in these settings further. To this end, we have established an in-situ deep-sea research platform designed to study adaptations, featuring modules for environmental monitoring, sample fixation, and even conducting experiments. Cutting-edge omics techniques were applied to reveal the ecological roles and regulatory mechanisms of symbiosis.

Our findings indicate that primary productivity in these communities has been previously underestimated, with carbon fixation rates in megafauna being 2.5 times higher than expected based on label-tracking incubations conducted on board. Symbionts not only provide nutrients but also assist their hosts in heavy-metal resistance, sulfide detoxification, and adaptation to fluctuating oxygen levels typical of cold seep environments. They convert unstable reductive compounds into intermediates using nitrate during hypoxic phases, which are then fully oxidized to generate energy when oxygen is available.

We also explored the structural and molecular foundations of these symbiotic interactions through micro-region analysis, discovering novel inner cellular membrane systems that facilitate connectivity and modularity among endosymbionts. Furthermore, our study provided the first cellular atlas of deep-sea symbiotic-containing tissues. By comparing gills with and without symbionts, we identified cholesterol as a potential regulatory molecule influencing the metabolic activities and development of bacteriocytes.

These insights underscore the importance of in-situ studies for future deep-sea research, offering a more accurate and comprehensive understanding of these complex ecosystems.

O3-3: An Evolutionary Perspective on Symbioses of Alvinocaridid Shrimps

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Alvinocaridid shrimps are a major component of the endemic fauna from chemosynthetic ecosystems, with a global distribution in numerous hot vents, cold seeps, and organic falls. The most emblematic species is certainly *Rimicaris exoculata* living in dense aggregations of thousands of individuals in close vicinity to hot vent fluid emissions. This shrimp hosts two distinct ectosymbioses: a chemosynthetic one in its cephalothorax cavity – or "head" – which provides most of its nutrition, and one with heterotrophic symbionts within its digestive system whose role remains unclear. However, symbioses in other alvinocaridid species have received little attention, unlike other chemosymbiotic lineages such as bathymodioline mussels. Here, we combine morphological and molecular examinations to study the two symbioses in 18 species of alvinocaridids from 26 chemosynthetic localities all around the world. We show that the "head" and digestive symbioses have followed distinct evolutionary trajectories with a more recent convergence of the "head" symbiosis in two pairs of sister species in *Rimicaris*, whereas main lineages of digestive symbionts are conserved across all species analyzed. We also highlight the presence of drastically different trophic regimes in this family, ranging from a complete dependence on chemosymbiosis to bacterivory and detritivory diets, including mixed feeding modes, depending on the species. Overall, our work greatly expands our understanding of alvinocaridid ecology, providing fresh perspectives and raising new questions on the influence of biogeography, host phylogeny, habitat, and diet on symbioses in chemosynthetic ecosystems.

O3-4: Host-symbiont Interactions in the Deep-sea Tubeworm *Lamellibrachia columna*

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Vestimentiferans are charismatic tubeworms thriving in deep-sea chemosynthetic ecosystems such as hydrothermal vents and hydrocarbon seeps thanks to their symbiotic association with bacteria. *Lamellibrachia* is the most diverse genus among vestimentiferans, with nine named species and several undescribed ones. Among these, *L. columna* exhibits a notably wide distribution in both vents and seeps, spanning approximately 9000 km from New Zealand to Japan, between depths of 800 to 3000 meters. *Lamellibrachia columna* is therefore an excellent model to study the adaptability and symbiotic relationships of vestimentiferan tubeworms. The genome of *L. columna* was recently sequenced but the lack of a complete reference symbiont genome and transcriptomes of the symbiont-housing trophosome hindered the study of this unique symbiotic model. Here, we fill this gap by sequencing the endosymbiont genome and holobiont transcriptome of *L. columna* from a cold seep in Sagami Bay, combining short- and long-read technologies. We elucidate the phylogenetic position of *L. columna* symbionts and investigate the variations in genome size, genome architecture, and intra-host diversity. We also characterize host-symbiont interactions, with a focus on symbiont establishment, population maintenance, and co-metabolism. Furthermore, we present a comparative analysis of host-symbiont interactions between hot vents and cold seeps, providing insights into the evolution of nutritional symbiosis that allowed tubeworms to colonize diverse deep-sea habitats. Our findings enhance the understanding of molecular mechanisms underlying the unique way of life in vestimentiferan tubeworms.

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O3-5: Novel Structural Integration of Chemosymbionts in A Giant Deep-Sea Caudofoveate Worm-Mollusc from Cold Seeps

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Symbiosis is a highly successful adaptive strategy for organisms across a wide range of environments, such as the relationship between invertebrates living in deep-sea chemosynthetic habitats and chemolithoautotrophic bacteria. Recently, our team named a giant caudofoveate worm-mollusc from methane seeps reaching over 15 cm in length: *Chaetoderma shenloong*. This is the first caudofoveate from a chemosynthetic ecosystem and the first aplacophoran mollusc associated with cold seeps. We confirm the presence of chemosymbionts within *C. shenloong,* the first case outside gastropods and bivalves among molluscs. We employ state-of-the-art HiFi and Hi-C sequencing strategies to obtain a chromosome-level genome of the host and the complete genome of the symbiont. Phylogenomic analysis reveal the symbiont to be a sulfur-oxidizing bacteria in the genus *Thiodubiliella*, clustering closely with the symbiont of the thyasirid clam *Conchocele bisecta*. Results from comparative genomics and transcriptomic profiling suggest significant interactions and co-evolutionary processes between the two parties, likely linked to their adaptations to anaerobic environments and contribute to the host's unusually large body size among caudofoveates. Our study further sheds light on a novel model of structural integration of chemosymbionts within this holobiont system, expanding the horizon of symbiotic mechanisms overall.

O3-6: Abyssal Deposit Feeder Utilization of Gut Microbiota is Reflective of Feeding Ecology

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Deposit feeders on the abyssal plain are adapted to survive on low-quality organic material, which often arrives in infrequent pulses. Stable isotope analysis has recently revealed that deposit feeders can be secondary consumers two trophic levels above the organic material they consume, and that their gut communities are instead the primary consumers. We combined compound-specific stable isotope analysis of amino acids (AA-CSIA) with 16S rRNA microbial community barcoding to relate the composition of gut communities with the trophic position and dietary preferences of abyssal deposit feeders. AA-CSIA allows us to distinguish the dependency of consumers on fresh phytodetritus and large marine snow particles from that on more degraded and recalcitrant small particles. We compared data for deposit-feeding echinoderms at two sites in the Northeast Pacific, the oligotrophic Station ALOHA and the relatively eutrophic Station M, to determine whether the quantity and quality of organic detritus affected the function and magnitude of animal-microbe symbioses. At Station M, relatively fast-moving taxa such as the holothurian *Oneirophanta mutabilis* consuming fresh phytodetritus had gut communities dominated by Cyanobacteria and other taxa unlikely to be resident microbiota. At Station ALOHA and for the slower-moving taxa at Station M such as the echinoid *Echinocrepis rostrata*, however, gut communities were dominated by archaea and bacteria potentially involved in nitrogen cycling. We found large variation among taxa at both sites in trophic level and consumption of different types of detritus based on isotope analysis, which was consistent with some of their known feeding behaviors. Taken together, we propose that niche partitioning and productivity regime drive deposit feeders that are less able to take advantage of fresh phytodetritus to rely on supplemental nitrogen and organic matter breakdown by their resident gut microbes.

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O4A-1: Exploring Deep Sea Biodiversity with Environmental DNA

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The deep sea, including the ocean's mesopelagic zone (or "ocean twilight zone"), harbors a vast biomass that is critically important to the global carbon cycle. However, the diversity of this biomass is understudied due to the immense size of the environment and the logistical challenges of collecting samples. More information is especially needed on diel vertical migration (DVM), where typically, mesopelagic animals travel to surface waters to feed at night and return to mesopelagic depths for the day, expediting the downward movement of carbon in the process. Environmental DNA (eDNA) metabarcoding analyses have great potential to provide information on deep sea biodiversity and address hypotheses related to DVM, species distributions, and ecological interactions. Furthermore, we have found that eDNA detects animal taxa that are missed in traditional net tow analyses. However, deep sea animal eDNA signals are dilute and patchily distributed, creating challenges for eDNA research. I will discuss recent advances and results in eDNA approaches to studying deep sea biodiversity with respect to sampling, reference databases, and data interpretation. Despite potential for vertical movement of genetic material, modeled and field-collected eDNA signatures appear to reflect the depth of their source, indicating that eDNA approaches are useful for studying vertical phenomena such as DVM. Consistent with this and using newly obtained reference sequences from deep sea fishes, we found a greater diversity of mesopelagic fish in surface waters at nighttime than in the daytime. Additionally, I will show how large-volume autonomous samplers can facilitate deep sea biodiversity exploration by enabling the detection of more taxa and through their integration with diverse oceanographic platforms such as the AUV *Mesobot*, a robot designed for midwater science and exploration.

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O4A-2: Multi-Marker eDNA Metabarcoding Reveals Patterns of Multi-Trophic Interactions and Ecological Connectivity in the Mesopelagic

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Midwater ecology and organismal interactions are difficult to study and as a result, are insufficiently accounted for in food web analyses and biogeochemical models. This hinders our ability to accurately model and forecast ecosystem function and formulate effective policies for conservation and management, especially given the growing interest in exploiting midwater resources. We used multi-marker metabarcoding of environmental DNA (eDNA) samples collected from the Northwest Atlantic Slope Water to resolve patterns of marine biodiversity from epipelagic and mesopelagic waters. Combined with statistical network analyses, we explored cross-kingdom eukaryotic community structure and taxonomic interactions with the aim of obtaining insights into food web dynamics. We found distinct, depth-specific communities comprised of unique protist, invertebrate, and fish assemblages. Ecological networks for the epipelagic, upper mesopelagic, and lower mesopelagic suggest that protists are key mediators of multi-trophic level interactions and ecological connectivity from the surface waters down to 1000 m. Additionally, network modularity and other topological features indicate greater interconnectedness in mesopelagic communities compared to the epipelagic, which may play a role in ecosystem stability and resilience. We will discuss our findings in the context of generating holistic ecological insights and the implications for deep sea ecosystems in a changing ocean to inform sustainable resource management and stewardship of the deep sea.

[This research is part of the Woods Hole Oceanographic Institution's Ocean Twilight Zone Project, supported by funding as a part of The Audacious Project, a collaborative endeavor housed at TED.]

O4A-3: Move Over Medusae: Trophic Ecology of Biomass-Dominant Gelatinous Zooplankton (Siphonophores and Pyrosomes) in the California Current Ecosystem

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Gelatinous zooplankton are increasingly recognized as key components of pelagic ecosystems. We focus on two abundant and biomass-dominant gelatinous taxa, siphonophores (Hydrozoa) and pyrosomes (Tunicata). We synthesized existing literature on the trophic ecology and predator-prey interactions of siphonophores and analyzed siphonophore-prey network topology across shallow and deep habitats. Diets were distinct between siphonophore suborders and species, indicating that siphonophores occupy multiple trophic niches and prey on taxa including crustaceans, gelatinous zooplankton, and fishes. Siphonophore-prey networks were more specialized in deep-pelagic compared to upper-ocean habitats. We then sampled particulate organic matter, zooplankton, and micronekton in the California Current, concurrent with blooms of *Pyrosoma atlanticum*, and measured gelatinous zooplankton size structure and biomass across stations and depth habitats. We used stable isotope analyses of bulk tissues and amino acids to infer trophic ecology and calculate the trophic positions of siphonophores and *P. atlanticum*. Siphonophore trophic positions ranged from 2.4-4.0, which illustrates their trophic diversity. Trophic positions were consistent across depth habitats. However, the highest trophic positions were restricted to deep-pelagic physonect species, and trophic positions were strongly related to siphonophore phylogeny. Stable isotope values also indicated that deep-pelagic siphonophores indirectly rely on food webs supported by deep, small particles, whereas *P. atlanticum* relies on a shallow particle food-web baseline. *P. atlanticum* exhibited lower trophic positions compared to siphonophores and other zooplankton, suggesting that they are isotopically distinct from the primary planktonic food web pathway in the California Current. Lastly, colony size greatly influenced *P. atlanticum* vertical habitat, whereby smaller colonies were restricted to the upper 200 m, which has implications for carbon cycling. Pyrosomes and siphonophores are both colonial gelatinous zooplankton but they employ different feeding mechanisms and occupy distinct niches in pelagic food webs. These insights enhance our understanding of their vertical distribution, trophic ecology, and roles in pelagic food webs.

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O4A-4: First Investigations of Dietary and Habitat Overlap in Three New Zealand Deep-Sea Squid Species

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Cephalopods are vital nutrient vectors between different marine habitats and from low level consumers to apex predators. Their ecological importance will continue to rise as cephalopods fill the vacant niches left behind due to the overharvesting of their competitors. Despite their importance, 90% of cephalopod species' diets remain undescribed, and the habitat preferences of many such species are equally unknown. In this study, I aim to describe the dietary and habitat preferences of three deep-sea squids from New Zealand waters: the Angolan flying squid (*Todarodes angolensis*), the Antarctic flying squid (*Todarodes filippovae*) and the rugose hooked squid (*Onykia robsoni*). To characterize target taxon diets, morphological identification and DNA barcoding of prey tissues from specimens' gut contents was undertaken, but this method only reveals recent prey items. Longer-term comparative data can be obtained through carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope analysis of squid beaks, which are chitinous structures that are formed in layers over their lives. Therefore, by sub-sampling the beaks at locations corresponding to different life stages of the specimens and measuring their $\delta^{13}C$ and $\delta^{15}N$ values, we can reliably quantify ontogenetic changes in habitat and assess trophic position. While there was a large degree of overlap in observed prey items from stomach content analyses between the study species, multivariate analysis reported that there was a species effect on dietary composition. This was attributed to *T. angolensis* having far more demersal and benthic prey species reported in its diet whereas *T. filippovae* and *O. robsoni* preferred pelagic prey items. All stable isotope results will be discussed during this presentation.

O4A-5: Examining the Diets of Deep-Sea Cephalopods from the Northern Gulf of Mexico Using a Metabarcoding Approach

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Cephalopods are integral to the trophic dynamics of the open ocean, including the poorly known deep midwater. They are well known as prey of apex predators such as marine mammals, fishes, and birds from techniques such as visual analysis of stomach contents to identify cephalopod beaks and other ingested parts. However, there is very little information related to the specific prey of deep-sea cephalopods. Most studies report only broad categories of prey items (e.g. crustaceans, fishes). Cephalopods have a beak-like mouth with radula they use to break up food and when the resulting fragments are passed through the brain to the stomach, there are very few, if any distinguishable parts for prey species identification. The DEEPEND/RESTORE Program has conducted multiple cruises in the Gulf of Mexico where deep-sea cephalopods have been collected (2019- 2023). Midwater squid and pelagic octopod stomachs are being used for a gut-content metabarcoding project in which the identification of the prey species is possible using various DNA gene regions for specific species identification. Results from the ongoing project will be discussed to highlight the variety of prey items cephalopod species ingest in the northern Gulf of Mexico.

O4B-1: The Hidden Diversity, Behaviour and Life Histories of Atlantic Deep-Sea Cephalopods

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Deep-sea pelagic cephalopods are pivotal components of Atlantic oceanic food webs, consuming a variety of mid-trophic prey and being prey for top predators. The biomass of deep-sea cephalopod populations is enormous but most species have never been documented alive in their natural habitat, and mature and reproducing individuals are unknown for many taxa. While, on a daily basis, populations of deep diving cetacean predators consume thousands, sometimes giant, cephalopods, these interactions have never been witnessed. The reason for the paucity in our knowledge on deep-sea cephalopods is the challenging environment they inhabit, and cephalopods' ability to avoid nets, cameras and submersibles. The ability to avoid oceanographic gear is likely linked to an ongoing arms race between whale predators to detect, hunt and capture cephalopods, and the selective pressure on cephalopods to evolve traits to avoid their predators. Here we present an overview of cephalopod traits, which we hypothesize reduce the detection chance by whale predators, and allow survival under high predation pressures. These include a vertical body position, an elongated body morphology, and solitary (non-schooling) occurrence and a semelparous life history. We discuss these traits in the context of whale foraging adaptations including echolocation. Additionally, we present novel insights in deep-sea cephalopod diversity and observations from recent ocean expeditions off oceanic islands in the Atlantic including new regional records. Finally, we present technological and methodological advances of a collaborative, multi-census approach to study deep-sea cephalopods.

O4B-2: *In Situ* Observations of Deep-Sea Cephalopods in Beaked Whale Predator's Foraging Habitat

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Off Terceira Island (Azores), different species of cephalopod-consuming cetaceans co-occur in a small geographic region and target prey at depths between 200 m to 2 km. It has been hypothesized that competition between co-occurring cetaceans is avoided by niche partitioning between species. One elusive deep-diving whale off Terceira is the goose-beaked whale, *Ziphius cavirostris*, foraging down to 3000 m. It is believed that these whales target larger, more calorific cephalopods occurring deeper as a result of ontogenetic migration. To test the hypothesis that larger cephalopods occur increasingly deeper in the *Z. cavirostris* foraging zones we aimed to document cephalopods in their natural habitat. During two field campaigns in 2023 and 2024 off Terceira Island, we deployed "Nautilus" pelagic drifting and seafloor lander camera systems *in situ* to record squids at different depths in the meso- and bathypelagic zones. Both systems carried an autonomous, ultra-low-light video imaging system that recorded videos under far-red and white light. To attract cephalopods, we used fish bait and an optical bioluminescence emitting lure called "eJelly". In 2023, we collected 89 hours of video at depths between 335-730 m and recorded 28 specimens of the family Ommastrephidae (flying squid), of which at least one species has been previously found in the stomach content of stranded *Z. cavirostris*, however not yet recorded in the Azores. Fifteen individuals were estimated to be between 19-89 cm in body length, with most (53%) in the size range of 36-70 cm. Combining the observations of both years, we present an assessment of cephalopod's size-distribution with increasing depth and preliminary observations of behaviour towards the eJelly and bait. These are among the first deep-sea observations of squids in the Azorean region and will further our understanding of foraging niche segregation of co-occurring deep-diving cetceans.

O4B-3: Accidental *In Situ* Observations Reveal Previously Unknown Behaviour Type in Cephalopods, Relevant to Bentho-Pelagic Coupling

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The biology of many cosmopolitan pelagic deep-sea taxa is only known from accidental opportunistic observations. Deep-sea cirrate octopods (Cephalopoda, Octopoda, Cirrata) from the family Cirroteuthidae are one of these taxa. Recently, we have used opportunistic observations from three deep-sea video imagery methods (Remoted Operated Vehicles, towing camera and autonomous lander systems) in the Arctic and North Pacific, and observed *Cirroteuthis muelleri* and *Cirrothauma* cf. *magna* in situ. Collecting all available video sequences, both species seemed undisturbed by the lights from the observational equipment, and as such the observed behaviour considered natural. Both species were recorded in close association with the seafloor, consistently repeating similar behavioural sequences which consisted of four consecutive phases, interpreted as feeding behaviour. In *C. muelleri*, supposed prey capture was observed, and the lebensspuren of such activities are known on the seafloor within the species range. *Cirroteuthis muelleri* was also repeatedly observed motionlessly drifting in an umbrella-posture in the water column 500–2600 m above the seafloor, which is supported by trawl catches data. Trawl captures of *Cirrothauma* spp. worldwide suggest it also lives in the water column at least 600–1300 m above the seafloor, but here we report it feeding on the seafloor. These benthic and pelagic observations suggest a feeding migration in Cirroteuthidae. Cirroteuthidae prey on small (hyper)benthic crustaceans and polychaetes, and are preyed upon by large fishes, sharks and deep-diving toothed whales. Therefore the benthic-pelagic feeding migration by Cirroteuthidae create a ‘carbon expressway’ from small bathyal seafloor invertebrates to large pelagic top predators. In some areas of the World, cirrate octopods reach high abundance (e.g., *C. muelleri* with 94.3 individuals/km^2 abundance density in the Baffin Bay). It means that this overlooked component of the biological carbon pump in the deep sea might be of worldwide importance but with local hotspots of increased impact.

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O4B-4: Trophic and Functional Specialization in Deep-Pelagic Fish Along the Depth Gradient in the Bay of Biscay

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Oceanic pelagic ecosystems are characterised by pronounced vertical gradients, particularly in light and food resources. Species have had to adapt to these conditions, resulting in a great diversity of species, morphologies and behaviours, particularly within the fish community. It was previously hypothesised that species inhabiting the deep pelagic zone would have a generalist diet, exploiting any potential feeding opportunities given the scarcity of food resources at depth. However, this is contrary to the theory of niche differentiation, which predicts that species should specialise to limit interspecific competition. We tested these hypotheses by collecting stable carbon and nitrogen isotope data on 16 deep-pelagic fish species from the Bay of Biscay (Northeast Atlantic) between 20 and 1335m depth. Comparison of isotopic niche size values with those obtained under null models revealed significant species specialisation, with less overlap than expected by chance. We then investigated the strategies used by deep pelagic fish species to obtain food in this vast, dark and food-poor environment. We measured 27 morphological traits related to foraging function in 42 species, including the 16 previously sampled, collected at night between 20 and 2000 m depth. Important differences emerged between surface species, which had larger eye sizes, possibly reflecting a prey-tracking strategy, and bathypelagic species, which had a large mouth opening and many species with large teeth combined with luminescent appendages, possibly reflecting an ambush hunting strategy. Functional uniqueness values revealed that several species had a unique combination of traits. These functionally unique species may represent highly specialised forms of resource use and perform unique functions within the ecosystem. The high level of trophic and functional specialisation observed could reflect a pristine community structure, unaffected by the impact of human pressures such as fishing, but it raises concern about their vulnerability to future climate change and potential exploitation.

O4B-5: From the Deep-Sea and Beyond: How Patagonian Toothfish, a Megafauna, May Connect Distant Biomes

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Patagonian toothfish (*Dissostichus eleginoides*) is a notothenioid fish, and has a circum-sub-Antarctic distribution. *D. eleginoides* is long-lived (33-54 years old; Horn 2002), and can attain >2.3 m and 200+ kg (Collins et al. 2010). Given its rich oil content and white flesh, toothfish are particularly sought after by chefs and seafood consumers worldwide.

How Patagonian toothfish are able to distribute across a broad latitudinal range (~50°) is unsolved. Equally intriguing is the mysterious capture of a 1.8-m specimen off Greenland (Møller et al. 2003), indicating a toothfish survived an uncharted journey of 10,000+ km. Most fundamentally, deep-sea megafauna are challenging to study, and their ecology remains a void in our understanding of the processes that bridge the deep-sea ecosphere with other parts of the ocean.

We successfully deployed 50 satellite tags on *D. eleginoides* in fishing grounds south of the Falkland Islands. Location, depth and temperature data returned from 44 instruments, logging 6000+ days at sea, have for the first time, independently verified the occurrence of long-distance (>200 km) dispersal for this species. Speed of their dispersals appears, contrary to prevailing theories, to be high (up to 33 km day^{-1}), and their movements be seasonal. We postulate that adult toothfish are capable of utilizing underwater currents to assist with their dispersal, a scenario analogous to us riding in the mass transit system.

Informed by satellite tracking, we will showcase current multi- disciplinary analyses on broader toothfish connectivity. Through fisheries data mining, circulation modeling, otolith chemistry and genetic techniques, we hope to uncover the potential mechanisms of dispersal, and the associated ecological implications. A greater understanding on megafauna movement and navigation will widen our perspectives and enhance the biological realism of fisheries and ecosystem models.

O4B-6: The Success of Spiny-Rayed Fishes in the Deep-Pelagic Ocean Discovered Using a Large Midwater Trawl

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The standard dogma regarding fish assemblages in the deep-pelagic ocean (water column below 200 m depth) is that they are comprised largely of basal, soft-rayed fishes such as Myctophiformes, Stomiiformes, and Aulopiformes. While the diversity of soft-rayed fishes in the deep sea is certainly much greater than the derived, spiny-rayed fishes, it is the abundance and biomass of the latter that has been historically underestimated. Our view of the deep sea has been framed by what we can catch with relatively small, research-sized, rectangular midwater trawls (RMTs) towed from single-warp oceanographic vessels. Large, dual-warp midwater trawls (LMTs) have only been used repeatedly for research in the last two decades. In 2011, the most extensive large-trawl sampling of meso- and bathypelagic fish assemblages occurred in the Gulf of Mexico as part of the *Deepwater Horizon* disaster damage assessment. During this sampling we found that spiny-rayed fishes were collected in much higher ratios than those of RMTs, and that this fauna represented a large proportion of fish biomass below 200 m. This program used both RMTs and LMTs to collect deep-pelagic fauna in the northern Gulf of Mexico between 0-1500 m depth. Data will be presented comparing the catches of basal, soft-rayed fishes to the more derived, spiny-rayed fishes using these two gear types. The resulting synthesis suggests that while soft-rayed fishes do indeed numerically dominate the deep-pelagic domain, the notion that spiny-rayed fishes are not successful in this habitat is likely a function of historical gear bias rather than evolutionary processes.

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O4B-7: To Brood or Not to Brood: Predicting Larval Strategies in the Asteroidea

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Larval strategies, the developmental progression from fertilization, through metamorphosis, to settlement, and the varying maternal input that characterizes such strategies, are fundamental to understanding biogeographic patterns in marine taxa. This is particularly true in the echinoderms, which, broadly sessile as adults, are reliant on pelagic larvae for primary dispersal and for the maintenance of connectivity between disparate populations. The Asteroidea, which span a known bathymetric range from the intertidal to more than 8,000m deep, have great diversities of developmental strategies, and these can, broadly, be categorized into three main types, free-swimming-planktotrophs, lecithotrophic-planktotrophs and benthic-lecithotrophs (often brooded). Each strategy represents a trade-off between reproductive considerations: is it more advantageous to produce numerous planktonic larvae with individually low survival rates but greater potential for exploitation of suitable but disjunct habitats or is it more favourable to invest in greater maternal input and individual larval survival rates at the cost of massively reduced dispersal potential and vulnerability to stochastic events? How too does this trade-off change in the deep ocean where adult population densities may be low and pelagic nutrition hard to come by?

Although a free-swimming planktotrophic larvae is generally considered to be 'typical' for the Asteroidea, developmental mode is only known for ~10% of asteroid species and is far less well characterised in the tropics and the deep ocean than in temperate and polar waters. Here, we have utilised a large, taxonomically almost comprehensive dataset of asteroid distribution data to fully characterise the biogeographic patterns of each larval mode at a fully global scale. We have further mapped reproduction across phylogeny and used these data to train models to predict, for the first time, across the unknown reproductive strategies of the class. We show substantial and surprising patterns of larval strategy distribution, discuss possible explanations for these pattern and show once again that the paradigms of shallow water are not always reflected in the deep sea.

O4C-1: Non-invasive Methods for Studying Midwater Jellyfish

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The midwater, the pelagic zone located beneath the euphotic zone and above the seafloor, is the largest continuous biome on our planet. It is primarily dominated by gelatinous zooplankton (e.g., medusae, ctenophores, siphonophores, and appendicularians), followed by other zooplankton and fish. Climate change, known for causing distribution range shifts in marine species, significantly affects biogeography and community compositions. Despite its significance in size and as an ecosystem, the midwater remains under-sampled compared to surface or deep-sea benthic habitats. This knowledge gap limits our understanding of how global changes will impact midwater organisms and the array of ecosystem services they provide. The lack of data also stems from traditional net sampling being inadequate for studying gelatinous zooplankton, as it easily fragments and/or destroys these fragile organisms. Here, the response of midwater organisms to environmental factors and global change was assessed and predicted using state-of-the-art non-invasive methodologies. These included metabarcoding of environmental DNA collected from seawater samples, as well as ecological niche modeling in three dimensions (latitude, longitude, and depth) based on optical surveys. Midwater communities detected through environmental DNA were linked to different water masses, and indicator species were identified, aiding in the prediction of future community shifts. Ecological niche modeling was used to test limiting environmental variables and to project the present and future three-dimensional distribution of midwater gelatinous zooplankton species of interest. Thus, the implementation of these non-invasive techniques allowed for testing the effects of the changing environment on midwater organisms, from species to community level.

O4C-2: Deep-Pelagic Nekton Research in the Gulf of Mexico: A 14-Year Synopsis and Future Directions

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The need for pelagic ecosystem data after the *Deepwater Horizon* (DWH) disaster precipitated a research program (DEEPEND; www.deependconsortium.org) spanning 14+ years (2010-present). The first iteration (2010-2015) focused on Census of Marine Life-like objectives (quantitative pelagic faunal inventories from 0-1500 m depth), the second (2015-2020) on population trajectories and ecological processes, and the third (ongoing) on continued time-series analyses and resource management utilization. We have learned much over this time. The deep-pelagic Gulf is exceptionally speciose, likely due to the combination of natural drivers and high sampling/analysis intensity. For example, more fish species occur in the deep-pelagic domain than in coastal waters, including coral reefs, a startling finding. We find that high vertical connectivity, from epi- to bathypelagic depths, is the Golden Rule, not the exception. The classical three-layer system concept becomes nonrepresentational once organisms cross the zooplankton-micronekton mobility threshold. This interconnectivity, coupled with extensive, multi-generational pollutant contamination, may be the reason that deep-pelagic populations have yet to recover from precipitous declines shortly after DWH. Extensive vertical distribution data reveal that diel vertical migration is rarely binary in a species; most have portions of populations migrating rather than all or none. Regarding diversity, our paired genetic and morphological studies highlight the need for continued and expanded specimen-based taxonomic training. We are nowhere near the point that genetic taxonomy alone is accurate or sufficient. In addition, areas of enhanced mesopelagic abundance have been detected in several Gulf of Mexico continental slope locations. This adds to a growing literature of such interactions in the Atlantic, Pacific, and Indian Oceans. Of particular interest in the Gulf are "triple junctions," namely mesopelagic aggregations over deep coral communities coincident with habitats of critically endangered cetaceans (e.g., Rice's whale) that feed on the mesopelagic fauna. DEEPEND's work will continue to address these and emerging topics.

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O4C-3: The Bathy and Abyssopelagic Micronekton Communities in the Eastern Pacific Clarion Clipperton Mining Zone

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Bathypelagic and abyssopelagic communities are poorly described worldwide. In the Clarion Clipperton Zone polymetallic nodule mining may occur in the near future leading to discharge plumes in the deep-water column and collector plumes in the benthic boundary layer. Therefore, it is very important to characterize baseline midwater diversity, community composition, and vertical structure prior to mining. We used 10-meter MOCNESS depth stratified sampling between 1500 and ~4200m water depth in the eastern CCZ to sample micronekton and macroplankton. Depth resolution was coarse given the broad depth range sampled and limited number of nets. Use of USBL beacons and fine-scale bathymetry enabled fishing these large nets to within 100m of the abyssal seafloor. Overall, crustacean taxa dominated the community in terms of density and often biomass. Large nemertean and polychaete worms were also important macroplankton. Density declined considerably below 2000m but caridean shrimp biomass was ~8-fold higher within 100-300meters of the seafloor in comparison to the rest of the bathypelagic. Elevated animal biomass or density above the deep-sea floor has been observed in other areas of the global ocean. Community composition was significantly different at every depth sampled suggesting that the bathypelagic cannot be treated as a single community nor as an extension of the shallower mesopelagic. Finer taxonomic and depth resolution sampling is required to evaluate species ranges and where faunal boundaries occur (e.g. to separate bathy and abyssopelagic communities) and whether the community composition and structure in the eastern CCZ is similar to elsewhere in the CCZ and Pacific.

O4C-4: Micronekton Community Assessment in A Deep-Sea Mining Site: Vertical Community Structuring and Biodiversity in an OMZ

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Micronekton are a vital part of midwater food webs and have the potential to be impacted by the release of sediment plumes and dissolved metals from deep-sea nodule mining (DSM) discharge. However, micronekton communities in the eastern Clarion-Clipperton Zone (CCZ) region are minimally studied, so baseline community descriptions are needed. Micronekton samples were collected day and night from 0 - 1500 m at both a control (intended for monitoring against mining impacts) and impact mining site in the NORI-D license area of the CCZ in Spring and Fall 2021. Using a 10-meter MOCNESS, nets were deployed across depths based upon dissolved oxygen patterns due to the pronounced oxygen minimum zone (OMZ) in this region and based on a previously planned midwater sediment discharge at 1200 meters. The micronekton community in NORI-D is clearly structured by oxygen; the migrating fish community exhibits species with daytime abundance peaks in the OMZ core and upper oxycline and nighttime abundance peaks in the upper oxycline and epipelagic. Non-migrating fish, such as *Cyclothone,* display biomass and abundance peaks in the lower oxycline. At the proposed discharge depth and below the OMZ, biomass and abundance of crustaceans and cephalopods were highest. The fish community displayed high rates of regional endemism suggesting this area is unique compared to other North Pacific regions. Total micronekton species richness ($q = 0$), Shannon diversity ($q = 1$), and Simpson diversity ($q = 2$) indices were highest from 1000 – 1500 m, the previously proposed discharge depth, followed by the OMZ core (450-700 m), suggesting midwater OMZs may hold higher diversity than expected. A sediment discharge depth shallower than 1500 m could not only affect the unique community in the 1000–1500m depth zone but also impact organisms adapted to extremely low oxygen levels due to the input of oxygenated discharge water.

O4C-5: Distinct Horizontal and Vertical Communities of Micronekton Across the Southern California Current Deep-Pelagic Ecosystem

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Quantifying the biomass and distribution of micronekton communities is critical for describing the ecological niches of deep-sea taxa and variability in food web structure across deep pelagic habitats. We collected micronekton in the southern California Current between the surface and 3000 m using a 10m^2 MOCNESS (n = 34 tows, n = 170 nets). Tows were performed annually from 2020-2023 along a 700 km transect (~East to West) sampling the water column above deep basin (three nearshore stations), escarpment (one station), and abyssal plains habitats (two offshore stations). For all animal groups, biomass generally decreased with depth and peaked above the escarpment. In the upper 1000 m, nearshore stations had higher biomass of fishes and crustaceans than offshore stations, with higher biomass of gelatinous zooplankton observed at offshore stations. Among daytime samples, depth was the primary driver of family-level community composition with respect to proportional mass and abundance (together referred to as "importance"). Micronekton community composition <200 m varied with season, but seasonal trends were less clear at greater depths. Gelatinous zooplankton dominated the community biomass at most depths with peaks in importance at <200 m (primarily tunicates, e.g., Pyrosomatidae and Salpidae) and >1000 m (medusae, e.g., Atollidae and Rhopalonematidae). The importance of fishes peaked at 200-1000 m (Myctophidae and Gonostomatidae), while crustaceans peaked at 500-1500 m, represented by a higher evenness of abundant families (e.g., Acanthephyridae, Eucopiidae, Sergestidae). Despite these consistent daytime vertical trends, there were clear differences in the micronekton communities sampled among habitat types. Each of the nearshore stations had distinct community compositions and were most different from the offshore stations. The escarpment was represented by a mix of nearshore and offshore taxa. Future work examining the size structure and vertical migration of each animal group will refine our understanding of their roles in deep-sea food webs.

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O4C-6: Biological Traits Influence Contemporary and Historical Temporal Genomics of Pelagic Deep-Sea Species from The Gulf of Mexico

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Investigating the temporal dynamics (e.g., population expansions and declines) of deep-sea species can help us better understand this mysterious habitat and provide information for species conservation. Such investigations can focus on changes that occurred a few or thousands of generations ago. Changes in population size are expected to impact genomic diversity (GD). GD describes a species' adaptive potential when facing environmental changes and represents a key parameter in species conservation. Deep-pelagic species from the Gulf of Mexico, an exceptionally speciose habitat, have experienced population crashes following the Deepwater Horizon Oil Spill (DWH). Here, we analyzed genomic data of a 12-year time series (2011-2023) of three species of fish (*Ceratoscopelus warmingii*, *Diaphus dumerilli*, and *Lepidophanes guentheri*) and an 8-year time series (2015-2023) of two of shrimp (*Phorcosergia grandis* and *Robustosergia robusta*) in the GoM following DWH. Moreover, we also used genomic data to investigate the historical demography of these species in the GoM. We detected different temporal GD changes depending on the species. Our results indicate that diel vertical migration behavior, depth range, and reproduction are important drivers of how GD changes over time in deep-sea animals, at both contemporary and historical time scales. From a conservation perspective, the results show how quickly GD can change over a few generations, but also how species have been going through distinct demographic trajectories, stressing the need to incorporate GD in future research as another indicator of potential anthropogenic impacts. Ongoing

work is expanding these analyses. Results are expected to deepen our understanding of the deep sea and inform conservation strategies for deep-sea pelagic species.

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Biological traits variation might determine how GD changes over time. GD studies are lacking for deep-sea species, especially over temporal scales.

In the northern Gulf of Mexico (GoM), some deep-sea pelagic species experienced population crashes following the Deepwater Horizon Oil Spill (DWH). Changes in population size are expected to impact genomic diversity (GD). GD describes a species' adaptive potential when facing environmental changes and represents a key parameter in species conservation. At the same time, biological traits variation might determine how GD changes over time. GD studies are lacking for deep-sea species, especially over temporal scales.

O4C-7: Hepatic Steatosis in Hadal Snailfish as an Adaptation to Extreme Environment

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The hadal trench (6,000-11,000 m) represents the deepest part of the ocean, is one of the most extreme environments on the Earth. Hadal snailfish are dominant bony fishes inhabiting in the hadal trench. In this study, we observed that the liver of hadal snailfish *Pseudoliparis swirei* tends to be enlarged (hepatomegaly) during several research cruise to Mariana Trench. Histological analyses including different staining methods showed excessive lipid accumulation but few fibers in the liver, suggesting that hadal *P. swirei* have severe fatty liver, but do not exacerbate to further liver fibrosis and worse. Proteomic and phosphoproteomic analyses were applied to gain insights into the metabolic pathways underlying the fatty liver. A total of 4533 proteins were identified and 5665 phosphorylated sites were found in the 2196 phosphorylated proteins. Further enrichment analyses and investigations of the liver proteins and phosphorylated proteins showed that the liver of hadal snailfish has active lipid metabolism and might serve as an “energy insurance” to deal with the extreme environment. High concentration of TMAO and potential hepatic insulin resistance might contribute to the excessive lipid accumulation in the fatty liver. Abundant enzymatic antioxidants and low inflammatory factors in the liver might prevent the deterioration of fatty liver, which might be shaped by the hadal environment. These results will deepen our understanding of deep-sea animals’ adaptive strategy to extreme environmental conditions and shed light on exploring deep-sea genetic resources for human disease control and treatment.

O5-1: Vision in the Deep – an Overview of Adaptations to Dim Light and Bioluminescence

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Adaptations of the visual systems of deep-sea organisms to dim light environments are driven not only by environmental light, but also biologically produced light, or bioluminescence. In both deep-sea crustaceans and fish, the dominant spectral sensitivity is to blue light, which is the color of light that transmits best in clear oceanic water as well as the color of most bioluminescent emissions. However, multiple species have unusual spectral sensitivities that have been correlated with bioluminescent light. In addition, many species are able to counterilluminate to hide their silhouettes from predators below them by precisely matching the intensity of light being blocked by their bodies. While the ability to do so is not clearly understood, recent evidence suggests that the photophores (light-emitting organs) themselves may be capable of sensing environmental light. Several species have also developed optical adaptations that allow them to "break" the camouflage provided by counterillumination.

O5-2: Shrimp Glow, Did Ya Know? Understanding Bioluminescence in Deep-Sea Decapods

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Bioluminescence, the emission of light by an organism, is rare on land but common currency in deep-sea ecosystems. Although the production of light can be used as both offensive and defensive behaviors, we are still “in the dark” on how most animals use light to survive. Our work on deep-sea shrimp has revealed that bioluminescence is much more common than previously reported, increasing the known occurrence of bioluminescence in deep-sea shrimps by 67%. The integration of -omics with morphology has revealed that light organs (photophores) come in a variety of forms and underlying genetic machinery. Over the past 10 years, my lab has traced the evolution of bioluminescent organs in the deep sea, demonstrated an expanded function of photophores beyond counterillumination and significantly increased the number of bioluminescent species. Recent work investigates the evolution of bioluminescence across the shrimp tree of life with the inclusion ~1000 taxa and a phylogenomic framework, while others explore the drivers of light on visual ecology and evolution. This talk attempts to summarize how the often unrecognized but awe-inspiring world of glowing shrimp has advanced our understanding of bioluminescence in the deep sea.

O5-3: Bioluminescence and Environmental Light Drive Visual Evolution in the Deep Sea

Danielle M. DeLeo, Heather D. Bracken-Grissom
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Light functions as the universal language in the deep sea (> 200 m), either dimly illuminating the water-column or emitted as bioluminescent bursts. Light is known to drive sensory system evolution due to the fundamental role it plays in the behavioral responses, fitness, and life history of many organisms. In pelagic environments, vertically migrating animals can experience drastic changes to their lighting environment across depth, subjecting them to unique selective pressures, possibly to distinguish between changes in ambient light and bioluminescent sources. In this study, we used a phylotranscriptomic approach to characterize the visual proteins (opsins) found across a group of variable vertical migrators- bioluminescent deep-sea shrimp (n=11) belonging to the Superfamily Oplophoroidea. We found that opsin diversity is higher among species who migrate to shallower waters and are exposed to more dynamic light conditions. Further, we provide evidence for adaptive evolution in the visual system of photophore-bearing species who have evolved a secondary mode of bioluminescence, including positive selection for a putative mid-wavelength sensitive opsin (MWS2) that may facilitate light source discrimination. Diversification of MWS2 appears to play an important role in the visual ecologies of photophore-bearing shrimp with its diversification in Oplophoroidea likely playing a critical role in the fitness and evolutionary success of this group.

O5-4: Ontogenetic Variation in Sensory Detection in Hydrothermal Shrimp Alvinocarididae

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Several species of shrimp in the Alvinocarididae family are known to occur in hydrothermal environments along the Mid-Atlantic Ridge (e.g. *Alvinocaris markensis, Rimicaris exoculata, Rimicaris chacei and Mirocaris fortunata*). In these species, the mechanisms involved in perceiving the environment in aphotic habitats are not completely understood. Recent studies have demonstrated a role for temperature in the localization of hydrothermal sites in adult individuals, whereas olfaction probably does not play an important a role as previously suggested (Ravaux et al. 2020). However, these two sensory modalities have never been studied at other life stages in our model species, notably in larvae. Being the dispersive phase, and traveling in the water column far from the hydrothermal emissions, their sensory modalities probably differ from those of adults. A study of the morphology of the sensory organs and receptors involved between life stages would provide a better understanding of how these species perceive their environment. In order to describe the processes involved in sensory detection by these species, we are examining both their sensory system (i.e. morphology of sensory organs, identification of receptors involved) and their central nervous system (i.e. brain areas). This presentation will focus on : 1/ the diversity and localization of receptors/co-receptors involved in two sensory modalities (i.e. thermodetection and olfaction), by a transcriptomic analysis of our four adult model species; 2/ the morphology of antennal appendages and central nervous system, throughout the development of these species using scanning and transmission-electron microscopy, as well as the structure of the brain using X-ray tomography (i.e. μCT-scan).

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O5-5: Bioluminescence in Deep-Sea Dragonfishes: Photophore Morphology and Proposed Functionality

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Bioluminescence is a common feature in meso- and bathypelagic fishes and has been proposed to play roles in prey attraction, predator avoidance, communication, and/or camouflage. Photophores, the light organs, are morphologically diverse among taxa, producing bioluminescence either exogenously (by bacterial symbionts) or endogenously (via neural innervation of photocytes contained in photophores). The most diverse and speciose order of deep-sea fishes, the Stomiiformes (>400 species, found worldwide), have a stunning diversity of photophores - including often complex hyoid barbels, sometimes sexually-dimorphic orbital photophores, large serial photophores organized in longitudinal lines, smaller photophores found in lines or scattered over the head and body, and unorganized, simple luminescent tissues. While some of these have been well-described (e.g serial photophores and photophores in hyoid barbels), other light organs in these fishes have been poorly recognized and rarely discussed in literature. We present a morphological review of the major photophore types found in stomiiform fishes and propose a unified nomenclature for them (complex serial, complex minute, simple pigmented, and simple unpigmented photophores) based on an examination of 35 species in 25 stomiiform genera. We present the first in-depth description of complex minute photophores, the numerically dominant photophore type found in stomiid fishes. Analysis of 14 stomiid species reveals the variability of size, density, and distribution of complex minute photophores. These data, in combination with an analysis of the predicted orientation of light emitted from the minute photophores, suggest that they may have multiple functions including camouflage and/or communication.

O5-6: Evolutionary Drivers of Eye Complexity and Transparency in Hyperiid Amphipods

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Although water depth, and more specifically the ambient light field, is an important evolutionary driver of vision in midwater animals, it generally fails to explain the diversity of eye designs in species with similar depth distributions. Our understanding of how ecological differences drive adaptations remains limited for all but a few species, yet is crucial for predicting how populations will adapt to environmental change. Here, we investigate the effect of swimming ability on visual adaptations and transparency in hyperiid amphipods, an abundant and diverse group of midwater crustaceans. By combining observations from nearly 30 years of remotely operated vehicle dives and a detailed functional analysis of visual abilities in the family Oxycephalidae, we show that swimming behavior (primarily free-swimming vs. in association with gelatinous animals) has a significant effect on eye complexity and transparency. Free-swimming hyperiids are generally transparent with complex eyes at shallow depths (<600 m), but are opaque with reduced eyes at deep depths (>600 m). In contrast, more sedentary species that associate with gelatinous animals have a reduced need for transparency or complex, energetically expensive, eyes. Functional analysis of oxycephalid eyes confirm these observations, with free-swimmers having more complex eyes due to a greater number of regional specializations for acuity and sensitivity. In contrast, visual fields in sedentary oxycephalids were relatively uniform and reminiscent of the simple, juvenile oxycephalid eyes. Our results highlight the importance of in situ observations in combination with detailed functional analyses to illuminate evolutionary mechanisms in the deep ocean.

O6A-1: Patterns of Genetic Diversity in Hydrothermal Vent Populations after the Hunga Tonga–Hunga Ha'apai Eruption

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Genetic bottlenecks are common evolutionary events that lead to a strong reduction in the effective size and diversity of natural populations. While genetic bottlenecks have been well described in a variety of biological systems, especially in the terrestrial realm, empirical data for deep-sea animal and microbial species remain scarce. The recent eruption of the Hunga Tonga–Hunga Ha'apai submarine volcano in the Southwest Pacific led to a drastic decline of animal symbioses associated with hydrothermal vents in this region, offering a unique opportunity to study bottleneck effects in the deep sea. In this study we applied metagenomic sequencing to pre- and post-eruption samples of mollusk-microbial symbioses from the Lau Basin to investigate patterns of genetic diversity and effective population size. Our data indicate that extant animal host populations show no observable changes in genome-wide variation but in most cases experienced an ongoing, long-term decline in effective size that was likely intensified by the volcanic impact. By contrast, symbiont populations exhibited a sharp decrease in genomic diversity, including potential loss of certain site-specific strains. These differences are likely related to the contrasting genetic structures of host and symbiont populations: host populations are overall poorly differentiated and genetically well connected, whereas symbiont populations are strongly partitioned between vent fields due to local adaptation. These results add to our understanding of the evolutionary dynamics of animal-microbe populations following a natural disturbance and help assess their resilience to potential future anthropogenic impact.

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O6A-2: Sequencing Ultraconserved Elements (Uces) in Conservation: A Case Study of Deep-Sea Mussel Population Genomics

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Ultraconserved elements (UCEs) have emerged as a powerful tool in deep-level evolutionary studies due to the low requirement for DNA quality, high sequencing depth, and resource-saving in expenses and computation. But there have been only a few tests of whether this technique can be successfully applied to answer shallow-level evolutionary questions. Here, we used for the first time the UCEs approach in the context of deep-sea conservation. The Western Pacific hosts active hydrothermal vents and methane seeps with close biogeographic ties, demonstrated by the similarity between faunas and the population genetic connectivity of several macrobenthic species, including the deep-sea mussel *Gigantidas platifrons*. Herein, we performed UCEs target capture sequencing for 123 *G. platifrons* individuals from six localities in the West Pacific using the Bivalve UCE 2k v.1 probes. To conduct variant calling and population genetic analyses, we used the available genome resource of *G. platifrons* and a pseudoreference of 1960 representative UCEs obtained from all individuals. We obtained 11870 SNPs by mapping to the genome reference and 8936 SNPs by mapping to the pseudoreference, with over 80% of SNPs found to distribute in intron and intergenic regions. Genetic structure and migration analyses revealed the existence of two genetic lineages from both SNP datasets—the South China Sea (SCS) and Okinawa Trough-Sagami Bay (OT-SB). A main gene flow from OT to SB was detected. These results are consistent with the results obtained previously using 2b-RAD SNPs. Overall, this work demonstrated that UCE probes for bivalves are a powerful tool to investigate shallow-level (i.e. population) genetic divergence even in the absence of reference genomes. The results have implications for delimiting genetic groups and establishing a network of reserves for deep-sea chemosynthetic ecosystems.

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O6A-3: Genetic Divergence and Migration Dynamics of Co-Occurring Vent and Seep Macrofauna Highlight the Need for Deep-Sea Conservation

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Hydrothermal vents and hydrocarbon seeps are two types of extreme habitats with remarkable biodiversity in the deep ocean. With over ninety hydrothermal vents and seventy hydrocarbon seeps discovered, the Northwest Pacific has been recognized as an evolutionary hotspot for vent- and seep-endemic macrofauna; moreover, it has also become a prospective target for deep-sea resource explorations, such as mining of polymetallic sulfide from vent fields and extraction of gas hydrate from seep areas. These anthropogenic disturbances can greatly impact vent and seep ecosystems by decreasing biodiversity and altering ecological functions. However, limited information on the life-trait history, population connectivity, and resilience potential of representative deep-sea macrofauna makes it challenging to exploit deep-sea resources sustainably while conserving deep-sea biodiversity effectively. To fill these knowledge gaps, we conducted large-scale population connectivity studies of three iconic deep-sea macrofaunal species, including the bathymodioline mussels *Gigantidas platifrons*, the patellogastropod limpet *Bathyacmaea nipponica*, and the munidopsid squat lobster *Shinkaia crosnieri*, which co-occur in multiple vent fields and seep areas in the Northwest Pacific. Combining population genomic tools with hydrodynamic modeling approaches, we investigated their biogeographical subdivisions and source-sink dynamics, unveiling that the southern Okinawa Trough vents and the Jiaolong seep in the South China Sea warrant imperative conservation efforts to sustain deep-sea biodiversity in the Northwest Pacific. These scientific findings will contribute to future decision-making on the informed designation of deep-sea reserves and the data-driven establishment of marine management plans in the Anthropocene.

O6A-4: Reduced Genetic Diversity and Limited Connectivity for Fisheries Impacted Populations of the Precious Coral *Hemicorallium laauense*

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Deep-sea precious corals in the octocoral Family Coralliidae are among the dominant megafauna at depths of 300-600m on the seamounts of the Northwestern Hawaiian Ridge and lower Emperor Seamount Chain. These seamounts have experienced some of the heaviest fisheries impacts of any seamounts in the world for both finfish and precious corals. Coralliids still occur on the fished seamounts but at low abundances. Since trawling continues on high seas seamounts, it is imperative to understand the impacts to and connectivity of this species. A total of 481 individuals for the coral fishery-targeted species, *Hemicorallium laauense,* were collected from 25 populations divided into 3 fishing treatments: Still Trawled, Recovering, and Never Trawled. Nine highly variable microsatellite loci showed significant departure from Hardy-Weinberg equilibrium, with moderate F_{IS} values (0.11-0.27), suggesting self-recruitment is common. Allelic Richness, H_o and H_e, were lowest in the Still Trawled sites and highest in the Never Trawled. The Still Trawled and Recovering seamounts had higher F_{IS} values compared to unfished seamounts. G'_{ST} indicated moderate genetic structure among populations. Among the treatments, mean pairwise G'_{ST} values for Still Trawled sites to Never Trawled sites was 0.23, which was much higher than for Still Trawled to Recovering sites (0.12). Migrate indicated that each sampled location represents a population exchanging a relatively small numbers of migrants with other populations. These results collectively indicate a loss of genetic diversity at impacted sites and that the Still Trawled seamounts are more well connected to the Recovering than either is to the Never Trawled seamounts. Continued protection of Recovering sites from additional fishing pressure will be critical for recovery of actively trawled areas. Additionally, the F_{IS} values and the relatively small immigration rates for each population indicate local recruitment from remnant populations will need to be a critical conservation and management consideration.

O6A-5: Life on Fire: Multiple-Omics Analyses Reveal Thermal Adaptations of Hot-Vent Endemic Alvinellid Worms

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Understanding the limit of life, and how life thrives under extreme conditions, is an intriguing topic of study. Alvinellid worms endemic to deep-sea hydrothermal vents are among the most thermal-tolerant metazoans, inhabiting chimney surfaces often bathed in hot water with dramatic temporal fluctuations. Among alvinellids, some 'hot' species prefer habitats right next to focused venting, while other 'cold' species live on diffuse venting at lower temperatures. Here, we performed comparative genomic analyses across three alvinellid worm species – *Alvinella pompejana* ('hot'), *Paralvinella* aff. *hessleri* ('hot'), and *Paralvinella palmiformis* ('cold'), as well as a species from their non-vent sister genus *Amphisamytha*. High-quality annotations of their chromosomal-scale genomes reveal a more streamlined and compact genomic architecture compared to many other deep-sea annelid lineages. Our genomic analyses uncover a significant expansion of various transferase gene families in alvinellid worms, potentially attributable to horizontal gene transfer. These enzymes may play important roles in their thermal adaptation, though the precise mechanisms require further studies. Through an acute heat shock stress experiment of *P.* aff. *hessleri*, we find the expression of key transcription factors and genes involved in sphingolipid metabolism to be significantly upregulated with increased temperature, in tandem with the well-established upregulation of chaperone proteins. Our findings indicate that sphingolipids, as major components of the cell membrane, play a crucial role in regulating the cellular response to temperature stress. Our new insights into the thermal tolerance mechanisms of alvinellid worms could inform the development of innovative biomimetic technological applications.

O6A-6: Convergent Evolution of Distinctive Adaption to Extreme Environment in Deep-Sea Organisms

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Prior studies on specific adaptation to the hostile deep-sea conditions has predominantly centered on selected deep-sea species or mitochondrial genomes. However, there has yet to be a systematic investigation of distinctive adaptations across a wide range of deep-sea species based on available genomes. In this study, we utilized assembled genomes to elucidate the phylogeny and environmental adaptation in deep-sea organisms. Phylogenetic analysis for deep-sea and shallow-water species showed that these deep-sea species diverged more than 300 million years ago. Gene families mainly involved in detoxification, protein stability, apoptosis, transmembrane recognition and heavy metal-binding were highly expanded in deep-sea organisms, which suggested their adaptation to extreme environments. Furthermore, comparative analysis identified positive selection genes (PSGs) in deep-sea organisms, including heat shock proteins (HSPs), transporter protein (ABC transporter, amino acid transporter), transmembrane pattern-recognition receptor (PRR), which was beneficial for deep-sea organisms to obtain their symbionts from the environment. Overall, our study provided novel insights into further research on the distinctive adaptation of deep-sea organisms to extreme conditions.

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O6B-1: Transmission Mode and Stability of the Scaly-Foot Snail Holobiont

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The scaly-foot snail, *Chrysomallon squamiferum*, which can be found in deep-sea hydrothermal vents in the Indian Ocean, depends on its sulphur-oxidising gammaproteobacterial endosymbionts for nutrition and energy. In this study, we investigated the transmission mode, specificity, and stability of multiple scaly-foot snail populations living in five vent fields with distinctly different geological, physical, and chemical environmental conditions. Population genomics analyses revealed an incongruous phylogeny between the mitochondrial genomes of the scaly-foot snails and their endosymbionts in the five sampled vent fields, indicating that the hosts obtain endosymbionts through horizontal transmission each generation. However, the genetic uniformity of several symbiont populations indicates that vertical transmission cannot be disregarded. Fluorescence in situ hybridisation of ovarian tissue showed symbiont signals around the oocytes, suggesting that vertical transmission co-occurs with horizontal transmission. Environmental measurements and gene expression analyses from in situ fixed samples showed that the snail host stabilises the endosymbionts' intracellular micro-environment by buffering the differences in environmental conditions. This provides the symbionts with a stable environment where they perform essential metabolic functions and benefit from the host's protection. The scaly-foot snail holobionts' evolutionary, ecological, and physiological success in different vents with unique environmental parameters is supported by the mixed transmission mode, symbiont specificity at the species level, and stable intracellular environment provided by the host.

O6B-2: Genomics Illuminates the Adaptation to Deep-sea chemosymbiosis in a Scallop

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Scallops from the order Pectinida are distributed from shallow water to the deep sea, making them ideal models for investigating adaptations to extreme environmental conditions. *Catillopecten margaritatus* (Pectinida: Propeamussiidae) living at a methane seep is the first discovered scallop forming symbiosis with chemosynthetic sulfur-oxidizing bacteria. Genomic studies of these ectosymbiotic bacteria have shown a strong dependency on their host. However, the scallop's adaptations to the deep sea and its role in ecto-chemosymbiosis remain largely unexplored. Here, we sequenced the genome of *C. margaritatus* to shed light on its adaptation to the deep-sea chemosynthetic habitats and symbiotic lifestyle. Our assembly generated a 1,115.87 Mb high-quality genome with 19 chromosomes and 98.4% complete BUSCOs. The deep-sea scallop genome maintains remarkably high macrosynteny with shallow-water scallops suggesting a broader pattern of evolutionary conservation within the order Pectinida. Phylogenetic analysis and divergence time estimation suggest the common ancestor of Propeamussiidae and Pectinidae diverged in the Early Devonian and may have colonized the deep sea during rising sea levels before establishing extracellular symbiosis. Analyses of the genome highlight several genetic adaptations related to the deep-sea environment and chemosymbiosis. These include 1) the loss of photoreception ability, 2) the development of sensory and defensive mantle, 3) immune mechanisms for recognizing ectosymbiont and facilitating their colonization, 4) a sophisticated sulfide detoxification system, 5) reciprocal nutrient supports within the holobiont, and 6) a mixotrophic lifestyle. Our findings clarify the adaptive strategies of C. margaritatus in the deep sea and enhance our understanding of symbiotic relationships within bivalves.

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O6B-3: Genomic Insights into the Deep-Sea Adaptation and Rapid Colonization of *Lindaspio Polybranchiata* in a New Cold Seep

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The genus *Lindaspio* is an intriguing group of spionid polychaetes endemic to chemosynthetic ecosystems such as hydrothermal vents, methane seeps, and whale falls. *Lindaspio polybranchiata*, a new species discovered in the Lingshui cold seep, forms a dense population around the methane seepage with extremely high abundance. We sequenced and assembled the genome of *L. polybranchiata* and performed comparative genomic analyses to investigate the genetic basis of deep-sea adaptation. With a size of 1.67 Gb, the genome of *L. polybranchiata* represents the first reference genome for deep-sea spionids and is notably larger than that of the shallow-water *Streblospio benedicti* (701.4 Mb). The larger genome size of *L. polybranchiata* is characterized by a higher proportion of repetitive sequences and more non-coding regions. Over long-term adaptive evolution, the visual system of *L. polybranchiata* has completely degenerated, and core circadian rhythm genes, such as CLOCK and period, have been lost. Comparative genomic analyses have revealed expansions in gene families associated with polyunsaturated fatty acid biosynthesis and chromatin stabilization, suggesting adaptations to high hydrostatic pressure. Furthermore, *L. polybranchiata* exhibits a broad digestive scope, enabling it to exploit the limited food resources of the deep sea and sustain large populations. As a pioneer species, *L. polybranchiata* has an expanded repertoire of genes encoding potential chemoreceptor proteins, including ionotropic receptors and gustatory receptor-like proteins, which likely facilitate the detection of chemical cues in chemosynthetic environments, and allowing it to quickly settle in suitable habitats. Our findings shed light on the adaptations of *Lindaspio* to the darkness, high hydrostatic pressure, and food deprivation in the deep sea, and provide insights into the molecular basis for spionids emerging as pioneer species in cold seeps.

O6B-4: Draft Genome of Abyssal Sea Cucumbers from a Region Targeted for Seabed Mining

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Deep-sea exploration in the eastern Pacific Ocean has recently increased owing to the interest in seabed mining. The Clarion-Clipperton Zone (CCZ) is the main region of interest, an area of approximately 6 million sq km harbouring relatively high macrofaunal biodiversity. Knowledge of the larger megafauna in this region mainly relies on videos and images due to the difficulties associated with sample collections. A dominant group is the Holothuroidea (sea cucumbers). They are the most abundant and diverse invertebrate megafauna, with at least 106 holothurian morphotypes catalogued in image-based assessments across or near the CCZ. An interesting question is how the deep-sea habitat has driven adaptation and evolutionary novelty in this group, such as body-wall thickness, feeding structures and ability to deal with low food availability. Despite the rapid development of sequencing methods, limited studies have been implemented to understand the relationship between holothurian phylogenetic and genomic features. Based on collections from the NERC SMARTEX project in 2023 and 2024 we report the *de novo* genome of two deep-sea holothurians from the Elasipoda (Psychropotidae and Elpidiidae). The genomic features are discussed regarding adaptation to an extreme and low-nutrient environment, focusing on genes that might play an essential role in molecular function and biological process (i.e., immune system, cell regeneration), as well as a genome-wide phylogenetic analysis. These genome drafts provide novel insights into deep-sea biodiversity and thus are highly significant from a conservation perspective, contributing to making a well-informed societal decision on deep-sea mining.

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O6B-5: Prokaryote-Eukaryote Co-Occurrence Predictions Using Multiomics to Link Ecosystem Function and Diversity in Deep-Sea Mining Areas

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In recent years, it was predicted that deep-sea mining will profoundly disturb benthic ecosystems, including microbial functions and interactions with faunal communities. Meanwhile, multiomic methods have matured to yield detailed taxonomic and genomic information that from growing amounts of environmental DNA samples for the global deep-sea benthos can help understand compositional changes and the ecology of prokaryotic and eukaryotic communities. Meiofaunal animals and protists thriving in metal-rich, deep-sea sediment are particularly elusive, and whether their diversity is maintained by that, and specific functions of prokaryotic partners, is only documented for a few, emblematic host model species. Here, we use multiple omics for a global set of abyssal, deep-sea sediment samples that mainly covers the Eastern Clarion-Clipperton Zone (CCZ), to integrate metagenomes with both DNA and RNA-based collections of amplicons targeting microbes, Metazoa, and Foraminifera. We predict with what bacterial and archaeal functions these taxa co-occur in the CCZ. We identify the functions of reconstructed microbial genomes and measure their evolutionary significance in gene phylogenies, with a focus on metal-dependent metabolisms enriched in the CCZ. We test for these functions as determinants for the maintenance of high eukaryotic diversity and of the high activity levels of specific metazoan and protistan taxa. We propose that compelling, prokaryotic-eukaryotic co-occurrence predictions substantiated by multiomics with underlying eco-evolutionary mechanisms are considered to prioritize the probing for new ecological models, and saveguard yet undocumented, but potentially key interactions in deep-sea benthic ecosystems designated for mining.

O6B-6: Characterization of Nuclear and Mitochondrial Genomes of Polynoids (Annelida: Polychaeta) in Deep-Sea Chemosynthetic Ecosystem

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Polynoids exhibit a broad ecological distribution, from polar to tropical waters and from shallow to deep-sea environments. The subfamily Lepidonotopodinae comprises species that inhabit deep-sea chemosynthetic ecosystems. Despite 55 recorded species within this subfamily, how these polynoids migrate and adapt to such environment remain poorly understood. With improvements in sequencing technology and cost efficiency, genomic-scale analysis is increasingly being used to study diverse organisms due to its ability to elucidate the origin and evolution of species, as well as species adaptation to various environments. As a preliminary study, we characterized the nuclear and mitochondrial genomes of eight Lepidonotopodinae species and two outgroup species. The nuclear genome sizes of Lepidonotopodinae species were estimated to range from 0.94 Gb to 2.79 Gb, with repeat content varying from 23.5% to 58.8% and heterozygosity levels from 0.64% to 10.7%. The assembled mitochondrial genomes revealed three variant gene arrangements, with sizes ranging from 15,399 bp to 23,294 bp. Across all species, the mitochondrial genomes consistently exhibited a bias toward the nucleotides T and C, as inferred from negative AT and GC skews. These foundational genomic data provide a basis for comprehensive analyses in the future, offering insights into the adaptations of polynoids to deep-sea chemosynthetic environments.

O6C-1: eDNA Metabarcoding Upholds the Patch-Mosaic Model for Meiofaunal Biodiversity in Deep-Sea Sediments

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Meiofaunal taxa (species 38µm-1mm such as nematodes, tardigrades, foraminifera, etc.) in deep-sea soft-sediment habitats exhibit high biodiversity despite an obvious lack of biogeographic barriers on the seafloor. The patch-mosaic model has been put forward to describe this phenomenon (Grassle & Sanders 1973), suggesting that deep-sea sediments comprise a "patchwork quilt" of microhabitats that drive species assemblages across space and time. Over evolutionary timescales, small patch sizes and slower colonization and community assembly rates in the deep-sea have resulted in uniquely high biodiversity. However, most investigations of the patch-mosaic hypothesis were carried out before the modern era of molecular biology. In this study, we used environmental DNA (eDNA) metabarcoding of deep-sea sediments in the Gulf of Mexico (~2100m depth) to provide new insight on species co-occurrence and biodiversity patterns at microscale (<1m) and mesoscale (~500m) distances on the seafloor. Two replicate grids of sediment push cores were collected via ROV, and microeukaryote biodiversity was assessed using both eDNA metabarcoding of the 18S rRNA gene (V1/V2 region) and parallel morphological identifications of abundant nematode taxa. Our eDNA results support the high patchiness of deep-sea species assemblages within a very small area of seafloor, showing that "hotspots" of biodiversity can exist directly next to species-poor areas. Furthermore, adjacent sediment cores exhibited highly dissimilar microeukaryote communities, in contrast to distant cores which displayed convergent community assemblages. Phylogenetic analysis of nematode ASVs supported a high degree of cryptic speciation with many rare lineages, as well as a small subset of “cosmopolitan” ASVs which were highly abundant across most patches. These eDNA results lend support for classical models of deep-sea biodiversity, and open up new research avenues for investigating microeukaryote community assembly at microhabitat scales.

O6C-2: Molecular Assessment of Deep-Sea Bony Fishes: New Findings from the Western South Atlantic

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The deep sea hosts some of the most extreme environments for life, harboring approximately 25% of bony fish richness. However, the diversity of deep-sea fishes is still underestimated due the difficulty in obtaining samples, resulting in considerable geographical gaps. Despite worldwide investigation of deep-sea fishes through DNA barcoding, the western South Atlantic remains a mystery in terms of biodiversity. To address this gap, two oceanographic cruises were conducted onboard the R/V *Alpha Crucis,* fishing between 250 and 1,520 m deep, and focusing on the continental slope off Southern Brazil. During these expeditions, around 103 species of deep-sea bony fishes were collected, including 1,400 tissue samples for molecular analysis. The COI fragments were amplified and sequenced using universal primers. A phylogenetic tree of maximum likelihood was constructed using the RAxML software and the inter-and-intraspecific distances were calculated using the K2P model. A total of 148 sequences of 85 species belonging to 42 families and 18 orders were generated, including a species incertae sedis in Eupercaria. The most diverse orders are Stomiiformes, Gadiformes and Ophidiiformes. DNA barcoding provided a high genetic divergence between species with K2P values from 4.1% to 36.6%. We identified three new species, including *Polymixia carmenae* (Polymixiidae: Polymixiiformes), in addition to a new species of *Bassozetus* (Ophidiidae: Ophidiiformes) and *Photonectes* (Stomiidae: Stomiiformes) under description. Additionally, the new occurrences of *Coryphaenoides subserrulatus* in the Brazilian Exclusive Economic Zone and of *Coryphaenoides striaturus* (Macrouridae: Gadiformes) in the Atlantic were recorded. The results also contributed to the first available sequences of 12 species and provided the first sequences for the western South Atlantic of 27 species, for the South Atlantic of 16 species, and for the Atlantic of 12 species. These findings significantly enhance our understanding of deep-sea fish diversity in the western South Atlantic.

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O6C-3: Vertical Biodiversity Zonation Revealed by Environmental DNA in the Molloy Deep, the Deepest Point in the Arctic

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The deep sea was long considered to be scarcely populated, with a negative correlation between species richness and depth. However, recent evidence suggests that deep pelagic ecosystems may contribute significantly to global biodiversity. The lack of sampling hampers the testing of ecological hypotheses on how biodiversity correlates with depth. The under-sampling of bathy- and abyssopelagic ecosystems mostly results from technological and logistical challenges to study these extreme depths. The goal of our study was to examine vertical zonation in metazoan biodiversity along a depth profile. Using environmental DNA (eDNA) metabarcoding, we investigated the biodiversity of invertebrates, vertebrates, and phytoplankton in filtered seawater and sediment samples collected at and above the deepest point of the Arctic, the Molloy Deep (5,607 m). We collected 68 eDNA samples in 2019 and 2020 at epi-, meso-, bathy- and abyssopelagic depths between 50 m and the seafloor. The used markers and primer sets targeted different organism groups: 12S rRNA gene for vertebrates, 18S rRNA gene for eukaryotes and cytochrome oxidase I (COI) gene for invertebrates, were analyzed via Illumina MiSeq sequencing. The preliminary analysis of the 12S gene identified 28 fish taxa, including capelin (*Mallotus villosus*). We also detected one arctic bird species (*Uvia lomvia*) and three marine mammals including the beluga (*Delphinapterus leucas*). Highest taxa richness for vertebrates was detected close to the seafloor at 5,000 (n=7) and 5,423 (n=10) m depth. The analysis of 18S and COI is ongoing.

Further analyses focus on comparing diversity across depths and organism groups and assessing potential vertical patterns within the Arctic deep sea. Our work will provide a first eDNA diversity study in the Molloy Deep, offering new insights into the ecology of remote marine environments with little knowledge on their biodiversity patterns.

O6C-4: Phylogenomics Shed New Light on the Placement of Siboglinidae

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Siboglinids are amongst the best-studied deep-sea worms but our knowledge of their evolutionary history is nevertheless limited. Indeed, although they are now widely known as annelids (and not another phylum as previously thought), their position within the annelid Tree of Life remains ambiguous and the relationships among the four major lineages of Siboglinidae (i.e. Vestimentifera, *Sclerolinum*, Frenulata, and *Osedax*) are unclear. Furthermore, little is known about the environmental changes that have driven their evolution and the specific adaptations they have acquired to successfully colonise and flourish in a wide diversity of deep-sea ecosystems. In this study, we resolved the phylogenetic position and the major internal relationships of Siboglinidae using all available genomic and transcriptomic data for the phylum Annelida. Using a genome-wide approach, we were able and explain previously observed phylogenetic incongruences and to identify groups of genes with unique evolutionary histories.

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O6C-5: Characterizing the Biodiversity and Bathymetric Distributions of Caribbean Deep-Sea Corals through eDNA

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Anthropogenic activities threaten the future of deep-sea animals; however, in many ocean regions, data regarding the diversity and distribution of deep-sea life remain scarce. Environmental DNA (eDNA) sequencing can accelerate the pace of biodiversity characterization, but effective eDNA sequencing relies on having a comprehensive reference database of DNA barcodes from voucher specimens. We conducted two research expeditions in 2022 and 2023, onboard NOAAs *Nancy Foster* and R/V *Falkor (too)*, and performed remotely operated vehicle (ROV) dives at coral and sponge communities using *SuBastian* and *Global Explorer* in Puerto Rico. During these ROV dives, we collected animal specimens and filtered water samples for eDNA at sites from 17 to 1,984 meters depth. DNA was extracted from corals and sequenced with whole genome skimming to build a comprehensive, vouchered DNA barcode database. Reference barcodes were assembled for 227 octocoral, 60 black coral, and 24 stony coral specimens. Leveraging this database, we conducted eDNA sequencing using primers that amplify the coral *28S rRNA* gene. From the sequenced eDNA, we detected 7 of 8 recognized black coral families, 19 octocoral families, and 7 stony coral families. 34 different eDNA sequences matched reference sequences generated from collected specimens exactly, representing species detections with high confidence. The diversity of coral genera and sequence variants detected in eDNA samples decreased with depth. Further, the taxonomic composition of the eDNA reflected the predicted bathymetric distributions of corals. eDNA sequence abundances from 11 coral families changed significantly with depth. The abundance of eDNA from mesophotic octocorals, like *Swiftia exserta* and *Muricea pendula*, decreased with depth. In contrast, the abundances of sequences from deep-sea corals, including golden corals (Family: Chrysogorgiidae) and bamboo corals (Family: Keratoisididae), increased with depth. Our results demonstrate the power of eDNA sequencing with comprehensive reference databases to characterize the biodiversity and distributions of deep-sea assemblages.

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O6-6: Advancing Deep-Sea Mollusk Shell Genomics: Insights from the Clam *Archivesica marissinica*

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Mollusc shells contain DNA that can be used to reconstruct the responses of molluscs to past climate changes and human exploitation. However, shell DNA recovery depends on their microstructure and preservation state. Here, we explore the use of the deep-sea clam *Archivesica marissinica* as a model to study ancient DNA due to it's the common occurrence of in a cold seep close to Hainan and its large shells. We aim to optimize the pre-PCR shell DNA extraction method by determining the influence of in-shell structure (fluorescent DNA stains in boundary, hint, and adductor muscle scar), pretreatment method (e.g. PBS and bleach washing), subsampling strategies (e.g. shell powder size), and DNA isolation conditions (e.g. silica column vs. phenol/chloroform extraction). Applying whole genome sequencing (WGS) and target capture sequencing (TCS), our preliminary results showed that samples with shell sizes smaller than 60 µm resulted in poor DNA recovery. In contrast, shell fragments of ~300 µm resulted in successful recovery of 164,978,600–204,364,280 and 32,002,158–98,788,696 clean reads from WGS and TCS. The endogenous nuclear reads varied between sequencing methods, resulting in 1,535,256–11,569,842 and 12,703,170–43,630,570 reads from WGS and TCS, respectively. Our ongoing experiments will provide a workflow to extract shell DNA from deep-sea clams to help elucidate the genetic history of deep-sea chemosynthetic ecosystems.

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O7A-1: Living on the Edge: The Mesopelagic Boundary Community of Monterey Submarine Canyon

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Mesopelagic Boundary Communities are most famously discussed in the context of the Hawaiian Islands, but reports of pseudo-oceanic species and bathymetrically-associated pelagic species can be found scattered throughout the literature. Here we describe the mesopelagic boundary community of Monterey Submarine Canyon, leveraging the MBARI midwater timeseries for context and a combination of video and active acoustics data. We find evidence of diagonal vertical migration for both fishes and zooplankton within 3.9km of the canyon wall. We also report a high frequency of sunrise topographic blocking of vertical migrators on the canyon rim and upper slope (>80% of sunrises sampled), which manifest as high density aggregations near the seafloor around sunrise. We also find persistent daytime aggregations of pelagic animals along the canyon wall and compare the boundary community composition to the local mesopelagic community. Moreover, video from a benthic timelapse camera on the canyon edge not only confirms the continuous presence of mesopelagic animals over the seafloor at the canyon wall, but also documents bentho-pelagic prey interactions. Thus, we not only describe an MBC at Monterey Canyon, but also present evidence that this mesopelagic boundary community provides high densities of prey to important local predators from commercially exploited fishes to socially important marine mammal species. In addition, these dynamics make the canyon edge a site of enhanced bentho-pelagic coupling. MBCs may be more common than currently thought and may perhaps not only exist at island slopes and in canyons, but at steep slopes throughout the oceans.

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O7A-2: Abundance, Niche Diversity, and Differential Species Effects Impact Ecosystem Function on the Bottom of the Ocean

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Biodiversity-ecosystem function (BEF) research stems back decades and has seen a recent exponential growth of the field. Many questions remain about the importance of functional diversity (complementarity) versus redundancy, differential species effects, and the effects of abundance versus different diversity components. We examined the BEF relationship in deep-sea xylophagous bivalve communities using 63 experimental wood falls deployed ~2000m deep in the Gulf of Mexico. We quantified the relationships between spatial and trophic partitioning, species dominance, individual species effects, and community level properties on total wood consumption, our metric for ecosystem function. A total of 26,324 individuals from 12 xylophagous bivalve species were identified. Individual species inhabited complementary spatial and trophic niches, but species effects on total wood consumption greatly varied. The amount of wood consumed increased significantly with total abundance and species richness, although the richness effects reflected increases in abundance. Ecosystem function among wood fall appeared to be predominately a feature of highly abundant core species with greater functional capacity.

O7A-3: Faunal-Mediated Ecosystem Functioning in a Benthic Deep-Sea Canyon Community Recovering from a Severe Seabed Disturbance

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Kaikōura Submarine Canyon is a deep-sea benthic biology hotspot with globally high faunal abundances. The 2016 M_w7.8 Kaikōura Earthquake triggered a canyon flushing event that evacuated an estimated 850 metric megatonnes of material down canyon, removing both seafloor substrate and associated organisms. Canyon habitats are now recovering from this large disturbance.

Here we relate post-event benthic macrofauna abundance and biomass to sediment community oxygen consumption (SCOC) and associated benthic macronutrient biogeochemical fluxes at ten sites along a depth transect down the Conway Trough and the main canyon axis. Infaunal bioturbation activities at three co-located sites down the main canyon axis are also presented.

We find distinct differences down-canyon in sediment organic matter composition and inputs, macrofaunal community structure, SCOC, nutrient fluxes, and bioturbation behaviour.

The relationship between canyon depth and the measured ecosystem function processes is not linear. The measured variables fluctuate along the depth transect, however SCOC and nutrient fluxes of NO_x-N and DRP from the sediment show a trend of increasing with depth, while infaunal biomass is greater in a known mid-canyon depositional “hotspot” but decreases at sites greater than 1100 m in depth. We find SCOC is linked to bioturbation behaviour and sediment organic matter content, rather than faunal abundance or biomass. We speculate that this finding is likely a consequence of the canyon flushing-event and post-event recovery processes.

These observations provide a benchmark for future measurements of faunal mediated deep-sea canyon processes and the recovery trajectory of deep-sea benthic communities after large seafloor disturbances.

O7A-4: Revealing the Assembly Rules of Scavenging Fish Faunas in the Deep Western Pacific

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Scavenging fishes are a diverse trophic guild which support unique and important functional roles on the deep-sea floor. Despite their functional significance, the environmental conditions that potentially drive community structure and biodiversity patterns remain poorly understood. We assessed the functional and taxonomic diversity of scavenging fish communities using 97 baited camera deployments across five archipelagos (Hawai'i, Marshall Islands, Micronesia, Niue, Palau) in the western Pacific and across a depth gradient of 214-2370m. Community structure changed significantly with location, sites and depth; however, depth explained more variation than spatial differences. Both taxonomic richness and functional diversity declined strongly between 214-1000m and then plateaued between 1000m and 2370m. Functional specialization, a measure of extreme traits in a community, and the trait dissimilarity between species also decreased with depth, suggesting functional community homogenization in deeper habitats. Bayesian hierarchical and joint species distribution modeling provided further insight into species and trait-specific relationships and co-occurrence structures in conjunction with environmental parameters. Functional structuring of deep-sea scavengers is correlated with environmental conditions such as oxygen and substrate type and contextualized by depth zonation - favoring trait similarity at deeper depths. These findings are preliminary macroecological insights into scavenger community assembly and the possible roles played by scavenging fishes across a variety of deep benthic environments. Further analysis will incorporate a wider geographic scope to better assess how local community ecology scales to a regional context and how relationships with environmental gradients change spatially.

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O7A-5: The Distribution and Trophic Structure of Gelatinous Zooplankton Across the Deep Pelagic

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Gelatinous zooplankton have prominent roles in marine food webs, yet their biogeography and feeding ecology are poorly resolved, especially across the deep pelagic. We quantified gelatinous zooplankton abundance and biomass along a nearshore-offshore transect within the southern California Current. We used stable isotope analysis of carbon (bulk tissue) and nitrogen (bulk tissue and amino acid-specific) to describe the food resources and trophic structure of gelatinous taxa representing a range of depth habitats and feeding guilds (pelagic tunicates, molluscs, ctenophores, chaetognaths, and medusae). We used a 10-m^2 Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS) to sample micronekton and zooplankton communities from 0-3000 m on four annual cruises. Gelatinous zooplankton comprised over 55% of total animal abundance and 75% of total biomass. Gelatinous zooplankton typically declined in abundance and biomass with increasing depth and distance from shore, coinciding with declines in surface fluorescence. Pyrosomes and calycophorans often peaked in abundance and biomass offshore during the summer, and chaetognaths often peaked in abundance within the upper mesopelagic (200 – 600 m). Gelatinous zooplankton spanned 2.4 trophic positions and gelativores (e.g., *Aegina* spp.) had some of the highest trophic positions (~3.8). Within feeding guilds, bulk nitrogen isotope ratios ($\delta^{15}N$ values) increased with increasing depth, but trophic positions did not, signifying differences in food resources across the water column. Unlike shallower taxa, taxa from the lower mesopelagic (600 – 1000 m) had similar $\delta^{15}N$ values regardless of season, possibly suggesting greater reliance on ambient, microbially degraded particles. Bulk carbon isotope ratios ($\delta^{13}C$ values) of gelatinous zooplankton decreased with distance from shore, reflecting the relative contributions of nearshore versus offshore production. We demonstrate that gelatinous zooplankton comprise a large portion of the pelagic community and have diverse roles as predators and prey.

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O7A-6: Squatlantis: Setting Physiological Baselines in the Seamounts of the SEP, Using New Records of Squat Lobsters

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The Salas y Gómez and Nazca ridges (SyG&NR) cover ~3000 km in the southeast Pacific (SEP) and possibly have the highest rate of endemism of all the open seas. The more than 110 seamounts within these ridges are benthic biodiversity hotspots. A reason for this level of diversity and endemism is an environmental transition zone.

We collected 51 morphospecies of squat lobsters, all new records for the area, including likely new species for science, of which 14 morphospecies were only collected outside the MPA's.

Within the transition zone the environmental conditions range from oxygen-poor, nutrient-rich, and cooler continental waters in the east to oxygen-rich, nutrient-poor, and warmer subtropical waters in the west. The environmental conditions change with seasons, El Niño-Southern Oscillation, Pacific Decadal Oscillation, and climate change.

To better understand the long-term effect of natural oscillations and anthropogenic changes on benthic species distribution, we need to know their minimal oxygen consumption, which has been modelled to be a limiting factor for adaptation of the benthic communities to climate change in the SyG&NR seamounts.

To set the first physiological baselines in this area, we measured the Standard Metabolic Rate (SMR), i.e., the minimal oxygen consumption needed for self-maintenance in rest, of squat lobsters. Squat lobsters are an excellent model organismal group; they are abundant, widespread, benthic, and survive great depth differences, which allows on-board experimentation. Using an ROV, 218 individuals were collected from 20 unique seamounts. On board the RV Falkor(too), SMR of 106 individuals was measured.

We found a significant weakly positive interaction between SMR and temperature, and the deeper the animal is collected the SMR decreases slightly, we did not find a correlation between SMR and longitude or oxygen. With this information we hope to facilitate an improvement of future climate models for this area.

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O7B-1: Animal Life in the Shallow Subseafloor Crust at Deep-Sea Hydrothermal Vents

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Many deep-sea hydrothermal vent animals are known to disperse as larvae via oceanic-, ridge-controlled, or bottom-currents. However, the larvae of the giant tubeworm *Riftia pachyptila*, a dominant species along the East Pacific Rise (EPR), have never been observed in the water column. We thus hypothesized that these larvae travel through subseafloor vent fluids.
During our expedition with RV Falkor too to the 9°50'North EPR, we used the ROV SuBastian to drill into the lobate shelves at "Fava Flow Suburbs" in 2500 meters depth. Lifting the lava shelves provided us a view into the underworld of hydrothermal vents: adult tubeworms and various trophic-level animals, including mobile and semi-sessile vent endemic polychaetes and gastropods, can use the fluid filled subseafloor cavities as habitat. Our finding therefore extends the known habitat of vent animals beyond the visible seafloor. Whilst we observed that some mobile vent animals can crawl through the lava cracks into the cavities, sessile tubeworms cannot migrate. We thus propose a subseafloor connectivity model, where vent tubeworm larvae can enter through the recharge zone along with cold seawater into the permeable oceanic crust, and recruit in vent discharge zones either in crustal subseafloor cavities or at the seafloor.
The discovery of animal life beneath the surface of the Earth's crust raises questions on the extent of this vent habitat and the role of subseafloor connectivity to maintain biodiversity where the habitat is patchy and transient. Whilst the three-dimensional extent of cavities filled with low temperature fluids is not quantified, the geological phenomena of hollow lobate lava are common. Until the true extent and breadth of the vent subseafloor habitat is fully ascertained, a precautionary approach with the protection against potential future anthropogenic impact such as deep-sea mining should be applied.

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O7B-2: Beta-Diversity Along the Hydrothermal Vent Fields of the Mid-Atlantic Ridge

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Hydrothermal vents are deep-sea oases of high biological productivity featuring unique vent-endemic life. Frequency of venting along the slow-spreading Mid-Atlantic Ridge (MAR) is several orders of magnitude lower than on fast-spreading ridges. With a hydrothermal vent field every 100-350km on the MAR, large distances separate the known active venting areas. Moreover, there is a visual shift in dominance between mussel- and shrimp-based assemblages with depth and latitude, at a time even hinting at two different biogeographic provinces.

Here, we investigate the beta-diversity among the deep-sea hydrothermal vent fields from 45.5ºN to 12ºN, in order to elucidate us on species overlap, ecological connectivity and role of the individual vent fields in maintaining biodiversity along the northern MAR. Presence/absence data matrices are compiled and analysed for this purpose. Species distribution is assessed and (dis)similarity along the nMAR is investigated at various levels. Pairwise pattern comparisons, including species turnover, nestedness and replacement, are analysed along directional environmental gradients such as depth, spreading rate, setting and temperature of the venting fluids. Depending on the analyses 2 to 3 different sub-regions are highlighted alongside outlying vent fields. Driving forces for directional community change are evaluated, revealing the joint interplay of various factors and threshold values of environmental constraints. Bipartite networks with iterative grouping are used to identify connector hubs (sites) and assess the contribution of each node (species). Contributions of each site are discussed as well as the implications for maintaining connectivity. The role of the recently discovered vent fields and future scenarios will be discussed, as well as importance for conservation measures.

O7B-3: Environmental Drivers and Microbial Mediation of Heterogeneity and Resilience of Carbonate Macrofauna at Methane Seeps

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Much of the variability in methane seep macrofaunal communities has been attributed to seepage activity, however, more attention is needed to the influence of other environmental conditions and animal-microbe interactions. With the goal of understanding how depth, dissolved oxygen, and the microbial community affect macrofaunal diversity and trophic structure and their recovery and resilience, we conducted mensurative and manipulative experiments that exploit natural seepage and hydrographic gradients at three seeps on the Costa Rican Pacific margin: (1) Quepos Landslide, at 400 m, within the oxygen minimum zone (OMZ), (2) Mound 12, at 1,000 m, just below the OMZ, and (3) Jaco Scar, at 2,000 m, well below the OMZ. We observed that seepage activity is the main factor influencing macrofauna at the deepest seep, where chemosynthetic production is the main food source, and fauna at active sites show faster responses to colonization and transplant experiments. At intermediate depth, where the seep is under the influence of both photosynthetic and chemosynthetic production, transition site fauna seem to have higher recovery and resilience rates. In contrast, within the OMZ, low oxygen conditions override the effects of seepage activity, yielding low densities, low diversity, and low resilience. In addition, we found significant associations between macrofaunal species and specific microbial Operational Taxonomic Units (OTUs) that reflect relationships of these OTUs with environmental conditions. Macrofauna responses to changes in seepage activity mirror the responses of the microbial OTUs they depend on for food and habitat provision. Our study highlights the heterogeneity of macrofaunal communities created by environmental conditions, as well as the importance of animal-microbe associations to the structure and functioning of seeps. With the expansion of OMZs due to ocean deoxygenation and possible expansion of seepage due to ocean warming, it is important we understand what factors affect recovery and resilience of seep communities.

O7B-4: Foundational Bathymodioline Mussel Larvae Preferentially Settle on Established Biofilm Surfaces Near Hydrothermal Vents

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Hydrothermal vent ecosystems are productive oases in the dark and vast deep-sea. The ability of vent endemic invertebrate larvae to successfully locate and colonize these environments is critical for the persistence, resilience, and survival of populations in the face of disturbance. Although microbial biofilms have been shown to provide settlement cues to various invertebrate larvae in other marine environments, the importance of microbial biofilms as mediators of larval settlement is relatively unknown in the deep-sea. Here, we present work from *in-situ* colonization experiments conducted at the highly disturbed, fast-spreading East Pacific Rise (EPR) hydrothermal system. Multiple short-term experiments (~2 weeks) were conducted at several vent sites by deploying colonization surfaces ("sandwiches") either with an established biofilm (developed for >1 year) or a fresh biofilm (developed throughout experiment) across zones characterized by different faunal assemblages. Recently settled *Bathymodiolus thermophilus* mussels were significantly more abundant on established biofilm surfaces compared to fresh biofilm surfaces across multiple sites and biogenic zones suggesting that microbial biofilms cue settlement for these foundational mussel species. Differences in biofilm characteristics such as microbial community composition, chemical compounds produced by microbes, biofilm biomass and bacterial density, and physical structure likely indicate suitable settlement habitat for larvae. Further analysis will explore the abiotic conditions and biofilm characteristics that appear to be the most important indicators for larval settlement.

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O7B-5: Potential for Recovery of Deep-Sea Hydrothermal Vents Ecosystems After Burial by the Catastrophic Hunga Volcanic Eruption

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On January 15, 2022, the Hunga submarine volcano (Kingdom of Tonga) sent a record-breaking explosive plume of material as high as 58 km. Rapid deposition of tephra from the volcanic eruption caused mass mortality of the foundational chemosymbiotic species (all IUCN-designated endangered or vulnerable) found at deep-sea hydrothermal vents on the Eastern Lau Spreading Center (ELSC), just 80 km from the eruption site. Here, we report the first observations of the potential for recovery after this major disturbance. From March 23 to May 8, 2022, we visited seven hydrothermal vent sites along the ELSC and collected samples using ROV Jason and the SyPRID plankton sampler mounted to the AUV Sentry. While the populations were decimated at three vent sites, conditions of the remaining *Bathymodiolus septemdierum* mussels and *Ifremeria nautilei* snails we collected were not significantly worse at the most ash-impacted sites. More than 1300 larvae were collected, with a clear variation in larval composition at the most versus least ash-impacted sites. Vent larvae, including those of the foundational species, were identified within our collections. Larvae of all three previously dominant *Alviniconcha* snails and *Bathymodiolus* mussels were found across all seven sites, including those most impacted by the ash, suggesting a potential for recovery. While more than 40% of our dissected *Ifremeria nautilei* snails (n = 467) were brooding or showed evidence of recent brooding or developing brood pouches, no *Ifremeria* larvae or juveniles were recovered at any site. Post-settler mussels and juvenile *Alviniconcha* were collected at multiple sites and showed evidence of early acquisition of symbionts. This discovery provides the unprecedented opportunity to study community recovery and succession of deep-sea marine ecosystems following a catastrophic disturbance such as a volcanic eruption.

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O7B-6: 'Gas'tronomy at Methane Seeps: Isotopic Indicators of Eukaryotic Methane Use

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Chemosynthetic production at methane seeps fuels complex communities, but detailed understanding of methane fates and pathways of methane use remains limited. We examined the incorporation of methane-derived carbon by protozoa and animals on carbonates at bathyal southern California methane seeps using short-term shipboard $^{13}CH_4$ isotopic enrichment experiments. Samples were collected from 6 seep location (310-1020 m) by the submersible ALVIN during AT50-12 and incubated for 4-5 d with 13-C enriched methane and various nitrogen substrates. Taxon-specific comparison of $\delta^{13}C$ signatures in incubation experiments with control samples and natural abundance data from seeps revealed methane uptake by agglutinating foraminifera (Pelosina-like taxa, mud-walled astrorhizinids), folliculinids, sponges, hydroids, stony/cup coral, pycnogonids, provannid snails and polynoid polychaetes. Incorporation of ^{13}C-labeled methane by eukaryotes can occur through symbiosis with or consumption of methane-oxidizing symbionts. Investigations into specific pathways of methane use for each taxon are ongoing. Because some of the taxa taking up methane form distinct habitats or zones around southern California seeps, our findings suggest that methane emissions from the seabed may have a broader ecosystem-level sphere of influence than originally assumed. These novel insights about biotic influence on methane fates have both conservation and climate relevance.

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O7C-1: Evidence of Dark Oxygen Production at the Abyssal Seafloor

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We carried out a series of in-situ benthic incubations from dozens of unexplored polymetallic nodule habitats in the eastern equatorial Pacific Ocean using a bespoke benthic lander system and found more O_2 was being produced at the abyssal seafloor than was being consumed. In 54 incubations of the seafloor, we found O_2 levels increased by more than 3-times background levels (from 185 to >800 μmol L^{-1}) over 48 hours. Dark oxygen production (DOP) was detected at sites up to 4000 km apart and occurred exclusively in the presence of polymetallic nodules and was unresponsive to experimental abiological treatments. Ex-situ shipboard incubations carried out in the dark at in-situ temperature also consistently showed DOP including in the presence of polymetallic nodules only, and when cores were poisoned, which collectively point to a geological origin. Electrochemical measurements of the nodules revealed extremely high voltage potentials (1V) across their surfaces most likely from the high concentration of metals precipitated onto the nodules. Based on these findings, we hypothesize that metal-oxide deposits in the deep sea may act as "geo-batteries" and facilitate seawater hydrolysis wherever they deposit (e.g., as polymetallic nodule fields or as ferromanganese crusts on seamounts). In the present day, DOP may also help explain the high abundance and diversity of megafauna found living on the surface of polymetallic nodules in the central abyssal Pacific, inviting the urgent investigation of how removal of potential oxygenic substrates during deep-sea mining would affect polymetallic nodule ecosystems. Future study of metal oxide-promoted DOP might also shed light on broader relationships that are known to exist between metal-oxide deposition, biological evolution, and the oxygenation of the Earth, as well as the potential for this process to impact aquatic habitats and potential life on other moons and planets.

O7C-2: Vulnerability of Tropical Fish Communities across Depth in the Central Indian Ocean

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Coral reefs and their fish communities below SCUBA diving depth (>30m), in mesophotic coral ecosystems (MCEs; ~30-150m), rariphotic (150-300m), and upper bathyal waters (300m-500m) are often underexplored, including in the Indian Ocean. This paucity of data, especially on the biodiversity, ecology and vulnerability of these habitats and the communities they support, leads to their omission from most conservation and management decisions and practices. Here, we investigated for the first time the structure and diversity (taxonomic and functional) of reef fish communities from the central and southern atolls of Maldives spanning a wide bathymetric gradient (2-500 m) to determine the functional composition of these little-known ecosystems and evaluate if their vulnerability changes across depth. We report distinct fish communities with depth showcasing the unique biological nature of MCEs and deep-sea coral habitats in the Indian Ocean. Decreasing taxonomic and functional diversity with depth combined with little overlap between species roles, makes deeper habitats more vulnerable to their shallower counterparts given that there is little ecological insurance against disturbance that leads to biodiversity loss. Moreover, some of the most functionally unique species were marine predators (e.g., sharks and rays) under extinction threat. Since many of these species occur in MCE and deep-sea habitats, conservation actions that not only avoids their extinction but also leads to their population recovery would restore their unique and specialised functional roles in the ocean. Overall, our results provide novel information on the ecology and vulnerability of sub-shallow fish communities in Maldives that can directly inform existing marine spatial planning activities in the region.

O7C-3: Habitat Distribution Modelling for the Azooxanthellate Coral *Madracis interjecta* in the Mesophotic and Deep Red Sea

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Corals of the genus *Madracis* have a global distribution, thriving in a remarkable variety of habitats from the shallows to 1220 meters depth. In the Red Sea, the azooxanthellate species *M. interjecta* is found in depths from 120 to 350 meters. While this species is most often observed as associated fauna of mesophotic habitats, it has also been reported to form sediment binding bioherms locally, yet the conditions required for this formation are not understood. Here, we compile data from three Red Sea expeditions and use an image-based method to identify the occurrence of *M. interjecta* for the first time along the whole Saudi Arabian Red Sea coast. We then complement this with a habitat suitability model to identify the potential habitat in the northern Red Sea and Gulf of Aqaba. For this approach, we combine presence data with geomorphometric variables and environmental data, including temperature, salinity and oxygen concentration. We identified both depth and seafloor ruggedness as main drivers of species distribution. Through multivariate statistics, we explore the different ecological spaces in which individual *M. interjecta* colonies and bioherms are found, identifying bioherms in deeper and cooler waters. The northern Red Sea and Gulf of Aqaba are undergoing continuous coastal development, resulting in threats not only to shallow habitats, but also to mesophotic and deep areas, due to a narrow continental shelf and steep slopes. This work provides both a baseline survey, and predicted distributions of an important habitat forming scleractinian coral which can inform conservation planning in the region.

[This work was supported by KAUST and baseline research funding awarded to Francesca Benzoni (BAS/1/1090-01-01). This work is based on data from three expeditions onboard M/V OceanXplorer funded by NEOM, the National Centre for Wildlife (NCW) and OceanX.]

O7C-4: Skeletal Growth, Micro-Anatomy and Metabolism of Cold-Water Coral Holobiont of Three Main Reef-Building Species

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As their tropical analogues, cold-water colonial corals are engineer species that create complex habitats among the richest in deep-sea biodiversity (Rogers 1999). Although living in deeper waters than tropical corals (from 5 m to over 3,000 m depth), cold-water corals will soon face the cumulative threats of ocean warming and acidification (Foley *et al.* 2010). As their tropical counterparts, specific host-bacteria associations have been highlighted (Neulinger *et al.* 2008, Meistertzheim *et al.* 2016, Kellog *et al.* 2017). But due to the difficulty of deep-sea sampling, detailed knowledge of the ecology and physiology of cold-water corals is still lacking to forecast the response of the coral holobiont to climate change.

Thus, we conducted an in-depth description of the coral holobiont, including growth and anatomy of the host to the localization and function of the associated bacteria. The study focused on 3 cold-water coral species present in the Lampaul canyon, Bay of Biscay (North-East Atlantic): *Madrepora oculata*, *Desmophylum pertusum* and *Solenosmilia variabilis*. *In situ* experiments using calcein staining and epifluorescence microscopy revealed particularly low polyp growth rates of *M. oculata* and *D. pertusum* in this canyon (respectively 0.6±0.3 mm/year and 2.9±1.3 mm/year) compared to the literature. A morphological description of different coral host tissues and the localization of the bacterial microbiome within these tissues, was carried out for the three cold-water coral species targeted, using respectively histological stains and electron microscopy approaches. These approaches have enabled us to gain a better understanding of the tissues' deep structure and the occurrence of bacteria within them. The host/bacteria interactions were investigated using secondary ion mass spectrometry approaches in *D. pertusum* (incubated with inorganic ^{15}N and ^{13}C), which revealed the presence of ^{15}N-enriched hotspots among the coral tissues. The involvement of bacteria in the incorporation of inorganic nitrogen has yet to be confirmed through the tissues' morphological description.

[The present work was supported by a grant (Project-ANR-20-CE02-0006) from French National Research Agency.]

O7C-5: Cost-Effective Deep-Sea Biodiversity Assessments Can Inform Conservation and Sustainable Management of Deep-Sea Ecosystems

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The deep-sea is characterized by complex marine seafloors home to rich benthic habitats, where hydrothermal vents, coral gardens and sponge grounds are commonly observed. These benthic habitats are, however, exposed to anthropogenic pressures, which can put their long-term preservation at risk. Identifying areas of ecological relevance is of upmost importance to inform management measures that would ensure the protection of the natural heritage. Thanks to the cost-effective video platform Azor drift-cam and other ongoing collaborations, the scientific knowledge of the deep sea in the Azores had increased significantly. Over the past five years, more than 1000 dives have been conducted at several seamounts, ridges and island slopes, resulting in over 700 hours of new deep-sea imagery, totaling approximately 600 kilometers of explored seafloor. We found that the Azores is a hotspot of cold-water coral diversity in the Atlantic, with more than 180 species identified to date. We have discovered the largest assemblage of the very slowly growing black coral of the genus *Leiopathes* ever observed in the Atlantic, the densest octocoral garden of the bubble gum coral *Paragorgia johnsoni*, and large aggregations of the endemic hydrocoral *Errina dabney*, among others. Several of the areas explored meet the criteria to be considered VMEs due to the high structural complexity and functional importance of their benthic habitats, with high vulnerability to human activities and potentially slow recovery after disturbance. These improved assessments of the deep-sea biodiversity have enhanced our ability to develop systematic conservation planning approaches and inform informed the Regional Government of the Azores on the expansion of the existing network of Marine Protected Areas to achieve the 30% targets. We argue that cost-effective technologies along with well stablished frameworks can democratize deep-sea exploration, produce transparent, data-driven and science-based scenarios, and inform conservation and sustainable management of deep-sea ecosystems.

[This work was supported by the Azores Government through the Contract 18/DRPM/2022 "Characterization of deep-sea habitats, for its mapping up to the outer limit of the Azores sub-area of the Portuguese exclusive economic zone".]

O7C-6: Trait-Based Approaches to Inform Conservation in the Deep Sea

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The study of traits (i.e., biological and ecological characteristics of species) complements species diversity studies to preserve and manage marine ecosystems. By applying trait-based approaches we can improve our understanding of ecosystem resistance, resilience, and functioning in front of environmental change and anthropogenic threats. Although far from our sights, the deep sea is not alien to the direct impacts of climate change nor potential human extractive activities such as deep-sea mining. The Azores Marine Park (AMP) is one of the largest Marine Protected Area networks in Europe, filled with seamounts and deep-sea ecosystems. After a collaborative effort with 30 researchers with different expertise, we built a trait database of the species found within, the FUN Azores trait database. We then developed different trait-based approaches to better understand vulnerabilities of our species to a changing climate and simulated the impact of extractive activities such as potential deep-sea mining on species and functional diversity of our ecosystems. The trait composition of each species informs on several aspects of its vulnerability (i.e., sensitivity, exposure, and adaptive capacity) to a particular threat. Knowing the species distribution within the AMP, we identified locations with different levels of vulnerability to temperature changes depending on the species present and their trait composition. Our results suggest that the Azores deep-sea benthos is highly vulnerable to both warming and wide temperature variations, more so than the pelagic environment. By identifying vulnerable species to deep-sea mining, we can simulate the impacts of diversity loss and recovery on species and functional (i.e., trait composition) diversity. Habitat loss and habitat quality degradation (i.e., increased sediment resuspension) significantly reduce the functional diversity of ecosystems in the AMP being the first one more impactful. Trait-based approaches, therefore, open the opportunity for biogeographic vulnerability assessments and simulation of human extractive activities that provide valuable insight for preservation of our deep-sea ecosystems.

O7D-1: Deep-sea Coral Ecosystem Dynamics through Space and Time: Implications for Conservation

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Elucidating the relationship between habitat heterogeneity and biodiversity has been the focus of many ecological studies. While there is a consensus that increased habitat heterogeneity is often associated with higher biodiversity, the influence of habitat heterogeneity varies depending on the species and scales considered. The effect of scale is particularly essential but rarely considered, especially in remote environments such as the deep sea. Unlike initially thought, the deep sea can be highly heterogeneous, both spatially and temporally, with variable environmental conditions affecting the physiology, distribution and behavior of deep-sea organisms. Focusing on deep-sea coral communities in Monterey Bay National Marine Sanctuary and the northern Gulf of Mexico, this presentation evaluates the role of habitat heterogeneity in the deep sea over multiple temporal and spatial scales. Relying on image-based surveys and monitoring, combined with seabed mapping and in situ environmental measurements, we show that deep-sea coral ecosystems are highly dynamic. Although deep-sea coral growth and recovery from injuries occur over time scales of decades, seasonal and tidal cycles (scales of a few hours to a few months) also affect their biology. Spatially, the distribution of deep-sea coral communities varies with substratum type and terrain characteristics across scales of few centimeters to kilometers. Together, these studies suggest that management approaches focusing on maintaining habitat heterogeneity at biologically relevant scales, rather than a "one size fits all" approach, are needed to preserve biodiversity in the deep sea. Studies evaluating the relationship between habitat heterogeneity and biodiversity are essential to set a baseline for deep-sea ecosystems, which is urgently needed in the context of climate change and emerging anthropogenic threats such as deep-sea mining.

[This work was supported by the David and Lucile Packard foundation (MBARI projects 901007, 901904, and 901101) and by the Habitat Assessment and Evaluation (HAE) Project, one of four projects selected by the interagency Deepwater Horizon (DWH) Natural Resource Damage Assessment Open Ocean Trustee Implementation Group to restore Mesophotic and Deep Benthic Communities injured by the DWH oil spill.]

O7D-2: Time-series Analysis of Benthic Megafauna in the Arctic Ocean

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Benthic megafauna communities in the Arctic Ocean are important for the functioning of deep-sea ecosystems by influencing the local biogeochemistry and the global carbon cycle. Variations in community structure of benthic megafauna are predominantly driven by food availability. The quantity and quality of phytodetritus reaching the seafloor depends on various factors such as sea-ice coverage and chlorophyll concentrations at the surface. With changing conditions at the surface ocean, impacts on the benthic megafauna are therefore inevitable.

In order to understand the dynamics in benthic megafauna communities in the Arctic Ocean, data from three stations in the HAUSGARTEN observatory (N3, HG-IV and S3) from a time span of six years (2016 - 2021) were analysed, as a continuation of the time series started in 2004. Benthic megafauna taxa were annotated on the image data and grouped into different functional traits. Data on sea-ice coverage and phytodetritus concentrations at the seafloor were included as environmental parameters.

The community structure of the benthic megafauna was highly dynamic within the six-year period. Compared to data sets from before 2016, similar dynamics were observed. However, these results indicate lower overall megafauna densities for the entire period. The year with the highest density, 2019, coincided with the highest phytodetrital matter at the seafloor for two stations (N3 and HG-IV). Simultaneously, a shift in dominant feeding type was observed from suspension feeders towards deposit feeders. This was the result of an increase in density of the opportunistic sea cucumber *Elpidia heckeri*, likely due to the increased phytodetrital matter.

These results indicate that the benthic megafauna community will likely exhibit strong variations in density and diversity in the future depending on the prevailing surface ocean conditions. The strong decrease in megafauna density highlights the need for further monitoring and reporting of changes observed in benthic communities in the Arctic Ocean.

O7D-3: Development of a Biologically-Validated, Global-Scale, Benthic Habitat Map for Use in Basin-Scale Marine Spatial Planning and Area Based Management

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The global ocean is critical to life on our planet and is increasingly the subject of human use. Society depends on services provided by ocean ecosystems in which ocean life plays an intrinsic part. Predicting how ocean life will respond to pressures, because of both increasing human use and impacts of climate change, is the central basis for science informed decision-making and sustainable use. At its heart this requires a comprehensive spatial understanding of the distribution of species and habitats, i.e. maps. While there have been notable efforts to develop habitat maps for the world ocean, few have been developed specifically to represent variation in biological diversity. The aim of this study is to develop and validate a global benthic biological habitat map for use in spatial management of the ocean. Environmental data layers (or proxies thereof) for the five most well reported drivers of marine species distributions (biogeography, water mass structure, substrate, primary production), are used in a multi-step classification process to develop two new global scale seafloor biological habitat maps. These new maps, together with existing published global and Atlantic scale habitat classifications are validated using a benthic 'clean' version of the OBIS database in a replicated permanova analysis at the genus level. Results suggest both new models explain almost 50% of the variance in benthic biological community composition at a global scale at genus level and are statistically significantly better (explain more variance) than previously published models. We suggest these maps may provide a useful decision-support tool for area-based management of the global ocean and particularly areas beyond national jurisdiction within the context of the new The High Seas Treaty.

O7D-4: What Is a Biotope? Thoughts From a Classification Methods Comparison

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A biotope is a set of environmental conditions that supports its own distinctive community. While the concept is theoretically easy to define, the practical description of a biotope is much harder to achieve. Anyone trying to classify deep sea benthic biotopes will likely be asking themselves: Which taxa should be included in a classification (all fauna, just benthic fauna, just sessile benthic fauna)? How much variation in species composition and environment should be allowed within a single biotope? How stable are biotope classifications across methods and assumptions? MAREANO, Norway's national seabed mapping programme, has been making biotope maps of deep-sea benthos for two decades. As our dataset has grown over time, our classification methods have had to adapt, providing us with an opportunity to test out and compare different classification methods with contrasting requirements and assumptions. Here we present a comparison of the results from these classification methods (e.g. TWINSPAN, hierarchical clustering, k-means, network analysis), highlighting the biotopes and characteristics that we found to be most consistent between methods and assumptions, the results that were most sensitive to the choices listed above, and the rules of thumb that we recommend when classifying biotopes (e.g. that mobile fauna and sessile fauna should not be treated equally). We also offer advice on the pros and cons of the different methods and thoughts on more established national and international classification systems (e.g. EUNIS) all framed in the context of usefulness to marine management.

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O7D-5: Fading to Black: The Ambiguous Journey of Deep-Sea Shark Fisheries in the Philippines

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Despite covering 87.2% of its territorial waters, the deep-sea ecosystems of the Philippines remain poorly understood. Deep-sea shark fisheries in the Philippines, primarily targeting squalene oil, have been sparsely documented. This study investigates recent and ongoing deepwater shark fisheries in Limasawa, Southern Leyte, and Cagayancillo, Palawan, focusing on vessel type, trip duration, target species, and trade routes. Operating at depths of 500-1,400 meters, these fisheries catch sharks from families Centrophoridae, Squalidae, and Etmopteridae, known for their squalene-rich livers. Recent declines in trade are attributed to a combination of catch decline, buyer shortages, the COVID-19 pandemic, and local regulations. Pre-pandemic, Limasawa supported two active boats conducting overnight trips, now reduced to opportunistic fishing. Cagayancillo's fishery, previously involving up to 30 boats with trips up to four weeks, is currently inactive. Based on interviews, these fisheries capture up to 20 sharks per night over an average of 20 fishing days per month. During landing site visits in 2017, 82 specimens were recorded in Cagayancillo in June-July 2017 and 74 in Limasawa in May-June 2017. Based on landing data, female *Deania profundorum* species were observed to reach sexual maturity at 62.18 cm ± 0.93 and became pregnant at 64.30 cm ± 1.59. In Cagayancillo, all male Centrophorus species were mature at 84.13 cm ± 6.55. Sex distribution showed *D. profundorum* catches predominantly female in both sites. Trade routes connect local fishers with intermediary local buyers, aggregators, and middlemen in the main cities of Cebu and Manila before the international trade of the purified squalene product, primarily to Japan. Given the small-scale fisheries' dependence on international trade, the current total shark trade ban in Cebu, and potential upcoming regulatory changes, understanding the economic and ecological impact of the fishery and its sustainability as well as exploring alternative livelihoods is essential.

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O7E-1: Seamounts and Pinnacles of the Global Ocean

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Seamounts are ubiquitous topographic features across the world's ocean. They rise steeply from abyssal depths, sometimes reaching the upper mixed layer of the water column. Depending on their size, shape and summit depths, seamounts may influence the physical flow regimes, affecting tidal currents, forming enclosed circulation cells, Taylor columns or cones, and enhancing vertical mixing Research has suggested that seamounts may promote the aggregation of zooplankton, micronekton, and top predators above or near their summits. However, the patterns of biological aggregations at seamounts vary globally. While some studies have identified seamounts as biodiversity hotspots, others have produced conflicting results.

The last decade has seen an increase in seamount literature, likely due to the ecological and fisheries significance of these features. The number of predicted seamount location has also increased in the last decade with improved datasets and observational methods. Despite the growing number of studies and research cruises conducted at seamounts, many knowledge and geographical gaps persist. Some seamounts are under enhanced fishing pressure, and there is an urgent need to study these ecosystems and to assess their vulnerability to anthropogenic activities. With the great technological development being made in our decade such as multi-sensored autonomous platforms, we anticipate new shifts in seamount research and knowledge globally.

O7E-2: Comparing Megabenthic Communities of Cobalt-Rich Manganese Seamounts of the Mid-Pacific Mountains, Necker Ridge, and Hawaiian Ridge

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Deep-sea mining on Pacific seamounts is an imminent threat to benthic megafaunal communities. Seamounts of the central and western Pacific (CWP) are prospective targets for mining activities due to cobalt-rich manganese crusts. While largely unexplored and undercharacterized, these seamounts are considered essential habitats to a wide diversity of deep-sea benthic megafauna. The Mid-Pacific Mountains (MPM) is an area that is poorly sampled outside the U.S. EEZ but may be targeted because of cobalt-rich crusts. Between the MPM and the Northwestern Hawaiian Islands (NWHI) is Necker Ridge, a feature that has been hypothesized to be a key stepping-stone in faunal dispersal between the two regions. This project aims to test this hypothesis by comparing the species composition of CWP seamount fauna between the three regions at a consistent depth of 1,500m while also characterizing the benthic habitat and communities of potential targeted areas for deep-sea mining both inside and outside the US EEZ. The ROV *SuBastian* was used to collect three replicate 500m long video transects, taken at a depth of 1,500m at each of 7 sites. Video transects were converted to screen grabs collected every 10 seconds. Images were annotated for morphology and taxonomy of benthic megafauna using the BioImage Indexing Graphical Labeling and Exploration (BIIGLE) website. Organisms were labeled with the Standardised Marine Taxon Reference Image Database (SMarTaR-ID) morphology and taxonomy label trees. Species composition, abundance, and diversity of the benthic community were determined at each study site. Preliminary results indicate octocorals were the dominant taxa for a majority of MPM and NWHI sites. In contrast, sites within Necker Ridge had higher abundances of crinoids and tunicates. Results of this study are essential to the conservation and management of vital deep-sea habitats since a majority of sites in this project are potential targets for deep-sea mining activities.

O7E-3: Diverse Megabenthic Communities Revealed by Video Surveys Along Boyd Seamount (Arctic Mid-Ocean Ridge), Norwegian Mineral-Exploration Area

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Increasing interest in deep-sea mining and the recent opening to seabed mineral exploration by Norway raises an urgent need for baseline ecological data from exploration-targeted areas, such as seamounts along the Arctic Mid-Ocean Ridge. Currently, few biological investigations have been conducted on Arctic seamount habitats, providing an incomplete picture of seabed biology and environment and preventing understanding of potential mining impacts. In this study, the first biological video surveys and species sampling of the Boyd Seamount (72°41' N, 2°55' E) was conducted using the ROV Ægir6000 to investigate both megabenthic diversity and distribution patterns and characterize their relationship to environmental conditions. Surveys and sampling were performed in summer 2023 from the base to the summit on the southern (2592 – 625 m) and northern (1265 – 593 m) flanks of the seamount. A total of 112 taxa were observed with a total density range from 9 to 109 ind. m^{-2}. The phyla Porifera and Echinodermata contributed the most to taxonomic richness, while Porifera, Annelida, and Chordata were the most abundant. Distinct biotopes were revealed by imagery analysis, namely base, slope, and summit, with the difference mainly explained by depth gradient and substrate variability. Base communities were represented by stalked crinoid fields. Slope communities were characterized by abundant tunicates, tube worms, and anemones. Summit communities showed rich sponge grounds inhabited by abundant epibionts, soft corals, anemones, tunicates, ophiuroids, and bivalves. Our study expands the current knowledge of deep seamount ecology and can be used to develop management and conservation measures considering the emerging deep-sea mining industry on the Arctic Mid-Ocean Ridge.

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O7E-4: Vulnerable Marine Ecosystem Patch Distribution and Abundance Hotspots on Seamounts of the Hawaiian-Emperor Seamount Chain

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Vulnerable marine ecosystems (VMEs) in the deep Pacific are at risk from anthropogenic impacts at multiple scales, however the patch sizes and distributions of patches of these communities have yet to be assessed. While the spatial scale of bottom-contact fishing can be tracked using AIS, the spatial distribution patterns of VME indicator taxa are not well understood. To better understand the spatial distribution patterns of VMEs, an existing dataset from AUV Sentry across 7 seamounts in the North Pacific was reanalyzed. The surveys contained over 500,000 images between depths of 200 m-800 m which were annotated for the taxonomic groups of coral, sponge, crinoid, and brisingid. Densities were categorized as sparse, medium, or abundant for each taxon. Density Based Spatial Clustering of Applications with Noise and local Getis-Ord were used to find patches and hotspots of abundance for individual taxonomic groups and for all fauna together. Patch sizes of Coral, Crinoid, and All Faunal groups varied by seamount (Coral and Crinoids: $p<0.001$; All Fauna: $p<0.01$) and depth ($p<0.0001$ for all three) but no significant pattern was found for Brisingids or Sponges. The area of hotspots of Coral, All Fauna, and Sponges varied by Fishing History (Coral and All Fauna: $p<0.00001$; Sponge: $p<0.05$) and Coral and All Fauna varied by Feature (Coral and All Fauna: $p<0.00001$), but no significant pattern was observed for Brisingid or Crinoid hotspots. Patch sizes ranged from 5 m to 2000 m in length, and hotspot area ranged from 500 m^2 to over 71,000 m^2. Move-on rules for many RFMOs stipulate a 2 nautical mile move with evidence of VME disturbance, but this distance would still be well within the range of the average Sponge hotspot. This study highlights the importance of scale as well as the usefulness of spatial analyses for conservation and management.

O7E-5: Cold-Water Coral Distribution Across Oxygen Minimum Zones in the Galapagos Islands and Isla Del Coco, Eastern Tropical Pacific

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Ocean warming caused by climate change promote the expansion of areas of low oxygen concentration in the deep sea. This could threaten cold-water corals (CWC), important ecosystem engineers. The Eastern Tropical Pacific (ETP) has one of the world's most pronounced oxygen minimum zones (OMZ) as well as some of the most biodiverse marine protected areas, the Galapagos and Isla del Coco. The pristine deep sea surrounding these islands is home to diverse CWC. Given the expected expansion of the OMZ in these critical areas, it is essential to understand the current distribution pattern of CWC and its implications for the local biodiversity. This study aims to investigate whether CWC distribution biodiversity and abundance across OMZ differ within and between islands and identify the environmental factors that may support CWC resilience under low oxygen conditions. In September 2023, the R/V Falkor (too) collected video, coral samples and environmental data using the ROV SuBastian at several sites across the islands. Video transects and environmental data were analyzed. We found large differences in the OMZ extension between the Galapagos and Isla del Coco, 160 m and 400 m, respectively, with Isla del Coco showing areas with O_2 concentration close to 0 umol/kg. There are different patterns in coral distribution between islands related to oceanographic variables. Diversity was lower within the areas with the lowest oxygen concentration, and one species of octocoral was abundant and dominated areas where the oxygen concentration was close to zero in Isla del Coco. Our findings provide essential information to understand the CWC adaptation and vulnerability in the ETP, which is helpful for the adequate development of the regional marine conservation corridor currently under implementation by bordering nations.

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O7E-6: Investigating Environmental Controls on Cold-Water Coral Distributions Using a Combined 3D Photogrammetric and Benthic Monitoring Approach

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Scleractinian cold-water corals (CWCs) build complex frameworks that can form CWC mounds in the deep sea, which have been regarded as biodiversity hotspots. Despite extensive mapping of CWC habitats and predictive modelling of CWC distributions, there remain gaps in our knowledge regarding the environmental variables that drive the distributions of scleractinian CWCs and their associated species at various scales. Thus, it remains difficult to define the boundaries of CWC habitats, especially at finer scales. To overcome this challenge, this study used a multidisciplinary approach to map CWC habitats and to determine the environmental variables influencing their distributions. Five sites within the Moira Mounds region (Belgica Mound Province, NE Atlantic) were examined using long-term data from benthic landers and structure-from-motion photogrammetric methods. Within each site, landers were deployed for one year and collected particle flux data within sediment traps, as well as current speed, direction, and temperature data. Remotely Operated Vehicle (ROV) video-data were collected around each lander and 3,499 images were extracted and exported to Agisoft Metashape to create 3D models, orthomosaics, and digital elevation models (DEMs) at a very fine scale (< 1 cm) for each site. Individual sites ranged in size from 58 – 178 m^2. DEMs were analysed using ArcGIS Pro to quantify terrain variables such as slope, aspect, bathymetric position index, and rugosity. Within Agisoft, the orthomosaics were utilised to identify, quantify, and geotag all observable species to ecologically characterise each site. The terrain and environmental variability across sites were compared, and their impact on the ecological composition of each site was described. This study illustrates how non-invasive and emerging methodologies can be used to understand the environmental variables which influence the distributions of CWCs and their associated species at a fine scale. This is critical for a more comprehensive understanding and effective conservation of these habitats.

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O7F-1: Bioturbation is a Key Function for the Preservation of the Abyssal Nodule Field Habitat

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Polymetallic nodules form a keystone habitat in abyssal plain ecosystems. The habitat heterogeneity created by exposed nodules in some areas, such as the Pacific Clarion Clipperton Zone (CCZ), increases diversity within these otherwise sedimentary habitats. Nodules take millions of years to form at the surface (~0.1 cm per 10^6 years), despite this process should be eventually inhibited by the accumulation of sediment (~1 cm per 10^3 years) and sinking due to higher density than the seafloor sediment. Today, it is unclear how the nodules remain on the surface, and hence available for benthic biota. At NORI-D, we use a set of seabed timelapse photographs to explore the potential role of biota in the maintenance of polymetallic nodules. We observed several taxa directly removing sediment from the nodule surfaces, mainly holothurians and gastropods, and infauna bioturbation causing nodule uplifting. Based on standardized bioturbation metrics, we described the temporal domains of bioturbation activity. These results show that some benthic organisms have a direct and significant influence on the nodule habitat, acting as ecosystem engineers that will allow the preservation of the nodule habitat over the longer term. As hypothesized for more than 40 years, this study provides the first empirical evidence that the bioturbation driven by habitat engineers keeps nodules on the seabed, which is an overlooked essential (and measurable) function for the maintenance of the abyssal nodule-field community. These findings expand our understanding of the functioning of the nodule abyssal plains. It also illustrates that unknown key processes might be threatened by the potential impacts of seabed mining.

O7F-2: Marked Variability in Distance-Decay Patterns Suggests Contrasting Dispersal Ability in Abyssal Taxa

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Species spatial turnover induces a decrease in community similarity with geographic distance known as the distance-decay relationship. Distance-decay patterns can reflect environmental and biotic controls on species distributions, but remain poorly assessed in the deep ocean, where this knowledge is urgently lacking. Here, we analysed beta-diversity patterns across space, depth and biotic components of abyssal megafauna communities (animals > 10 mm), based on seabed imagery data (>36,000 specimens across 402 species) collected across the Clarion Clipperton Zone (NE Pacific), a seascape spanning over 4,000 km. We unveil consistently steeper species turnover rates in benthic communities below 4,400 m and variations among functional groups. Our results support Young's abyssal dispersal hypothesis; turnover was higher for sessile taxa growing only on scattered hard bottom patches than sediment-dwelling or swimming organisms, depicting a more restricted dispersal in polymetallic nodule-dependant fauna. Overall, our study suggest that carbonate saturation boundaries associated with depth are a very relevant factor driving community turnover via niche-sorting with respect to a threshold, whereas dispersal limitation seems to be a more relevant mechanism within the regions above and below that threshold. We provide some of the first empirical evidences of regionally shifting turnover rates and contrasting dispersal abilities across functional groups in wide abyssal seascapes, key to assess the resilience of deep ocean biodiversity and functions to rapidly growing human disturbances in one of Earth's last wildernesses.

O7F-3: Feeding Niche Varies with Organismal Body Size in Abyssal Deposit Feeders

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Abyssal plain ecosystems (4000-6000m water depth) rely directly on surface ocean productivity to sustain benthic communities. Phytodetritus settles on the seabed, acting as the primary food source. It is necessary to decipher how organisms use this source to fully understand their roles in ecosystem functioning and carbon storage. We used carbon and nitrogen stable isotope ratios to explore the relationships between feeding niche and body size of abyssal plain megafauna (456 specimens, across 18 species and 4 feeding guilds) from the Porcupine Abyssal Plain (north-east Atlantic). Initial results across all individuals showed that $\delta^{15}N$ was significantly correlated to wet weight, but $\delta^{13}C$ was not. Differences in $\delta^{15}N$ were observed between feeding guilds: in both surface and subsurface deposit feeders $\delta^{15}N$ and wet weight were correlated, but not in suspension feeders and scavengers. Significant differences in $\delta^{13}C$ were also observed between feeding guilds. The nitrogen results indicate that smaller deposit feeding organisms are consuming mostly fresh phytodetritus, while larger individuals consume more reworked sediment. This is likely due to physiological changes with growth, where larger organisms have a longer gut and thus the ability to extract sufficient nutrients from sediments where the smaller organisms may struggle. The carbon results indicate that each identified guild is exploiting a different food source, including the surface and subsurface deposit feeders. Together, these results highlight that the functional role of each organism differs depending on feeding guild and body size. Futher analyses will identify variations in isotopic values within and between species to determine if smaller individuals of a species have differing functional roles to their larger counterparts. This research emphasises the vulnerability of small organisms and surface deposit feeders to the reduced phytodetritus input which is anticipated as a result of climate change.

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O7F-4: Disparity of Dominant Species Across Three New Hydrothermal Vent Fields in the Mid-Atlantic Ridge

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Highly specialized animals densely colonize deep-sea hydrothermal vents, forming island-like communities that are supported by chemoautotrophic microorganisms. Over four decades of exploration have revealed differences in the dominant species inhabiting vents along the Mid-Atlantic Ridge (MAR). However, the underlying causes of these community differences remain poorly understood, a concerning issue given that mining exploration contracts targeting mineral deposits at vents have been issued on the MAR. Here, we report the discovery of three new hydrothermal vent fields on the MAR during the Schmidt Ocean Institute cruise FTK230303 within the Russian and French mining exploration areas. These vent fields, named Puy des Folles, EMARK, and Hydra, show communities with similar species compositions but strikingly different species dominance patterns, particularly in diffusive-flow habitats. At high-temperature, focused-fluid flow habitats, the chemosymbiotic shrimp *Rimicaris exoculata* dominates, forming dense swarms at all three vent fields. In contrast, lower-temperature, diffusive-flow habitats exhibit distinct dominance patterns: beds of the chemosymbiotic mussel *Bathymodiolus puteoserpentis* at Puy des Folles, carpets of the carnivorous anemone *Maractis rimicavora* at EMARK, and dense populations of the carnivorous/scavenger snail *Phymorhynchus* sp. at Hydra. These findings contribute to our understanding of the biological heterogeneity at MAR vents and underscore the challenges of designing representative networks of protected areas for active hydrothermal vent habitats.

O7F-5: Abyssal Megafauna Communities and the Potential Influence of *Sargassum* Sedimentation – A Qualitative and Quantitative Assessment

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It is assumed that the abyssal fauna is extremely food-limited and relies mainly on slowly sinking organic material from the euphotic zone. In recent years, however, several studies have revealed a surprising phenomenon in the North Atlantic - the rapid sedimentation and accumulation of the brown macroalga *Sargassum*. The regularity of these *Sargassum* deposits combined with the associated carbon input into the abyssal plains raises questions about the adaptability and ecological significance of these macroalgae in an area characterized by extreme food limitation. Despite their potential ecological importance, the number of studies that have investigated and compared megafauna communities in abyssal areas with and without frequent *Sargassum* falls has been small to date.

Here, we provide new data on the abyssal epi-megafauna inhabiting two abyssal plains in the Sargasso Sea, compared to stations in the Great Atlantic Sargassum belt with documented *Sargassum* falls. By utilizing both an ocean-floor observation system (OFOS) as well as an automated underwater vehicle (AUV), calibrated videos and images were taken and either manually (OFOS) processed or automatically processed by a model (AUV). Taxa were morphologically distinguished, their diversity and density estimated and related to the occurrence of *Sargassum* falls. Stations with and without *Sargassum* sedimentation hosted unique communities with several taxa significantly associated to *Sargassum* falls. Further, megafauna density and diversity were significantly greater at stations in the Great Atlantic Sargassum belt if compared to the Sargasso Sea. Overall, our findings imply a potential positive impact of *Sargassum* falls on abyssal megafauna communities.

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O7F-6: Exploring the Growth of Deep-Sea Bivalves in Areas of Potential Seafloor Mining: Methods in Sclerochronology

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The Clarion-Clipperton Zone (CCZ) is a region in the Pacific Ocean between 0°-20°N and 110°-160°W where seafloor polymetallic nodules occur in high abundance on the abyssal plains. These nodules are rich in manganese, nickel, copper, cobalt, and other valuable ores, and are being targeted by deep-sea mining for green technology. Polymetallic nodules in the CCZ are one of the few hard substrates in this region and they provide a diversity of habitats for fauna living on and within their crevices (and in the surrounding sediment). Of these, bivalve molluscs are abundant. Bivalves grow by accretion, where new material is added onto the shell's growth margin, creating consecutive growth lines. The study of shell growth—sclerochronology—has been largely confined to shallow water bivalve taxa which are relatively large and show growth on a variety of tidal, daily, monthly, seasonal, and yearly schedules. This research aims to extend the techniques of sclerochronology (e.g., cross-sectioning, staining) to the tiny and fragile bivalves of the deep CCZ (some of which have only been recently discovered or still remain undescribed) to address questions of age, growth rate, and longevity. To date, the most abundant mollusc found in the benthic CCZ is the bivalve *Nucula profundorum* (Smith, 1885), a small (<5mm, typically 1-2mm in length) protobranch that has received little academic attention since its discovery. Specimens of *N. profundorum* collected from the UK-1 claim region of the CCZ have been examined to better describe this species with respect to shell microstructure, ontogeny, and larval ecology (from juvenile shell morphology). With a clearer understanding of this species' shell development, growth patterns may be more clearly analysed. Results from studies such as these will be critical for the International Seabed Authority in order to establish fair environmental regulations for the deep-sea mining industry in the coming decades.

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O8A-1: Long-Term Impact and Biological Recovery in a Deep-Sea Mining Track after 44 Years

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Management of polymetallic nodule mining requires scientific evidence on the effects of activities on deep-sea ecosystems. A key part of this is describing the ability of seafloor ecosystems to recover from impacts, a process which is poorly understood but expected to take many decades. Some studies of abyssal disturbance over relatively long time periods have been carried out but they are evaluating impacts that were caused by dredges or ploughs and not deep-sea mining machines. In addition, limited data are available more than 26 years after disturbance. Here, we present newly collected data from the site of test mining done by the OMCO consortium with a prototype nodule collector in 1979. We show the long-term impacts on the physical environment and subsequent biological effects remaining after 44 years and compare these to control areas with no impact. We focus on areas directly disturbed by the collector tracks, adjacent areas impacted by near seabed sediment plumes and background conditions in the central Clarion Clipperton Zone. Our results will show whether mining impacts in the abyssal ocean are still visible over at least decadal timeframes, whether communities remain altered in directly disturbed areas and how areas experiencing impacts from sediment plumes differ. The outputs of this work are discussed in the context of potential measures for effective management including minimising the direct impacts of mining activities and setting aside an effective network of protected areas.

O8A-2: Long-Term Impacts of Deep-Sea Mining on Benthic Macrofaunal Communities

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Polymetallic nodule deposits in the Clarion-Clipperton Zone (CCZ), central abyssal Pacific, are a major target for potential seabed mining. The extent of environmental impacts of seabed mining on biological communities and the capacity for ecosystem recovery remain poorly understood, particularly over long-term temporal scales. Here we examine the long-term environmental impacts of a nodule mining collector test conducted in the eastern CCZ in 1979 (Ocean Minerals Company, OMCO) on specieslevel benthic macrofaunal abundance and diversity. The historic mining track, revisited in March 2023, and the area affected by an associated sediment plume are assessed, with both sessile nodule dwelling fauna and motile sediment dwelling fauna examined. Our results reveal the degree of impacts four decades since the mining test took place as well as insights into community-level succession and recolonisation patterns. Decisions by stakeholders regarding if and how mining occurs, in addition to implementing any management of potential industry, requires detailed knowledge of the long term effects on deep-sea ecosystems. This study provides a rare opportunity to understand the impacts of mining disturbance on these ecosystems on a decadal time frame.

O8A-3: Impacts of an Industrial Deep-Sea Mining Trial on Seafloor Biodiversity

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Deep-sea mining represents one of the largest potential industrial activities in the ocean. However, there have been no empirical studies of the impacts of commercial-scale mining on infaunal biodiversity at the seabed. The Clarion-Clipperton Zone (CCZ) is an area of commercial importance owing to the growing interest in mining high-grade polymetallic nodules at the seafloor for battery metals. In 2022, a mining test was carried out, removing over 3000 tonnes of nodules from the seafloor − the largest complete mining test ever undertaken in the CCZ by a large margin. Here we present the largest quantitative abyssal dataset on macrofaunal metazoan biodiversity collected anywhere globally to date, based on a 4-year program at the test site, sampling multiple control and impacted sites both pre- and post-impact. These include sites directly impacted by the mining machine, and sites potentially impacted by sediment plumes. Our results have profound implications for understanding the degree and spatial extent of nodule mining environmental impact. While further study will be required of recovery rates and long-term impact, our results provide the first data on the impacts of large scale deep-sea mining on seabed abundance and biodiversity.

O8A-4: The Environmental Impacts of Deep-Sea Mining

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Although deep-sea mineral deposits were first discovered over 150 years ago, the concept of deep-sea mining as a commercial business is fairly recent. Debate on the environmental advantages or disadvantages of deep-sea mining has grown dramatically; 25 nations have called for a unilateral 'moratorium' on deep-sea mining despite also being signatories to the United Nations Law of the Sea, which created a *de facto* moratorium in 1982. Deep-sea mining debate has moved from the academic and governmental sphere to the public - films, debates, petitions, celebrity endorsements in favor or against, alongside a multitude of journalistic reviews and NGO reports have firmly placed it as one of the most current of environmental causes. Most of these campaigns have been based on precautionary principles, owing to the general lack of data. However, the last decade has seen a dramatic increase in available baseline knowledge for some types of deep-sea mining, two large scale mining tests for polymetallic nodules and the first study of the long-term impacts of a mining test carried out in the 1970s. Here we review the environmental impacts of deep-sea mining for all resource types based on the latest empirical data. We rank the different types of impacts across resource types, providing we hope a useful way of focussing environmental science on key priorities to help guide all the stakeholders involved in the discussion.

O8A5: The Persistent Impact of Abyssal Seafloor Disturbance

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Anthropogenic impacts to ecosystems can interact to intensify or alter effects, so understanding these effects is important to environmental impact assessment and the management of industrial activities. Despite the need to characterise cumulative effects, they are not often observed over long periods; this is particularly true on abyssal plains, despite increased industrial interest in this environment. We present observations of the persistent impacts of seafloor disturbance caused by epibenthic sledge operations 30+ years after their deployment at the Porcupine Abyssal Plain Sustained Observatory, assessed primarily by seabed photography. The sledge tracks appeared to result in three interactive impacts: (i) redistribution of sediment and a presumed disturbance of biogeochemical conditions by the creation of furrows, (ii) accumulation of organic matter in the furrows, and (iii) directly observed accumulation of plastic debris, concentrated 1000 times relative to the surrounding abyssal plain. These latter two impacts are likely the result of the topographic low and adjacent associated sediment spoil berm of the furrow trapping material that was advecting across the seafloor. Increases in the abundances of some fauna were potentially related to this localised organic enrichment and the increase in hard substratum availability to an otherwise soft-sedimented habitat. These observations of persistent and interacting impacts at a multidecadal scale provide an important benchmark useful to the assessment and management of activities causing abyssal seafloor disturbance.

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O8A-6: Environmental Challenges of a Green Energy Transition in the Offshore Energy Sector: A Review to Guide Global Marine Planning in a Green Future

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The green-energy transition poses significant environmental challenges to the offshore energy sector in the decommissioning, repurposing and installation of marine artificial structures (MAS). As we progress towards net-zero, the potential solutions to realise sustainable, nature-positive industry use of the ocean need urgent analysis. Supplying energy demand, whilst keeping resources secure and affordable, reorienting towards renewables and prioritising global ocean health is a complex, multifaceted task that requires the commitment and collaboration of science and all offshore energy sectors. Sectors reviewed include offshore oil and gas, wind, cables and emerging renewable industries. Leaving MAS offshore as part of decommissioning to create artificial reefs (ARs) may enhance marine habitats and develop additional ecological resources. However, this approach should only be considered after a comprehensive case-by-case risk assessment including, reef efficacy, invasive species and pollution. Moreover, with high demands for and the associated impacts of sourcing certain materials, recycling MAS elements should not be dismissed. Spatial planning is a critical step in optimising ocean space, planning MPAs, generating connected ARs, assessing cumulative impacts and initiating interindustry collaboration. Finally, the installation of new MAS should learn from the past energy sector and increasingly focus on science and nature-inclusive-design, particularly 'design-for-decommissioning', which may generate valuable data sets and more persuasive AR cases respectively. However, forward thinking must be supported by science, whereby design is informed by current MAS ARs, comprehensively studied using long-term imagery, isotopic, organic indicator and molecular biology investigations. This requires regular collaboration between industry and science to build adaptable strategies that have the potential to achieve nature-positive outcomes. Our reliance on the marine environment for energy and connectivity is only growing. Planning for a future that includes science and focusses on nature could go some way in achieving biodiversity and climate targets as well as facilitate the sustainable use of our oceans.

O8B-1: Marine Litter in Brazilian Deep-Sea Fish Gastrointestinal Contents

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While the use of plastic has increased in the past century, it has become a major pollutant, now ubiquitous in the marine environment, including the deep sea. The presence of deep-sea litter along the Brazilian coast has been confirmed with a major presence of plastic items. Once in the ocean, these objects became subject to fragmentation, producing smaller particles (< 5mm) known as microplastic (MP). The microplastic can be mistaken with food and ingested by marine organisms. This work aims to investigate and evaluate the ingestion of MP by deep benthopelagic fishes collected on the Brazilian continental slope, from 200 to 1,500 meters deep. A total of 122 specimens from seven species were analyzed: *Allocyttus verrucosus*, *Argentina brasiliensis*, *Bembrops heterurus*, *Coelorinchus marinii*, *Monomitopus americanus*, *Polymixia carmenae*, *Xenolepidichthys dalgleishi*. Their gastrointestinal tracts were removed and digested in 1M NaOH at 40°C for 48h, the derived solution was filtered through a GF/F filter, and the product was sorted under a stereomicroscope for manual particle separation; and then, the polymers were identified using a Raman spectrometer. Twenty specimens from all species analyzed were contaminated with a total of 97 particles, 26.8% (n=31) of which were identified as either microplastic (12.1%; n=14) or blue dye (14.7%, n=17); 26.0% (n=30) as organic matter; and 47.2% (n=54) could not be identified. The MP particles were composed of polyaryletherketone, polystyrene, polyacrylamide, PET, thermoplastic, polymethylhydrosiloxane, silicone, or rubber. Previous studies reported the ingestion of microplastic in mesopelagic fishes from Northeastern Brazil. Therefore, our results warn that MP contamination is a widely spread problem in the deep-sea ichthyofauna, but the actual environmental impacts are still poorly understood, and may affect not only the individuals that ingested the MP but also the entire deep-sea community, since MP can be transferred along the food chain.

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O8B-2: Long-Term Ecotoxicological Effects of Sediment Plumes on Deep-Sea Invertebrates Following a Polymetallic Nodules Collection Trial

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Polymetallic nodules (PMNs) contain high levels of manganese, iron, nickel, copper, cobalt, and rare earth elements (REEs) and occur in the abyssal plains of the oceans. Due to the increased demand for critical minerals and REEs required for modern technology, PMNs have become a target for the mining industry. However, the environmental consequences of exploiting such resources on the structure and functioning of the unique deep-sea ecosystems are still unknown, and a careful risk assessment associated with deep-sea mining must be carried out. In addition to the local impact, PMNs collection generates sediment plumes characterized by a complex mix of elements that can spread across large areas with potential toxic effects on the pelagic and benthic fauna. Therefore, this study investigated the ecotoxicological effects of the sediment plumes generated during the Patania2 nodule collector system trial in the Clarion-Clipperton Zone (CCZ) in the Pacific Ocean. Eighteen months post-impact, benthic megafauna samples were collected from reference and impacted areas (4100-4500m depth) using the ROV Kiel 6000 during the SO295 cruise in 2022. Sponges and brittle stars samples stored at -80°C were analyzed for metal bioaccumulation, biomarker levels indicative of metal exposure (metallothioneins - MTs), oxidative stress (catalase - CAT, superoxide dismutase - SOD, glutathione-S-transferase - GST), and oxidative damage (lipid peroxidation – LPO). These results may provide valuable insights into the still unclear physiology of these animals and on their potential for recovery from impact. This information may also contribute to establish future regulatory thresholds for sustainable practices if deep-sea mining at the industrial level occurs.

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O8B-3: Ecotoxicological Effects in Hydrothermal Vent Shrimp and Polychaetes Exposed in Situ to Sulphide Particles

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Deep-sea mining (DSM) industries have been increasingly interested in the metal rich seafloor massive sulphides (SMS). However, the possibility of sulphide particles plumes being formed during the extraction of the SMS raises ecotoxicological concerns, given the proximity of the inactive SMS, likely the targets of exploitation, to active hydrothermal vents. The potential harmful effects of these plumes on the living fauna of the active sites are still unknown. The Sulphide PartIcle spreaDER (SPIDER) chamber is a new device developed for semi-contained *in situ* exposures. It was first tested during the MOMARSAT 2023, Ifremer cruise, in the Lucky Strike (LS) vent field at the depth of 1700m. This study assesses the toxicity of sulphide particles on the hydrothermal vent shrimps (*Mirocaris fortunata)* and polychaetes (*Branchipolynoe seepensis)*. For this experiment, the SPIDER chamber was deployed in a mussel bed releasing sulphide particles that settled on the fauna. The chamber was left in place for 15 hours. The empty chamber was then reallocated to another mussel bed, to serve as a reference and was left in place for 33 hours. After the exposure, the fauna was sampled, sorted by size and preserved at -80ºC. Twelve individuals of *M. fortunata* and *B. seepensis* were collected from the exposed and reference experiments. The levels of lipid peroxidation, induction of metallothionines and metals concentration (As, Cd, Co, Cr, Cu, Mn, Ni, Pb, V, and Zn) will be analysed in both species. The results from these analyses will help to better understand the impact of the sulphides on vent fauna and contribute with essential knowledge to the future establishment of ecotoxicological thresholds.

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O8B-4: Are Sea Anemones Useful Tools for Assessing the Ecotoxicological Impact of Deep-Sea Sediments and Manganese Exposure?

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Interest in deep-sea mining (DSM) of manganese-rich polymetallic nodules (PN) from the Clarion-Clipperton Zone (CCZ) is high. During DSM, the generation of sediment plumes may increase metals bioavailability which can induce toxicological harm. In addition, deep sea faces the projection of rising seawater temperatures, which further threatens these ecosystems, since the cold-adapted fauna have limited thermal plasticity. To address these challenges, this study used shallow-water sea anemones (*Paranemonia cinerea*) as a proxy bioindicator model. Anemones were exposed to deep-sea sediment (SD) from CCZ (SD, 50 mg/L), a mixture of SD+PN (50 mg/L), and two concentrations of Mn^{2+} (1 and 20 mg/L) plus control treatment, at two different temperatures (22 and 26 °C). Anemones were sampled after 2, 14, and 28 days of exposure. Elemental screening was performed to reveal metals and rare earth elements in the anemone tissues and experimental waters. A set of biochemical biomarkers were evaluated in whole soft tissue, including those involved in the antioxidant defense: superoxide dismutase (SOD), catalase (CAT), glutathione peroxidases (GPx); xenobiotic biotransformation system: glutathione S-transferase (GST); oxidative damage: levels of lipid peroxidation (LPO) and protein carbonyl (PC); metal metabolism: metallothionein (MT); neurotoxicity: acetylcholinesterase (AChE); and reactive oxygen species (ROS). Results from the exposed waters and anemone metal accumulation showed a myriad of bioavailable metals in the water tanks. Biomarker responses induced changes in antioxidant defenses, biotransformation systems, and oxidative damage in sea anemones. Our findings suggest that sea anemones may serve as a model to evaluate the ecotoxicological impact caused by DSM, although validation with deep-sea relatives is essential.

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O8B-5: Metal Impacts on Deep-Sea Microbial Diversity and N Cycling Potential

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Deep-sea mining of minerals is expected to increase in the next decades, potentially exposing microbial communities to toxic concentrations of metals, such as cadmium (Cd) and copper (Cu), among others. These microorganisms are responsible for crucial ecosystem services in the deep-sea, including genetic diversity and driving nutrient cycles, such as the nitrogen cycle. However, the impacts of metal exposure on deep-sea microbial communities are still largely unknown. This study aims to explore the effects of Cd and Cu on microbial diversity and N-cycling potential in deep-sea sediments.

Aboard the RV Falkor(too) (2023), in the East Pacific Ocean, and RRS James Cook (2024), in the Northeast Atlantic Ocean, collected deep-sea sediments were subjected to 96-hour exposure experiments with varying Cd and Cu concentrations. Total DNA and RNA were extracted from exposed sediments and used for high-throughput sequencing of the 16S rRNA gene (prokaryotic diversity marker) and for real-time quantitative PCR of genes involved in different N-cycle pathways (denitrification, nitrification, anammox, DNRA).

In the microbial communities from the Pacific Ocean sediments, exposure to high concentrations of Cd caused a significant decrease in community heterogeneity, despite no significant effects on alpha or beta-diversity. Regarding the N-cycling communities, most pathways revealed a strong resistance to Cd effects on gene abundance or taxonomic relative abundance, but exposure effects were observed at the gene expression level.

We believe our observations and findings regarding metal exposure effects on deep-sea microbial diversity and N cycling potential will contribute to the global efforts of assessing the potential impacts of deep-sea mining on ecosystem functioning.

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O8B-6: Ecotoxicological Response to *in situ* Exposure to Sulphides in *Bathymodiolus azoricus*

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Seafloor massive sulphides (SMS) have raised interest for deep-sea mining (DSM) industries. Although active hydrothermal vents are not the targets, the inactive SMS structures are. Since inactive SMS deposits usually occur in proximity to the active ones, there are concerns that potential sulphide particle plumes may be released during mining activities. These plumes hold the potential to cause harmful effects on the abundant fauna living in active sites, such as on large mussel beds. This study evaluates the toxicity of sulphide particles on the hydrothermal vent mussel *Bathymodiolus azoricus* using a recently developed Sulphide PartIcle spreaDER (SPIDER) chamber. This chamber was developed for semi-contained *in situ* exposures and was first tested at 1700m depth in the Lucky Strike (LS) vent field during the MOMARSAT 2023 Ifremer cruise. The SPIDER chamber was deployed on a vent mussel bed releasing sulphide particles directly over the organisms inside the chamber. An additional similar experiment was made, during which no sulphides were released, to use as control. Mussels (n=12) were sampled after 15 hours using the ROV (Victor 6000), brought to the surface, dissected for gills and remaining tissues, and stored at -80 ºC. A battery of biomarkers (superoxide dismutase, catalase, glutathione peroxidase, glutathione S-transferase, acetylcholinesterase, metallothionein, lipid peroxidation, and protein carbonylation) and metal concentrations (As, Cd, Co, Cr, Cu, , Mn, Ni, Pb, V, and Zn) were analysed. Preliminary results show induction of metallothionein's in the gills and increased levels of lipid peroxidation in the remaining tissues, which supports the hypothesis that sulphides particles released *in situ* might be toxic to deep-sea fauna.

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O8B-7: *In situ* Disturbance Effects on the Proteome of the Hydrothermal Vent Mussel *Bathymodiolus azoricus*

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The rising metal demand led to increased interest in Deep-Sea Mining (DSM) whose activities will remove extensive accumulations of minerals from the deep ocean. Those activities are expected to release potentially toxic metal mixtures through the generation of sediment plumes near the seafloor or from the dewatering ore slurry after the ore process. These plumes may spread and impact larger areas and may disrupt the normal functioning of biological mechanisms, adversely affecting deep-sea fauna. The discovery of optimal biomarkers of metal toxicity in deep-sea species is a crucial step towards the supply of important ecological information for environmental impact assessment. In the present study, the impact of sulphide particles on the proteome (by SWATH mass spectrometry) of the hydrothermal vent mussel *Bathymodiolus azoricus* was investigated. A sulphide particle spreader (SPIDER) was used to induce an *in situ* disturbance event over the mussel beds, for 15 hours, at the Lucky Strike Hydrothermal vent field, Mid-Atlantic Ridge. Our findings revealed that proteins differentially modified were mainly related to metabolism, oxidative stress and immune system processes. These protein biomarkers, from distinct biological mechanisms, may be useful in future environmental impact assessment and monitoring. Future work will assess their suitability for other deep-sea species.

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O8C-1: Deep Pelagic Micronekton Reflect Differences in Mercury Bioavailability Within the Southern California Current Ecosystem

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Mercury (Hg) is a neurotoxicant that – in its organic form, methylmercury (MeHg) – accumulates in marine organisms through trophic interactions. Micronekton (swimming animals 2 – 20 cm) are key prey for top predators and transfer Hg assimilated by primary producers to higher trophic levels. However, few studies examine how environmental variability influences Hg bioaccumulation in these midtrophic organisms, especially in the deep pelagic (>200 m) where microorganisms transform inorganic Hg into MeHg. We examine how surface productivity and vertical habitat depth affect Hg concentrations in micronekton fishes and crustaceans from the Southern California Current Ecosystem (CCE). The Southern CCE is characterized by upwelling nearshore and lower nutrient availability offshore. Both surface productivity and microbial methylation in deep, oxygen-depleted waters influence Hg bioavailability throughout the deep pelagic. We collected micronekton from nearshore (0 – 1000 m deep) and offshore (0 – 2500 m deep) stations in the Southern CCE in October 2023 using a 10-m^2 Multiple Opening/Closing Net and Environmental Sensing System (MOCNESS). We analyze total Hg and MeHg concentrations in non-migratory taxa collected from epipelagic to bathypelagic depths to constrain the effect of vertical migration on Hg sources, and migratory taxa to examine exposure to multiple sources. We describe how Hg concentrations vary between major taxonomic groups, nearshore and offshore regions, and habitat depths, and evaluate whether differences in surface productivity are reflected in the Hg burdens of micronekton in the deep pelagic. We also compare Hg concentrations in muscle tissue with whole body burdens, since muscle tissues reflect Hg assimilated by an individual while whole body concentrations represent Hg exposure to predators. This research improves our understanding of how interactions between surface productivity and habitat depth affect Hg burdens in micronekton and Hg transfer through deep pelagic food webs.

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O8C-2: Maternal Transfer of Polycyclic Aromatic Hydrocarbons in Mesopelagic Fauna from the Northern Gulf of Mexico

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Maternal transfer of persistent organic pollutants, such as polycyclic aromatic hydrocarbons (PAHs), exposes developing embryos to high concentrations of toxic and mutagenic compounds. This exposure poses conservation concerns due to the potential impact to subsequent generations. To understand exposure trends in PAH composition and concentration in the open-ocean ecosystem of the northern Gulf of Mexico (GoM), collections of deep-pelagic fish, cephalopod, shrimp, and gelatinous zooplankton species were conducted as part of the Deep Pelagic Nekton Dynamics of the Gulf of Mexico (DEEPEND) Consortium. The maternal tissue of each taxon studied was compared to unhatched eggs or gonads over a period of several years during the last decade. Results indicate non-selective maternal transfer of individual compounds and significantly higher concentrations in eggs/gonads, suggesting a sink for organic pollutants in deep-pelagic organisms. In addition, the temporal trends observed show exposure to high PAH concentrations from an episodic contamination event in 2010 (*Deepwater Horizon* oil spill) that continued through the following years with long-term bioaccumulation driven by dietary intake and maternal transfer of PAHs. We hypothesize that the high PAH concentrations observed in the egg/gonad tissues may have influenced offspring's survival and affected the abundance of deep-pelagic species since the spill. A fundamental understanding of the persistence of organic pollutants in deep-sea habitats is critical for effective management and restoration initiatives.

O8C-3: Zooplankton Community Structure in the Abyssal Benthic Boundary Layer Varies Over Time with Organic Matter Flux

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The abyssal benthic boundary layer (BBL) community is broadly reliant on pelagic organic matter (OM) export, yet community dynamics under changing surface productivity remain poorly understood. Here, we describe temporal variability within the BBL zooplankton community, focusing on benthopelagic adults and meroplanktonic larvae, at a site with seasonal OM flux to depth. We test the hypothesis that BBL community structure is stable over time, with higher absolute abundances occurring under greater OM flux. Zooplankton were collected from three meters above the seafloor in the NORI-D mining contract area of the Clarion-Clipperton Zone in spring (March - April 2021) and fall (October - November 2021) using a benthic lander mounted with two large-volume pumps (22 deployments, avg. 14 m^3 seawater / pump). Using both morphotaxonomic and metabarcoding analyses, we observed elevated abundances (1.7X greater) of benthopelagic adults as well as bryozoan, bivalve, and gastropod larvae in spring, in addition to increased body size in pelagic polychaetes. Community structure was distinct between sampling periods ($p << 0.01$, $R^2 = 0.18$) with high rates of species-replacement. Springtime patterns co-occurred with elevated surface productivity and OM flux, supporting our alternative hypothesis that BBL community structure is variable over time due to non-uniform species responses to OM input. The BBL serves as a critical habitat for benthopelagic adults and as a dispersal conduit for larvae, and our observations of a temporally variable BBL community suggests that anthropogenic impact management may require species-specific information, necessitating greater knowledge of the taxonomy and life history of abyssal taxa, combined with an understanding of climate-related shifts in OM fluxes to the seafloor.

O8C-4: Predicting Habitat Suitability Changes for Vulnerable Marine Ecosystems in the Northeast Atlantic under Future Climate Scenarios

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Species are expected to adapt their distributions in response to climate change to stay within preferred environmental conditions or adapt physiologically to avoid extinction. Vulnerable marine ecosystems (VMEs), like cold-water corals and sponge grounds, provide essential ecological and biogeochemical services, and represent hotspots of biodiversity in the deep sea. However, the species that form VMEs have evolved under the relatively stable conditions of the deep sea, resulting in narrow environmental tolerance ranges and low growth rates, which might limit their resilience and resistance to future climates. We compiled over 4,000 records of VME species collected by monitoring programs across the northeast Atlantic to model their current (1990-2014) distributions and future (2056-2070) habitat suitability using three recently developed climate models of the deep sea. Two climate models, with 25 × 25 km resolution, include a broad range of environmental variables like silicate and phosphate, while the third, with finer 10 × 10 km resolution, only provides temperature, salinity, and current speed. We used MaxEnt, random forest, and boosted regressions models to study the effects of the climate models. The models predict significant reductions in habitat suitability across the southern and eastern parts of the northeast Atlantic for several VMEs. The models also predict increases in habitat suitability along the continental slope off Greenland and north of Svalbard, regions which are currently poorly surveyed, if at all. Lastly, we examine how predictive certainty varies across the study region and propose regions that might benefit from more monitoring. Our study does not consider aspects such as potential physiological adaptations, nor the effects of extreme events. Still, we find a high degree of vulnerability of deep-sea ecosystems to climate change and highlight the importance of monitoring programs that collect the data needed to develop effective management strategies for VMEs in the deep sea.

O8C-5: Testing the Deep-Sea Glacial Disturbance Hypothesis of Norwegian Sea Diversity, Using Fossil Records

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Aim: Within the intensively-studied, well-documented latitudinal diversity gradient, the deep-sea biodiversity of the present-day Norwegian Sea stands out with its notably low diversity, constituting a steep latitudinal diversity gradient in the North Atlantic. The reason behind this has long been a topic of debate and speculation. Most prominently, it is explained by the deep-sea glacial disturbance hypothesis, which states that harsh environmental glacial conditions negatively impacted Norwegian Sea diversities, which have not yet fully recovered. Our aim is to empirically test this hypothesis. Specific research questions are: (1) Has deep-sea biodiversity been lower during glacials than during interglacials? (2) Was there any faunal shift at the Mid-Brunhes Event (MBE) when the mode of glacial–interglacial climatic change was altered?

Location: Norwegian Sea, deep sea (1819–2800 m), coring sites MD992277, PS1243, and M23352.

Time period: Middle Pleistocene–Late Holocene.

Taxa studied: Ostracoda (Crustacea).

Methods: We empirically test the deep-sea glacial disturbance hypothesis by investigating whether diversity in glacial periods is consistently lower than diversity in interglacial periods. Additionally, we apply comparative analyses to determine a potential faunal shift at the MBE, a Pleistocene event describing a fundamental shift in global climate.

Results: The deep Norwegian Sea diversity was not lower during glacial periods compared to interglacial periods. Holocene diversity was exceedingly lower than that of the last glacial period. Faunal composition changed substantially between pre-and post-MBE.

Main conclusions: These results reject the glacial disturbance hypothesis, since the low glacial diversity is the important precondition here. The present-day-style deep Norwegian Sea ecosystem was established by the MBE, more specifically by MBE induced changes in global climate, which has led to more dynamic post-MBE conditions. In a broader context, this implies that the MBE has played an important role in the establishment of the modern polar deep-sea ecosystem and biodiversity in general.

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O8C-6: Lipid Dynamics in the Cold-Water Coral *Dentomuricea* aff. *meteor*: Effects of Ocean Warming and Reproductive Condition

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Dentomuricea aff. *meteor* is an important bioengineering cold-water coral gorgonian, in the Azores seamounts. It forms extensive coral gardens mostly at depths of 200 to 400 meters, that provide essential habitat, used as shelter, breeding and feeding grounds for other organisms, contributing significantly to the biodiversity in the Azores region. However, these coral gardens face increasing threats, such as ocean warming.

In corals, lipids constitute up to 40% of dry organic matter and are vital for their health, and physiological processes such as metabolism and reproduction. These essential nutrients are categorized into neutral lipids, serving as energy reserves, and polar lipids, contributing to cell membrane structure. Lipid class composition respond to environmental factors such availability of food and changes in environmental parameters (temperature and pH), making them valuable trophic biomarkers and indicators of physiological performance and stress.

Considering the threat presented by ocean warming and the importance of lipids in coral physiology, the primary focus of this study was to investigate the potential dynamic changes in the lipid class composition of *D. meteor* colonies under different temperatures: 14°C, 16°C, corresponding respectively to the species' minimum and maximum natural temperature range, and 19°C corresponding to the IPCC RCP8.5 prediction scenario (+3°C from the species' maximum natural temperature range). The study was conducted over a period of 6 weeks to evaluate potential changes over time. Additionally, we explored these variations during the reproductive season. Lipids were extracted using a modified Folch method then separated by High Performance Thin Layer Chromatography. For the results, we anticipated variabilities in the distribution of neutral lipids *vs* polar lipids, and even within the polar lipid classes due to adaptation to the different temperatures.

Furthermore, we expected higher lipid concentrations in females compared to males and before spawning due to their higher reproductive investment. Then, a post-spawning decrease in lipid content is expected for both sexes, particularly pronounced in females at higher temperatures, considering the energetic costs associated with spawning and ocean warming.

O9-1: Progress in the Development of Standards and Best Practice in Benthic Imagery Annotation and Onward Data Use in AI Applications

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Image based platforms are now firmly cemented into the future of marine benthic biodiversity survey and monitoring. The datasets delivered by these platforms are vast and have the potential to transform our understanding of the deep ocean. However, there are widely recognised challenges in extracting consistent and robust biological and ecological data from imagery relating to both the lack of standardisation in approaches used and the time taken to process such data. We report here on actions to progress the development and adoption of standards in benthic image annotation and the provision of training resources and best practice approaches in this field. Specifically, we consider these actions with respect to the development of novel deep-learning artificial intelligence (DL-AI) approaches to imagery data analysis. DL-AI holds significant promise in helping to break the bottleneck of manual biological image analysis. We report on multiple studies within the Plymouth University and Plymouth Marine Laboratory teams that assess the performance of DL-AI trained on benthic annotated datasets using different approaches to animal classification and annotation, and different imaging platforms. Our work highlights the intrinsic link between the development and adoption of standards, the need for formal training and quality control procedures, and the potential for DL-AI to support deep-sea biodiversity research into the future.

O9-2: Towards Fully Open and FAIR Deep Sea Biology Data

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Deep ocean data are limited and expensive to acquire, making it critical to share and re-use data broadly to foster scientific progress globally. This presentation will overview current initiatives from programs such as the Deep Ocean Observing Strategy and DeCODER that are improving how FAIR – Findable, Accessible, Interoperable, and Reusable – deep ocean data are. The landscape is changing around data accessibility and tools: there are new resources and approaches available to you as a deep-sea biologist, and areas where your effort and input is needed to work towards open and functional data infrastructure.

O9-3: Capture by Hybridization, State of the Art Tool for Unravelling the Biodiversity of the Deep

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Methods like metabarcoding allow us to analyse complex ecosystems across the Tree of Life. One aspiration is to use such standardised environmental genomic approaches for biomonitoring and impact assessment of the deep sea. However, the largely unknown diversity still limits the application outside of research. Despite significant recent developments, even the most versatile primers still result in biased results, with essential lineages only being revealed in very partial ways. Moreover, the short nature of metabarcode fragments, mainly due to Illumina limitations, limits the resolution and the potential for phylogenetic or phylogeographic reconstructions. Here, we present a new optimised protocol based on Captured by Hybridisation (CBH) applied to the poorly known deep benthic communities. The different enrichment methods allow for obtaining less biased full-length Prokaryotes and Eukaryotes sequences. We assembled Metazoan mock communities from DNA extracts from 110 specimens spanning 13 phyla and four times 40 specimens with variable DNA concentrations. Results showed a significantly higher sensitivity and sensibility of CBH than metabarcoding, reaffirming the advantage of Captured by Hybridization across a broad range of taxonomic lineages. All species could be detected by CBH, and even more, most specimens could be differentiated. In contrast, many were lacking in metabarcoding results that also lacked the resolution to discriminate close relatives. Bioinformatic analyses are also optimised with a novel developed RiboTaxa pipeline for metagenomic analyses, which offers a standard and repeatable protocol. While developed for 16S, 18S and COI to capture prokaryotes and metazoan biodiversity, it can be adapted for different genes and taxa groups. This approach will improve the resolution of community characterisation, the description of new species, and phylogenetic or connectivity analyses. This outlines one future opportunity for improving the metagenetic approach in deep-sea habitats and helps to develop assessment protocols, thereby enhancing our understanding of deep-sea biodiversity and its conservation.

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O9-4: Mapping Tetractinellid Sponge Abundance and Sizes with Instance Segmentation: Exploring the Potential of New Technologies for Understanding Deep-Sea Ecosystems

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The role of Sponges in deep-sea benthic ecosystems is critical. In Norway, sponge aggregations (ostur) form an important portion of the benthic habitats but their spatio-temporal dynamic and ecology is still poorly understood. Measurement of their abundance and size are important factors to consider when trying to quantify - and eventually, model - their contribution to and ecosystems' diversity and function at local and basin scale.

Image-based sampling, while non-destructive more spatially explicit than physical sampling, makes identification and quantification slightly more complicated than measuring physical samples. The sponge size, shape and surface area can be inferred from calibrated image but this approach is time-consuming and difficult to standardise if performed manually. Instance segmentation, a computer-vision powered analysis methods can automate this process and make it viable for large scale analysis.

Owed to the relative novelty of this approach, it is not yet clear what the best annotation strategy can maximize time efficiency, taxonomic resolution and measurement precision.

We used a set of 453 ROV images of the Norwegian Seabed calibrated and manually annotated in Biigle with 3 sets of classes reflecting different annotation strategies. We trained Ultralytics YoloV8m-seg models to identify and measure the size of 6 tetractinellid sponge species and perform quantitative comparisons between these CV predictions and manual segmentation.

The results show that the morphology classes produced a higher F1 score (0.712) than taxonomically explicit classes (0.574) while a single class models had the highest accuracy (0.733). The quantification of the sponge's relative coverage of the seabed according to these models correlates to the manual equivalent but differences can occur in challenging visibility conditions.

We describe the method used to achieve these results and discuss the practical implications of our findings for the implementation of segmentation for sponge aggregation ecology as well as the potential for improvement.

O9-5: Deep-Sea Neoichnology: New Lebensspuren Classification Scheme and Applicability

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Detailed deep-sea neoichnological studies have increased in number during the last decades, mainly through advances in visual instrumentation used to observe this underexplored environment. The appearance of new technology has enabled the acquisition of highly detailed images over large-scale areas of the deep-sea floor, and the subsequent characterization of biogenic traces (lebensspuren) and trace makers. Lebensspuren are common features of deep-sea landscapes, being more abundant than their tracemakers, rendering them promising proxies for inferring biodiversity. We propose a new classification system for marine lebensspuren that integrates three key labels: 1) morphology (e.g., M-ridged trail), 2) behavior determination (e.g., locomotion and feeding), and 3) tracemaker taxonomy (e.g., Echinocrepis rostrata). We offer recommendations to address each of these labels and we discuss the utility of open nomenclature. This classification scheme facilitates consistent comparisons of lebensspuren worldwide.

Here we present a study case of eight deep-sea stations in the Kuril Kamchatka Trench area to address density-diversity relationships between lebensspuren and benthic fauna (e.g., trace makers). Diversity correlation was observed at specific stations, showing both negative and positive correlations depending on: 1) the number of unknown tracemakers (especially significant for dwelling lebensspuren), 2) the multiple origins of particular lebensspuren, and 3) the tracemakers producing different lebensspuren. Lebensspuren density was either positively or negatively correlated with tracemaker densities, depending on the lebensspuren morphotypes. A positive correlation was observed for resting lebensspuren, while negative correlations were observed for locomotion-feeding lebensspuren. Thus, lebensspuren diversity may be a good proxy for tracemaker biodiversity when the lebensspuren-tracemaker relationship can be reliably characterized. Lebensspuren-density correlations vary depending on the specific lebensspuren residence time, tracemaker density and associated behaviour. We suggest that lebensspuren density and diversity correlations should be related specifically to tracemakers rather than to the benthic fauna in general.

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O9-6: Computer Vision to Unravel Biotic and Biotic Factors Explaining the Fine-Scale Distribution of Cold-Water Corals

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Computer vision offers fascinating opportunities to study deep seascapes at unprecedented levels of spatial resolution, thus providing insights into the factors and scales that structure benthic communities. This is particularly valuable in complex habitats such as deep-sea coral reefs, where it could facilitate the disentangling of biotic and abiotic interactions. The aim of this study is to present a novel methodology for the comprehensive use of imagery data at high spatial resolution in benthic studies. Based on videos and images recorded by a Remotely Operated Vehicle (ROV), three-dimensional (3D) models are constructed utilising Structure from Motion (SfM). To assess the influence of topography, 3D geomorphometrics (terrain descriptors, e.g., slope, aspect, roughness, Benthic Position Index…) are computed. The original images and videos are then manually or automatically annotated for corals and associated fauna using the online collaborative tool Biigle and deep learning algorithms. To combine the ease of 2D annotation with the accuracy of 3D model positioning, these annotations are reprojected onto the 3D model (conversion into 3D annotations). This process results in an accurate 3D representation of the seascape at a centimetre resolution. Point Pattern Modelling (PPM) and Species Distribution Models (SDM) analyses are performed to elucidate the patterns of faunal distribution and the underlying structuring factors. This process pipeline was applied to two Cold-Water Coral (CWC) habitats of the Lampaul Canyon off Brest (France), mapped in 2022: a 46 000 m² vertical cliff dominated by *Desmophyllum pertusum* and a 11 000 m² coral garden dominated by *Madrepora oculata*.

O9-7: Application and Transferability of Object Detection Models to Support the Identification of Benthic Epifauna from Imagery

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Technological advances over recent decades have seen the proliferation of accessible deep-water imaging platforms. The acquisition of vast amounts of image data has resulted in an image analysis bottleneck, taking annotators months to years to annotate imagery collected from a single survey. This challenge could be compounded further as ocean observing strategies become increasingly autonomous, higher image resolution and the rate of data collection proliferates. Object detection is now being applied to assist the image annotation process to potentially reduce analysis time. However, for object detectors to effectively tackle the scale of the challenge, models need to be transferable between imaging platforms and in space.

This study trains YOLOv5 object detection models to identify six coral morphology classes using annotated imagery collected by ROV ISIS in the UK deep sea (JC136). Model performance was then tested with independent datasets to inspect different aspects of transferability. Imagery collected with ROV Holland I (SeaRovers Project) from the Irish deep-sea was used to test the transferability of models between ROVs in the same region, while imagery collected on Tropic Seamount in the Canary Islands (JC142) with the same ROV, ISIS, was used to test spatial transferability. When validated, model performance overall was moderate (adjusted recall = 0.58, adjusted precision = 0.80) with variable class performance (recall = 0.44-0.69, precision = 0.67-0.78). Model performance decreased substantially when tested across all the independent testing datasets (adjusted recall = 0.23-0.34, adjusted precision = 0.33-0.47). Results suggest that these models do not perform better in either transfer scenario (platform or spatial). The analysis supports the conclusion that the poor testing performance was not strictly the result of poor transferability, e.g. differing image quality, but instead the sampled biological assemblages and structure of datasets. Here, we will present our subsequent recommendations for improving model transferability and unresolved questions.

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O10-1: Broadening Our Views on Common Heritage: Factoring in Art, Science and all Forms of Knowledge in the Politics and Regulatory Framing of the Deep Sea

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The deep sea plays a pivotal role in delivering towards human wellbeing. This includes sustaining the healthy functioning of our ocean and regulating the global climate, as well as an embodiment of our intrinsic values. The deep sea is, therefore, a global commons in a broad sense – belonging to everyone – and in the case of the mineral resources of the international seabed, the 'common heritage of humankind'. Regrettably, the contemporary political and regulatory framing of the deep sea often neglects or sidesteps scientific information and other forms of knowledge (including local and traditional knowledge). Indeed, two of the key barriers that stands in the way of strong ocean protection and marine conservation efforts are global politics and the surrounding legal frameworks. The solution, fortunately, also lies in international law and politics, in what may be termed as 'ocean diplomacy'. The argument here is essentially that science and other forms of knowledge must all factor into the politics and regulatory framing of the deep sea. This is, easier said than done, as the ocean space is highly contested and national interests often takes precedence over community interests. In most controversial cases, like deep seabed mining, emotions prevail over logic and sentiments tend to fuel arguments. This gives rise to the question on how can emotions be swayed through ocean diplomacy when it comes to the deep sea in particular? One possible answer worth exploring is the role of art, which can serve as an object of communication but also act as an intermediary. In this context, art could be the missing tool to broaden our thinking on the ocean as a common heritage and help bridge the interface between ocean science and knowledge on the one hand, and the politics as well as regulation of the deep sea on the other.

O10-2: Measuring the Success of the Kunming-Montreal Global Biodiversity Framework in the Deep Sea

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A biodiversity crisis is unfolding in our world ocean with direct exploitation, climate change, pollution and alien invasive species as the main anthropogenic drivers. To respond to this crisis, the Kunming-Montreal Global Biodiversity Framework (GBF) set an ambitious plan to protect biodiversity on land and in the ocean through 4 Goals and 23 Targets to be met by 2050. To assess progress towards meeting those goals and targets, a monitoring framework of the GBF includes proposed headline, component and complementary indicators. However, many of these indicators have originated on terrestrial ecosystems and their applicability in the ocean has not been evaluated. For the deep ocean in particular, even some of the headline indicators may not be feasible to use. For example, Goal A aspires that the integrity, connectivity and resilience of all ecosystems are maintained, enhanced, or restored, substantially increasing the area of natural ecosystems by 2050, and will be assessed based on four indicators. Two of these, A.2 “the extent of natural ecosystems” and A.4, “the proportion of populations within species with an effective population size > 500” are not quantifiable in the deep ocean presently because of lack of data. However, indicator A.1, “Red list of ecosystems”, may be useable, at least for some deep-sea ecosystems. In this presentation, I will discuss the current feasibility of using the proposed indicators in the deep-sea context. I will address some of the current gaps in scientific knowledge that may hinder the application of the monitoring framework of the GBF in the deep ocean and suggest ways forward. It is anticipated that the GBF will form the basis for the implementation of many elements of the BBNJ agreement and identifying the science needs that can support concurrently the implementation of both agreements will help advance the conservation of deep-ocean biodiversity.

O10-3: Communicating Azores Deep-Sea Benthic Communities through Scientific Illustrations

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The Azores deep seafloor is a hotspot for benthic communities dominated by cold-water corals and sponges. These communities supply a myriad of ecological services, providing habitat for many associated species. Over the last decade, Azorean deep-sea research has grown considerably, mostly due to low-cost exploration technologies such as the Azor drift-cam. The large volume of images/data produced have advanced our understanding of Azores deep-sea ecosystems and informed management and conservation. Despite advances, there is still a general lack of public comprehension about biological diversity, natural value, and ecological importance of deep-sea habitats. To this end, the Azores Deep-Sea Ecology research group developed a communication plan to increase public awareness on the Azorean deep-sea. Although the research group now holds an immense video/image dataset, obtaining a still image portraying all aspects of a given community remains elusive – either because not all species are found within the same frame, or the image might be unfocused. Since scientific illustration can help fill this gap in conceptualisation, video image information was used to create scientific illustrations that faithfully represent key deep-sea Azorean benthic communities. Selection was based on prevalence, structural complexity and depth distribution. Selected communities included three types of coral gardens, one scleractinian reef, two types of sponge fields, and xenophyophore and sea urchin aggregations. Besides using illustrations for scientific publications that visually describe important deep-sea communities, they will enhance our ability to translate scientific knowledge into an approachable visual format for people previously disconnected from it. Illustrations can also communicate differences between pristine versus impacted communities and will be merged to form a conceptual design representing community distribution along the depth gradient (200-1000m). By investing in deep-sea ocean literacy targeting the general public, conservation decision-makers, the scientific community and other marine stakeholders, we are fostering more effective deep-sea management and conservation actions.

O10-4: Tracking Bottom-Fishing Activities of the European Union's Deep-Sea Fishing Fleet in Vulnerable Marine Ecosystem Areas

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'Vulnerable Marine Ecosystems' (VMEs) represent deeply sensitive habitats in the ocean, susceptible to human activities. These ecosystems boast diverse arrays of habitat-forming organisms, such as deep-sea sponge clusters, cold-water corals, sea pens, and crinoid fields, alongside distinctive features like seamounts and hydrothermal vents. Extensive research has underscored bottom-contact fishing gears as the primary threat to VMEs.

In our study, we examined bottom-fishing activities within closed VME areas and on seamounts across European Waters and the Mediterranean Sea, leveraging publicly available Automatic Identification System data from Global Fishing Watch to calculate apparent fishing effort. Our analysis revealed that despite closures established in 2022, approximately 3,500 hours of fishing persisted within closed VME areas in EU waters in the following year. Moreover, we identified up to 17,600 hours of bottom-contact fishing occurring in unprotected areas where VMEs are known or likely to occur, based on annual assessments by the International Council for the Exploration of the Sea (ICES).

On the Mediterranean seamounts, we found that the EU fleet spent 32,000 hours trawling between 2022 and 2023, with additional hours allocated to trawling seamounts in EU waters. These findings underscore the profound impact of the EU fleet on VMEs, including seamounts, signalling an urgent need for states to prioritize the safeguarding of these ecosystems. Enhanced surveillance and monitoring of fishing fleets are imperative for effective fisheries management, and crucial in mitigating further degradation of VMEs, including seamount habitats.

O10-5: One Thousand Reasons – An Inspiring Step Towards the Protection and Sustainable Use of the Deep Sea

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The sustainable use of the ocean and its resources, a core principle of the United Nations Convention on the Law of the Sea, demands a fine balance between human activities and proper conservation and management measures. Enhanced understanding of deep-sea ecosystems and biodiversity is needed to implement this mandate.

After the DNA revolution in the early 2000’s, artificial intelligence has now become the cutting-edge technology supporting a whirlwind of new species discoveries. Navigating along these scientific advancements, exploration of mineral resources in the international seabed area is contributing to increasing knowledge of biodiversity in remote deep-sea ecosystems.

Estimating biodiversity in the world’s oceans has been possible after large, global initiatives, such as the Census of Marine Life (2000-2010), leading to the creation of several open-access databases sharing species occurrences, taxonomic information and molecular data. On the margins of the 2022 UN Ocean Conference, the International Seabed Authority (ISA) launched the Sustainable Seabed Knowledge Initiative (SSKI) as a flagship initiative under the ISA MSR Action Plan in support of the UN Ocean Decade. SSKI serves as a catalyst for advancing deep-sea biodiversity knowledge, facilitating capacity building efforts for deep-sea taxonomy and informing relevant decision-making processes.

In 2023, the 1,000 reasons call for taxonomic projects awarded 10 deep-sea taxonomists to describe over 70 new species across deep-sea ecosystems in areas beyond national jurisdiction, ranging from sharks to minute often neglected mud dragons (Kinorhyncha) in hadal trenches. This presentation will highlight the results of the 1,000 reasons campaign and other SSKI achievements since its inception. It will also share opportunities for new collaborations to advance taxonomic research in the deep-sea as a contribution to achieve the ambitious goals of the UN Agenda for Sustainable Development, in particular sustainable development goal 14, and inform global ocean agendas for sustainable development of deep-sea resources.

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O10-6: Coupling “Arts & Sciences”: Inspiration and Innovation to Increase Ocean Literacy

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Projects that combine "art & science" are quickly gaining popularity, with innovative initiatives such as performance projects, artist residencies, training courses, and festivals receiving support across France over the last decade. These projects aim to transcend the boundaries of individual disciplines to create new forms of communication and experimentation. Public enthusiasm highlights their significant impact on knowledge dissemination and environmental awareness, especially regarding remote deep-sea ecosystems. This interdisciplinary dialogue inspires students and early-career scientists by offering new perspectives, emphasizing creativity, and fostering a broader understanding of their fields.

One notable example is a long-term collaboration between scientists from the Ifremer deep-sea laboratory and a professional theater company –Teatr PIBA- in Brest, Brittany. This partnership has produced two sensory plays using 3D sound, which immerse the audience in deep-sea environments and raise awareness of environmental issues linked to the potential exploitation of their resources. The conference will detail this six-year collaboration, including the initial meetings, joint work on scientific cruises or on stage, and the development of scientific mediation surrounding the plays. Additionally, the collaboration has spawned various parallel projects, including a making-of film, two publications, a short animation, and "art & science" workshops now part of the University of Western Brittany's Marine Biology Master's program. The conference will end up with a quick glance into a few other “art & science” projects developed more recently in our lab.

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O11A-1: The African Network of Deepwater Researchers

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The African Network of Deep-water Researchers (ANDR) is a network of deepwater researchers developed under Challenger 150 Programme, one of the United Nations Decade of Ocean Science for Sustainable Development endorsed programs. The main objective of the ANDR is to build capacity for Africa's deep-water research. Although the continent of Africa is surrounded by two of the most important global oceans (the Atlantic and the Indian Ocean) and the Mediterranean Sea, capacity for ocean research in African is wanting, in particular capacity for deep water research. The notion of Blue Economy as the next frontier for economic development has given many countries the impetus to venture into the ocean. Additionally, the call by the Decade of Ocean Science has challenged the world over to do the science we need for the ocean we want. The deep-sea science has had little attention in Africa due to several challenges including human and infrastructure capacity, funding among others. Therefore, the network was formed with a view to identify where we are, where we wanted to be and how we want to get there.

O11A-2: Deepening the Decade: Collaborative Action for Advancing Deep Ocean Science and Policy in the United Nations Decade of Ocean Science for Sustainable Development

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The current United Nations Decade of Ocean Science for Sustainable Development (hereafter, the Decade) offers a unique opportunity and framework to globally advance ocean science and policy. Achieving meaningful progress within the Decade requires close collaboration and coordination across Decade Actions (Programmes, Projects, and Centres). This coordination is particularly important for the deep ocean, which remains critically under-sampled compared to other ecosystems. To address the coordination needs across the deep-ocean Decade community, we gathered representatives from Decade Actions that focus (at least partially) on the deep ocean for a workshop hosted by the Deep Ocean Observing Strategy, a Decade-endorsed Action, in October 2023. Together, we identified five broad thematic areas that connect across our Decade Actions and aim to advance deep-ocean science in alignment with the Decade's overarching goals and ten Challenges: natural capital and the blue economy, biodiversity, deep-ocean observing, best practices in data sharing, and capacity building. Within each of these themes, we pose concrete objectives (termed Cohesive Asks) and targets for the deep-ocean community. These span a range of topics including seafloor mapping, physical and biogeochemical data generation, efficacy of carbon removal, identifying exploration priorities, advancing eDNA technologies, biodiversity-carbon cycle linkages, FAIR and CARE data, digital twins, deep-ocean science training, the science-policy interface, and co-design principles including with Least Developed Countries, Small-Island Developing States, and Indigenous communities. Lastly, the conversations within the deep ocean Decade community led to a 'Deepening the Decade' satellite event at the Decade Conference in 2024 and the creation of a deep ocean Task Team within the global Early Career Ocean Professionals (ECOPs) programme. The new task team will provide engagement opportunities for the next generation of deep-ocean leaders and a connection between deep-Decade Actions and ECOPs. Altogether, these collective efforts reflect a commitment to better coordination across deep-ocean Decade Actions.

O11A-3: Prioritisation of Ocean Biodiversity Data Collection to Deliver a Sustainable Ocean

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Fundamental ecological questions about the distribution of ocean life remain unanswered, hindering both the effective management of the ocean, and our comprehension of life on this planet. The benthic and pelagic realms are subject to different methods of study, and to understand where to best focus effort, a thorough understanding of existing information is required, allowing identification of critical knowledge gaps. Open-access data repositories provide a valuable means to identify such gaps; however, these repositories are subject to challenges in separating benthic from pelagic data. Here we demonstrate an automated data pipeline for extracting and separating benthic from pelagic data in open-access repositories. By stratifying data against essential ocean variables in a critical gap analysis, we show that large spatial and taxonomic biases exist in both the benthic and pelagic global datasets, favouring depths shallower than ~100 m, the northern hemisphere, and vertebrate species. The newly compiled, cleaned, and classified dataset is used to identify areas of chronic under sampling and high priority regions for exploration. We argue that coordinated strategic prioritisation of sampling is needed to support modelling and prediction, enabling us to better manage our oceans, and comprehend life on Earth.

O11A-4: Deep-Ocean Stewardship Initiative: The Decade that was for the Decade that is

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In April 2023, almost at the start of the UN Ocean Decade (2021-2030), the Deep-Ocean Stewardship Initiative (DOSI) celebrated its 10th anniversary. DOSI and the Decade share a common vision, which the Decade succinctly states as 'the science we need for the ocean we want'. Over its first 10 years, DOSI has grown in size, influence and reputation, giving a hitherto largely absent voice – impartial, independent and science-based – to the deep ocean in national, international and intergovernmental negotiations. These negotiations aim to regulate human activities in the marine environment that affect its inhabitants, natural resources, and life-supporting ecosystem services. Whilst DOSI's anniversary celebrations were duly observed, there is still much work to be done, not least in supporting and contributing to the mission and outcomes of the still-young UN Ocean Decade. To that end, this presentation will briefly highlight the achievements of DOSI over the past 10 years, including its own Decade-endorsed Programme – Challenger 150 – and importantly, will expand on what DOSI is doing now on several rapidly evolving fronts to inform and provide responsible, fair, and equitable stewardship of the deep ocean.

[DOSI receives core support from Arcadia (2017-2031).]

O11A-5: Climate Change and Deep Ocean Microbiomes and Ecosystems (DOME)

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For the first time in Earth's history, climate change is being driven by human forcing and proceeding at a pace that may outstrip evolutionary change. Climate change is affecting the marine environment, inflicting ever-increasing pressures on marine microbiomes and ecosystems. The resulting cumulative impact has substantially eroded the ocean ecosystems, and often leads to ocean ecosystem degradation or even collapse. It is supposed that we are now firmly entrenched within the sixth mass extinction event with loss of biodiversity being most prominent. As the oldest and largest biome on Earth, the deep ocean contains a trove of microbial diversity with unique physiology, metabolism, and genetic resources that provide ecosystem services of enormous values to the mankind. The deep ocean microorganisms, and the communities they form, drive global biogeochemical cycles, including those that regulate the Earth's climate. Although our understanding of marine microbiomes has increased, deep ocean microbiome research, particularly in the context of ecosystem processes and functions, is still in its infancy. The DOME programme adopts the PMO concept – People, Microbe, and Ocean, that is, the interactions and connections between people, microbes, and the ocean, aiming to generate the knowledge on how ecosystem services provided by deep ocean microbiomes impact the societies. DOME will determine microbial diversity of the deep ocean, assessing the ″Deep Ocean Genome″, that is, all the genes and the information they encode. Further, DOME will utilize an ecosystem-level biology approach, combining the study of molecules, cells, populations and communities to assess their ecosystem impacts and multidirectional connections between them. DOME will contribute the needed knowledge and information about the deep ocean microbiomes and ecosystems to enhance understanding of the ocean-climate nexus and generate knowledge and solutions to mitigate, adapt and build resilience to the effects of climate change across all geographies and at all scales.

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O11A-6: UN Ocean Decade Project COESS: Chemistry, Observation, Ecology of Submarine Seeps

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COESS (Chemistry, Observation, Ecology of Submarine Seeps) was established and recognized by UNESCO as an Ocean Decade Project in September 2022. Now in its second year, the project involves 27 researchers from 15 different institutions in 3 countries and is still growing. At present we have carried out 3 deployments of a FullDepth underwater drone prototype to capture video footage of seafloor life at Torigakubi Spur located offshore near the Toyama underwater canyon. The Spur is an area of active hydrocarbon seepage and methane hydrate accumulations, as well as being productive grounds for local fishing communities. In order to monitor long term episodic changes, we have deployed two seafloor landers (Fugro Shallow Environmental Landers) equipped with CTD and sensors for measuring dissolved methane, pH, oxygen, turbidity and current movement. During our last underwater drone deployment, we found the landers to be actively inhabited by tunicates and deep-sea whelks (Buccinidae). As a participant in the Ocean Decade, our project has the commitment to not only carry out scientific research, but also create educational materials and public awareness materials illustrating the role of submarine seeps in hosting a variety of seafloor organisms. We presently have over 3 hours of high-resolution video footage and will be recovering the lander sensor data in the near future. In addition to publishing our results in research journals, we are also sharing information in social media, including FaceBook, Google Sites, and YouTube.

O11A-7: Deep Ocean Discoveries in The UN Ocean Decade: Opportunities for Science, Development and International Cooperation

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Despite significant technological advancements that have revolutionized our ability to explore the deep ocean, seamount systems remain one of the last great frontiers in human discovery. Although more than 70% of nations have exclusive economic zones that contain deep-sea environments, the majority of deep-sea research is conducted by a few economically developed nations, institutions, and private entities. Consequently, the data populating the current knowledge base of the deep oceans are biased toward the interests of these economically developed countries. A more comprehensive understanding of seamount systems, including their physics, chemistry, geology, and biology, will be instrumental in assessing their current state and resilience. We propose that enhancing and interconnecting research in these areas will be a prerequisite for informed decisions regarding protection and sustainable use of these ecosystems. We are spearheading an initiative that involves collaboration among experts, organizations, and governments across multiple disciplines and nations to identify major information needs and critical bottlenecks in 1) deep-sea research, 2) technologies, 3) policy, and 4) capacity. A key component is to increase awareness, philanthropic and international support, and bolster the research capabilities of less developed nations, ensuring they are equipped to contribute to and benefit from deep-sea exploration. The new initiative aims to determine priorities for action during the Ocean Decade and beyond. By leveraging ongoing UN Ocean Decade activities and fostering global partnerships, the initiative seeks to develop calls-to-action to support understanding, data sharing, and knowledge exchange, as well as provide critical information for deep ocean governance in the context of protection and sustainable use.

O11B-1: The Development and Upcoming Challenges of Area-Based Management Tools for the Areas beyond National Jurisdiction

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Deep-sea habitat is the largest ecosystem on Earth, with extremely abundant biodiversity and a large number of unknown species. In recent years, the impact of climate change and human activities on deep-sea habitats has received widely international attention. The most significant progress is the conservation and sustainable use of "Biological diversity of areas beyond national Jurisdiction" (BBNJ) negotiation, which will provide legal basis for area-based management tools (ABMTs), including marine protected areas. ABMTs, including marine protected areas, are considered as the most effective measures for conserving marine biodiversity at present. In addition to the BBNJ agreement, International Maritime Organization (IMO), International Seabed Authority (ISA), and other international organizations have developed various ABMTs for types of human activities. Taking ISA as an example, the Regional Environmental Management Plan (REMP) has been developed, which includes various ABMTs for different types of deep-sea habitats. Given that the BBNJ Agreement is a global legal instrument under the United Nations Convention on the Law of the Sea, future ABMTs developed under BBNJ agreement need to be coordinated with existing ABMTs. This work systematically reviewed the existing ABMTs for the area beyond national jurisdiction, with focus on the REMP under ISA. In addition, we analyzed the challenges may arise in coordinating among current international organization and enforcement body of BBNJ and proposed the corresponding suggestions.

O11B-2: Population Genetic Structure of the Deep-Sea Ophiuroidea across the North-Western Pacific: Subtle Differentiation within High Connectivity

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Knowledge regarding dispersal mechanisms in deep-sea ecosystems, providing key scientific evidence for marine protected area designing, remains limited. The western Pacific has the highest density of seamount around the world, providing stepping stones for long distance dispersal of deep-sea animals. Understanding patterns of gene flow is crucial for protection of this vulnerable deep-sea ecosystem. This study conducted a population genomic analysis of an abundant brittle star, *Ophioplinthaca defensor*, across its distribution range on both sides of the Marina Islands. We analyzed 94 individuals from nine deep-sea seamounts utilizing a fragment of the mitochondrial cytochrome c oxidase subunit I (COI) and 16S gene, along with 26,844 genome-wide single nucleotide polymorphisms (SNPs) derived from double digest restriction-site associated DNA sequencing (ddRAD-seq) for population genomic analyses. Our findings revealed exceptional population homogeneity across seamounts on both sides of the Mariana Trench (from the Kyushu-Palau Ridge to the Malkuswick seamount chain), spanning approximately 3,135 km at depths ranging from 1,245 to 2,070 meters. This remarkable level of panmixia is likely attributable to a prolonged pelagic larval duration and recent demographic expansions. Notably, when applying 1,184 outlier SNPs, we detected minor genetic subdivision between populations from the KPR, OH, and other seamounts. This finding suggests the presence of subtle geographic barriers, such as environmental gradient, possibly influencing genetic differentiation despite the overarching influence of Subtropical recirculation and North Pacific Intermediate Water. Historical demographic reconstruction of these three groups indicated that their differentiation times corresponded to two glacial periods during the Pleistocene, further highlighting that deep-sea provided “refuges” for the species during the ice ages, with the relative stable environmental conditions promoting population proliferation and genetic divergence among seamounts. Given the increasing anthropogenic activities, including mining and gas hydrate extraction, impacting the deep ocean, our results have significant implications for the conservation of deep-sea biodiversity and the establishment of marine protected areas.

O11B-3: Time in the Deep: Insights from the NorthEast Pacific Deep-sea Exploration Project (NEPDEP)

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Climate change and human activities are altering deep-sea ecosystems, yet empirical data documenting the rate and nature of these changes remains scarce. That said, the NorthEast Pacific Deep-sea Exploration Project (NEPDEP) — a Challenger 150 program and Ocean Decade initiative—is uniquely positioned to provide insights to help address this knowledge gap. NEPDEP, led by federal and Indigenous scientists and managers, monitors a network of deep-sea Marine Protected Areas (MPAs) spanning over 160,000 km² to assess the effectiveness of conservation measures by documenting the environmental conditions and indicator species, including cold-water corals, sponges, fish, and invertebrates. Since 2017, the NEPDEP team has conducted annual surveys across dozens of monitoring sites at depths ranging from 100 to 2,500 m, providing robust datasets relating to climate change and human impacts. Our results reveal diverse responses to impacts, from rising acidity leading to mass mortalities (e.g., *Primnoa pacifica* corals), to rapid declines in oxygen causing habitat shifts of mobile species (e.g., ophiuroid mats)—and all at rates that are magnitudes faster than previously predicted. Some areas exhibit stark evidence of ecosystem decline, such as *Lophelia pertusa* coral reefs and methane cold seeps. Conversely, our time-series data have also shown some offshore habitats are serving as refuges, where healthy populations of critically endangered animals (e.g., *Pycnopodia helianthoides* seastars) have survived the decimation of a coastal climate-linked marine disease and deep-sea nursery grounds are so stable as to support species requiring over 4-year incubation periods. Key findings underscore species- and depth-specific responses to environmental pressures. Compelling before-and-after photographic evidence paired with oceanographic data highlights the transformations occurring otherwise 'out of sight and out of mind.' Our NEPDEP research and time-series data underscore the critical role of long-term monitoring in understanding deep-sea ecosystem resilience and vulnerability and informed conservation and restoration strategies to safeguard deep-sea biodiversity amidst a rapidly changing ocean.

O11B-4: Searching the One and Finding the Other: A Story of Corals, Hydrothermal Vents and Cold Seeps

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This talk tells the story of successful expeditions 2018 - 2024 studying Vulnerable Marine Ecosystems (VMEs). On an expedition with RV Maria S. MERIAN in 2018 we were searching for geothermal activity, but did find huge deep-sea coral reefs. Just recently, with RV SONNE in 2024, we did search for corals, but did find a mud volcano. Our findings unite one thing: hydrothermal vents, cold seeps, and cold-water corals (CWC) are VMEs and provide biodiversity hotspots for a unique fauna. We present research highlights of four expeditions embedded in international research projects like IceAGE (Icelandic marine Animals: Genetics and Ecology since 2011) and IceDivA (as UN ocean decade action), ALONGate (A Long-term Observatory of the North Atlantic Gateway to the Arctic Ocean 2024 - 2030) and CoWIO (Cold-water Corals of the West Indian Ocean 2024 - 2026) with the aim of contributing to the Challenger 150 UN ocean decade program. The study areas of these expeditions include the subarctic waters around Iceland, extend to the South in the North Atlantic and even towards the tropical West Indian Ocean along the continental margin of Africa. Based on video observations with Remotely Operated Vehicles (ROVs GEOMAR Phoca, Kiel6000 and MARUM Squid) we present an overview over newly discovered “shallow” (300– 000m depth) hydrothermal vents and cold seeps, new CWC reefs and single coral occurrences forming microhabitats with specific associated fauna. The comparison of the associated fauna inhabiting the different coral taxa using an integrative taxonomy approach was of specific interest.

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O11B-5：From Barriers to Biodiversity – Phylogeographic Patterns in Deep-Sea Isopods in Two Major Oceanic Regions

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The deep seabed is largely unexplored and presents a complex array of life forms with unique patterns of distribution and divergence. As human activities increasingly encroach on these remote environments, understanding the mechanisms driving species distribution and divergence becomes critical for effective conservation. Here, we present genetic diversity and biogeography of deep-sea Isopoda across the North Atlantic and Pacific oceans, focusing on the role of barriers such as ridges, trenches, and geographic distance in shaping species distribution. Specifically, we focus on the isopod families Dendrotionidae collected in the North Atlantic and Desmosomatidae and Nannoniscidae from the North Pacific. In the North Atlantic, the Mid-Atlantic Ridge (MAR) serves as a key biogeographic divide, shaping species differentiation. Additional factors, including water-mass distribution, productivity regimes, and historical climatic fluctuations, may further contribute to the observed distribution patterns in its abyssal isopod fauna. In the North Pacific and adjacent Bering Sea, we examine the genetic structure of isopods in the abyssal and hadal zones, identifying depth constraints, like the Aleutian Trench, along with geographic distance as important factors in species divergence. Samples were collected during several expeditions conducted between 2015 and 2022 exploring the sea floor in the North Atlantic as well as North Pacific. Via integrative taxonomy approaches, we identify patterns of diversity and isolation across these northern hemisphere deep-sea ecosystems. Our results underscore the importance of bathymetric barriers and geographic distance in shaping the genetic diversity of asellote isopod families. This research, in alignment with the goals of the UN Ocean Decade 2021–2030, enhances our understanding of deep-sea biodiversity and provides critical insights for mitigating the impacts of human activities on these vulnerable ecosystems.

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O12A-1: Thinking Deeply: Reflections on Experiences, Practices and Values in Deep-Sea Science

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Let's face it. Despite some recent glimmers of hope, the deep-sea science community is still lacking in diversity, inclusion, and equity. Diverse teams result in more innovative and effective problem solving, and likely higher-quality and more impactful science. As such, this prompts a need for a critical look at how deep-sea science is conducted globally in order to move towards a more inclusive and equitable future. In the hope of contributing to ongoing conversations, I will reflect on some of my experiences and learnings as a Caribbean deep-sea biologist, from project inception to at-sea research practice and taking science to policy.

O12A-2: Democratising the Deep Sea

Sheena Talma

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Deep-sea research in the Indian Ocean is crucial for understanding one of Earth’s least explored and biodiverse regions, which plays a vital role in global environmental health. However, this research is hampered by significant challenges, including limited technological infrastructure and high operational costs. In this presentation, I will examine the current state of deep-sea research in the Indian Ocean, focusing on the key players shaping the research agenda and assessing whether their efforts truly represent the region’s needs. By addressing these barriers, we can highlight the urgent need for enhanced collaboration, technological advancements, and sustainable funding to unlock the ocean’s mysteries and drive future discoveries.

O12A-3: "Costa Rica Desconocida" - A Campaign for Awareness and Cultural Integration of Deep-Sea Environments

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Costa Rica's territory is 92% ocean, with 97% of it being deep and largely unknown. The "Costa Rica Desconocida" campaign, translating to "Unknown Costa Rica," is a cross-disciplinary framework dedicated to raising awareness and integrating Costa Rica's deep-sea environments into the national consciousness. The campaign focuses on communicating the significance of deep ecosystems, introducing the general audience to the rich biological and geological diversity of Costa Rica Through a multimedia strategy including talks, fora, mural paintings, art exhibitions, and web platforms, the campaign aims to promote a cultural and intellectual appreciation of our deep environments among diverse national stakeholders. The "Costa Rica Desconocida" campaign responds to the growing volume of deep-sea footage generated by multiple expeditions, developing a multidisciplinary approach that could be replicated in other countries experiencing similar increases in deep-sea video, ensuring that the wealth of information gathered is used effectively in both scientific research and policy development. By fostering stronger connections between marine scientists and decision-makers, the campaign seeks to enhance ocean governance for a science-based marine management model aligned with the precautionary principle. As we explore the vast and mysterious depths of our ocean, we invite both nationals and foreigners to join us in safeguarding our deep-sea heritage and contributing to a forward-thinking marine governance framework for Costa Rica.

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O12A-4: ‘Dos’ in Deep-Sea Research: The Case Study of the Octopus Odyssey

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The deep ocean, poorly known and largely never seen by the human eye, currently represents 82% of area of all States’ jurisdictions and the vast majority of areas beyond national jurisdiction (ABNJ). Barriers in capacity have led to inequitable access to the open and deep ocean, as well as its resources. The *status quo* is near complete dominance by more economically developed countries, both scientifically as well as industrially. Power imbalances often lead to other problematic practices, including parachute or colonial science, tokenistic behaviour, harassment/bullying, as well as dependency on resources and infrastructure from more economically developed countries. Undertaking open-ocean and deep-ocean science can and must be reformulated to move away from tokenistic action and achieve fair, inclusive and equitable practices. Here, we share learnings from an important effort towards equitable deep-sea research, the ‘OctoMESS’ Project, which is researching the Costa-Rican deep. In this work, we critically assessed this project’s development and execution, including the missteps, challenges, successes and lessons learned, so that future efforts can bring the deep-ocean community collectively closer to achieving a more equitable ocean. We argue that by learning from past experiences, revisiting values and rethinking how science is made, including by whom and for whom, are key steps towards changing the status quo. We hope this case study can serve as inspiration for researchers to more readily share practices and opinions, and therefore act more reflexively before, during and after deep-sea expeditions take place.

O12A-5: Understanding Human Values and Risk Perceptions in Deep-Ocean Stewardship

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Understanding the risks associated with human impacts on deep-sea ecosystems is crucial for the sustainable stewardship and management of the deep ocean. Effective management of deep-sea spaces and resources requires more than technical risk assessments; it depends on individual perceptions of potential risks that guide decision-making. However, human values and emotions toward the deep sea are often overlooked, despite their significant influence on our commitment to marine stewardship and actions to protect these environments. This study explores how to incorporate human values and emotions into technical risk assessments within the context of ocean resource management, including deep-sea environments. It highlights the importance of understanding the factors that shape people's risk perceptions of maritime activities, which is essential for fostering a sustainable blue economy. Using an interdisciplinary approach, the research evaluates the relevance of current risk assessment methodologies and examines how people perceive the severity of impacts on deep-sea ecosystems and broader social-ecological systems. Focusing on offshore activities such as deep-sea mining and bottom fishing, the study analyzes public sentiments and the specific risk perceptions of scientists, environmental managers, and policymakers involved in assessing these activities. By examining these perspectives, the research aims to align technical risk assessments with personal risk perceptions, ensuring they reflect the values and emotions people hold towards the ocean. Ultimately, this study emphasizes the need for a holistic approach to risk management that integrates human dimensions into decision-making processes. By connecting public perceptions with principles of stewardship, it advocates for more comprehensive and sustainable management of deep-ocean resources, ensuring their preservation for future generations.

O12A-6：Enhancing the Voices of Deep-Sea Early Career Ocean Professionals – a Framework

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Recognizing the critical role that early-career professionals (ECOPs) play in shaping the future of ocean governance, there is a growing emphasis on enhancing their engagement, particularly those from developing countries, in key decision-making processes. However, the deep-sea - a vital yet often understudied area of ocean research and policy - requires more focused efforts to ensure that ECOPs are given the space and opportunity to share their voices, needs and challenges. Aware of the importance of engaging ECOPs more closely, the Deep Ocean Stewardship Initiative (DOSI) - a global network of deep-sea experts that aims to advise on ecosystem-based management of the deep ocean – is engaged in efforts to explore and identify pathways to strengthen the involvement of ECOPs withing the network and in the diverse fora for deep-sea decision-making. This oral presentation aims to share with a wider audience the results of such efforts by introducing to the public a framework adopted by DOSI to amplify the engagement of deep-sea ECOPs from around the world, in line with the mission of the United Nations Decade of Ocean Science for Sustainable Development to build a transformative and inclusive science for a sustainable ocean until 2030. We hope this presentation serves as an inspiration to other organizations and groups currently enrolled with deep-sea science and policy-making to further look into options to engage ECOPs. Finally, we expect this can be an opportunity to kickstart collaborations with individuals, especially ECOPs from developing countries.

O12B-1：Blue (Un)certainties: Deep-Sea Mining Policy Process in the Arctic Mid-Ocean Ridge, Norway

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Deep-sea biology is often presented as one of the key knowledge sources for deep-sea mining policy decisions. While deep-sea mining topic resulted in rich and diverse body of literature, there seems to be a lack of works that look at how scientific and expert knowledge is translated into policy. How are science and expert knowledge (and their uncertainties) translated for policy use? Therefore, in this paper, we analyze the opening process of the Norwegian Continental Shelf with attention to the policy context – the knowledge base and its uptake. We conduct document analysis, focusing on the Impact Assessment and the associated commissioned expert reports. The total document sample is 324,817 words. Through qualitative and quantitative text analysis, we find strong patterns of certainty/uncertainty dichotomy. This central theme indicates the tension between various knowledge uncertainties and the need for certainty for policy decisions. We find that in the impact assessment, uncertainties are dealt not with quantitative or qualitative methodological approaches to plan for future work, but rather verbally, by downplaying them, using irrelevant proxy studies or introducing generic mitigation measures. For example, we explore what enabled the following: how the impact of mining of inactive vents was concluded as having a small impact on benthic communities. In sum, uncertainty is a common component in the deep-sea mining context, from policy to biology. Yet, its political treatment in the Norwegian policy space is questionable.

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O12B-2 : Perspectives on Part II: Science-Policy Engagement, Challenges, and Opportunities for the Marine Genetic Resource Provisions of the BBNJ Agreement

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After almost two decades of negotiations, the United Nations Convention on the Law of the Sea on the conservation and sustainable use of marine biological diversity in areas beyond national jurisdiction (BBNJ Agreement; A/CONF.232/2023/) was adopted by consensus in September 2023. The BBNJ Agreement marks a new phase in global governance for the deep ocean. However, many details on the marine genetic resources (MGR) provisions of the Agreement and how the requirements may operate in practice are yet to be decided by the future Conference of the Parties to the Agreement (COP). This raises many questions but also provides a key opportunity for science engagement. The research and development (R&D) pipeline for MGR can be highly complex and it is important that the requirements are examined in this context. Here we focus on the required benefit sharing associated with MGR and associated digital sequence information (DSI), discussing consistency of the requirements with current scientific practice, and potential challenges for implementation. We develop scenarios for how the MGR requirements could be applied, covering a range of R&D activities and addressing areas of complexity, e.g. automation in collection and R&D; fishing-related activities and potential retroactive application of the Agreement. We explore how the new requirement of the BBNJ Standardised Batch Identifier could be implemented and integrated into scientific infrastructures, including databases and repositories. We explore opportunities for increased harmonisation in deep-sea science activities (e.g. data and sample sharing) and capacity development initiatives to both support practitioners and the implementation process. Awareness and engagement of the scientific community is crucial to an effective Agreement that achieves the stated objectives of benefit sharing and capacity development for activities relating to MGR, and ultimately the conservation and sustainable use of marine biodiversity.

O12B-3: The Ghost Net Movement Raises Awareness on the Vulnerability of Deep Sea Habitats

Lynette Griffiths, Marion Gaemers, Virginie Tilot

https://www.ghostnetcollective.com.au/

The Australian "Ghost Net Art movement" began in 2009. Lynnette Griffiths and Marion Gaemers went on to form the Ghost Net Collective in 2020, they create Art from abandoned industrial fishing nets and associated marine debris to raise awareness on the vulnerability of marine species and habitats. This movement is rapidly expanding worldwide, striving to generate awareness to the state of world oceans. Virginie Tilot fosters the movement to go deeper with the urgency to address the vulnerability of deep sea ecosystems to cumulative human impact with an oceanian community based creative approach.

The movement expanded with the collaboration of indigenous and non-indigenous artists to achieve common goals on raising awareness that recognise and celebrate cultural diversity. These artists are recycling and bringing sustainability options that will share and raise awareness on rogue fishing gear, industrial fishing nets and associated marine debris, that destroys marine species and habitats. The Ghost Net Collective are weaving and stitching massive installations that engage with conservation groups, children, museum's and collectors on a world stage. It is an "ocean-centric" arts practice with a recycling, educational and global philosophy connecting conservation to community, education, personal connection, cross cultural linkages to creating Art.

Large-scale industrial fishing operations are the source of vast amounts of marine pollution. 46% of the total amount of plastic floating in the world's oceans has its origins in industrial fishing practices. Ghost nets drift aimlessly, indiscriminately killing as they travel with the ocean currents or clogging benthic fauna and destroying habitats. According to a recent World Wildlife Fund for Nature report, since 1970, barely 50 years ago, 90% of marine life has disappeared due to human activity, directly or indirectly. The ultimate and important message is that no place on earth is immune and time is running out.

Through a shared vision of the world connected by oceans and belief in the opportunities for regeneration that repurposing presents, the Ghost Net Collective's immersive woven and stitched installations raise awareness of the dangers of environmental marine pollution, both in their own home waters and throughout the world's oceans.

The aim through Art, education and science is to weave together a process that will embed an understanding of cultural storytelling and its relationship to place whether that is shallow waters or the more unknown ocean depths. Through Science, Art and Education, the collective hopes to connect people, understand the greater world position on rogue fishing gear and by creating visually stimulating and thought provoking works, open opportunities and a platform for discussion.

O12B-4: A Different Approach to The Research Internship

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The Monterey Bay Aquarium Research Institute (www.mbari.org) has been running an internship program since 1997 – the primary purpose of the internship program is to provide for the specific educational benefit of the intern and to make a contribution to the general good of the oceanographic community (with a wide range of potential projects focused on science, engineering, and/or education). During the ten-week program, interns will work on their specific research projects and also interact with other interns and mentors working on different projects. This helps emphasize the peer relationships between scientists and engineers, part of MBARI's mission. While some internship programs focus on trying to get more students into the discipline, MBARI wants to help the interns find what research is really about and where their interests lie. In some cases this has meant that exposing an intern interested in research to the sometimes harsh reality of oceanographic research (a lot of laboratory and computer time will be required) means that an intern may decide to switch careers. While this might be considered an adverse outcome in other internship programs, MBARI views this as a 'win' for both the intern and the oceanographic community. The MBARI program is unique in that it is open to undergraduates, graduate students, and educators – both domestic and foreign. It is a ten-week program (originally started as a 12-week program but reduced to ten weeks to better fit academic calendars of the interns). The funding for the program is internal and MBARI budgets support for up to 12 interns although we have had as many as 19 interns in one summer. Support for additional interns comes from external grants and partners. At the conclusion of the summer, all of the interns give formal presentations.

O12B-5: A Streamlined Data Pipeline for Image Contribution and Archiving in FathomNet

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FathomNet, a community resource for sharing high-quality, expert-annotated image training sets focused on marine life, has a new feature for seamless user contributions to the National Oceanic and Atmospheric Administration's National Centers for Environmental Information (NOAA-NCEI) archive. This presentation will showcase the user-friendly process for submitting annotated image sets to FathomNet, enabling researchers and scientists to effortlessly contribute valuable data to a permanent public archive.

Benefits:

● Simplified Submission: The FathomNet data pipeline streamlines the process of submitting image sets to NOAA-NCEI, removing technical barriers for data contribution.

● Public Availability: Images submitted through FathomNet become publicly accessible, fostering collaboration and knowledge sharing within the marine science community.

● Long-Term Archiving: NOAA-NCEI ensures the secure storage of submitted images for 75 years, guaranteeing data preservation for future generations of researchers.

● Expert-Annotated Training Sets: FathomNet leverages the expertise of marine scientists to provide high-quality, annotated image sets that benefit the development of advanced machine learning models for oceanographic research.

This data pipeline empowers a broader range of participants to contribute to critical marine image datasets. By facilitating data sharing, long-term archiving, and the creation of expert-annotated training sets, FathomNet fosters advancements in marine research, promotes open access to valuable deep-sea image data, and accelerates the development of powerful AI tools for ocean exploration and discovery.

O12B-6: Sustainability and the Common Heritage of Humankind: What It Means to Safeguard the Area for Current and Future Generations

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The deep seabed beyond national jurisdiction, known as the Area, is recognized as the common heritage of mankind under international law. A core element of this principle is the requirement to preserve the Area and its resources for current and future generations. But what does it mean to preserve these resources "for current and future generations," and does this obligation carry legal weight?

My paper examines the legal implications of this requirement, arguing that it imposes distinct obligations on both states and the International Seabed Authority (ISA), the international body responsible for managing the Area. The preservation for current and future generations connects with the principles of intergenerational and intragenerational equity and sustainability, shaping how the common heritage of mankind principle is understood in the modern era of deep seabed mining.

In doing so, the paper explores the ISA's mineral production policy, addressing the management of deep seabed minerals as a non-renewable resource. Sustainable management, in this context, means that resources cannot be fully depleted by the present generation but must be used in a way that leaves sufficient reserves for future generations. This requires the ISA to carefully balancing of economic development and resource conservation when developing its mineral production policy.

The second obligation emerging from this requirement is reflected in the specific the obligations of states, the ISA, and contractors when conducting activities in the Area, to protect the marine environment. These obligations include ensuring that the marine environment is preserved, minimizing harm to deep-sea ecosystems, and implementing effective conservation measures. This analysis highlights how the preservation requirement for future generations is intertwined with broader environmental sustainability goals.

In conclusion, the requirement to preserve the Area for current and future generations carries substantial legal weight, promoting a framework of equitable, sustainable resource use and robust environmental protection in the governance of deep seabed activities.

C.

ABSTRACTS OF POSTER PRESENTATIONS

P1-1: Integrative Taxonomy of the Southwest Atlantic Dragonfishes and Their Allies (Stomiiformes), Revealing of a New Species

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Stomiiformes includes more than 450 species of meso- to bathypelagic fishes classified in 53 genera, and the following four families: Gonostomatidae, "Phosichthyidae", Sternoptychidae, and Stomiidae. The dragonfishes are among of the most iconic deep-sea fish, and the common name recalls the mythical Chinese dragons, because of their body ornamented with photophores that can produce either blue/green or red/orange bioluminescence, the head with a large mouth sometimes armored with fangs, the well-developed eye that can detect even the minimum intensity of light, and a chin or hyoid barbel with a bioluminescent lure. Up to date, 116 species from the four families had been recorded in the Southwest Atlantic. For the first time, a taxonomic revision of the Southwest Atlantic stomiiforms is being conducted combining integrative taxonomy, allying the traditional morphometric and meristic taxonomy to modern techniques of DNA barcoding and microtomography. The specimens were obtained during the cruises conducted onboard the RV Alpha Crucis off southern Brazil, natural history museums, and collections. The COI fragments were amplified and sequenced using universal primers, and the sequences compared to others available on-line in public databases. A phylogenetic tree of maximum likelihood was constructed using the RAxML software and the inter-and-intraspecific distances were calculated using the K2P model. The 3D reconstructions were obtained from images produced by high resolution x-ray computed tomography produced by a ZEISS Xradia Versa XRM-510, using. A total of 15 species were investigated, including eight stomiids, four gonostomatids, and two sternoptychids Molecular data revealed a high genetic divergence within the stomiiforms (mean K2P=25% +- 1.6). Our results confirm the occurrence of 14 previously recorded species and a new species of Photonectes Günther, 1887 that is currently being described based on molecular and morphological evidence.

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P1-2: Characterization of Biofluorescence in Deep-Sea Fishes Collected off Southern Brazil

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Biofluorescence occurs when an organism absorbs high-energetic electromagnetic radiation (i.e., UV or blue light) from the environment, and re-emits light at a longer, lower-energetic wavelength (green, yellow, or red). In oceanic waters, the sunlight is rapidly attenuated at shallow depths (< 50m), resulting in a spectrally restricted, blue-shifted illumination (450–480 nm) that reaches the dim twilight zone (200–1,000m). Our collections were made onboard the Brazilian N/Oc Alpha Crucis in depths between 150 and 1,500 meters using bottom trawling. To simulate the natural conditions, soon after the collection, the specimens were brought into a dark room and exposed to a 470 nm wavelength blue light. Then, if present, biofluorescence was recorded using an Ocean Optics Flame spectrometer and the specimens were photographed. Biofluorescence was observed in species collected up to 900 meters, including two synodontids and two chlorophthalmids (Aulopiformes), a bembropid, a serranid and a setarchid (Perciformes), a mullid (Mulliformes), a centriscid (Syngnathiformes), and two scyliorhinid sharks (Carcharhiniformes). Only green biofluorescence was observed, with peaks ranging from 501 to 523 nm, in structures such as the eye iris and crystalline lens, and the skin. The unique lightening conditions of the twilight zone drove the independent evolution of biofluorescence in fishes that are capable to transform the ambient blue-light into wavelengths otherwise absent in the environment.

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P1-3: Rissoid Snails (Gastropoda: Rissoidae) From Arctic Chemosynthesis-Based Ecosystems

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One of the most common taxa inhabiting Arctic chemosynthesis-based ecosystems (CBEs) are microgastropods of the family Rissoidae Gray, 1876. However, their diversity, taxonomy and ecology remain understudied. Rissoidae has a complex taxonomy, with a recent phylogeny revealing that many genera are non-monophyletic. We aim to delimit the rissoid species in Arctic CBEs and infer their phylogenetic position within Rissoidae. The examined material was collected from hydrothermal vents, cold seeps, colonization experiments using bone and wood substrates, and a natural whale fall. DNA sequences were obtained for three molecular markers (COI, 16S and 28S) for species delimitation and phylogenetic analyses. Based on a combination of morphological and molecular data, we identify several species of rissoids from Arctic CBEs. One of the species corresponds to *Rissoa griegi* Friele, 1879, originally described from a deep-sea wood fall near Svalbard, Norway, and here shown to be broadly distributed in other Arctic and sub-Arctic CBEs. The other species have a more restricted distribution, possibly controlled by species-specific habitat preferences. Our updated phylogeny of the family Rissoidae (16S, 28S) confirmed that many genera are non-monophyletic and supported that rissoids from Arctic CBEs do not belong to the genus *Rissoa*; instead, they form a monophyletic clade which may constitute a new genus.

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P1-4: Three New Species of Deep-Sea Wood-Associated Sea Stars (Asteroidea: Caymanostellidae) from the Eastern Pacific

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Caymanostellidae is a group of rarely collected and morphologically unusual sea stars that have been exclusively encountered on wood falls in the deep sea. There are currently 3 genera and 7 species described, occurring in the Atlantic, Pacific and Indian Oceans with a depth range between 418 and 6780 m. Three new species are here described from specimens collected from wood falls in multiple localities across the Pacific margin of Costa Rica and near the Gulf of California (Mexico): *Caymanostella scrippscognaticausa* n. sp., *Caymanostella davidalani* n. sp. and *Caymanostella loresae* n. sp. These records expand the known geographical distribution of caymanostellids and constitute their first report from wood falls found at methane seeps. This study also includes the first descriptions of early-stage juvenile caymanostellids, which reveals that traits previously considered useful for diagnosis might represent intra-specific ontogenetic variability, with important consequences for caymanostellid taxonomy.

P1-5: Southwest Indian Ocean Ridge Seamounts: What Influences Changes in Diversity

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Despite the prevalence of seamounts in the global ocean they are often described as unique underwater features. The size and topography of the seamounts can influence circulation, internal waves as well as deflecting ocean currents and some seamounts associated with increased levels of productivity. Seamounts are often observed to have high levels of diversity which support a range of benthic assemblages and communities, including e.g., corals, polychaetes, echinoderms and fish with the latter found in large aggregations and hence increasing the economic importance of the seamount.

To date seamount ecology and biodiversity research has focussed on areas of the Atlantic and Pacific oceans and comparatively little in the southern Indian Ocean. In this study five seamounts situated on the Southwest Indian Ridge were examined. The south-west region of the ridge is located under an area of relatively high productivity, whilst the north-east is characterised by relatively low productivity and weak currents. The seamounts along this ridge system have provided us with an opportunity to investigate the macrofaunal benthic community across multiple variables including changes in primary productivity and substratum type.

The benthic samples were collected from a variety of substrates ranging from mobiles sediments and coral rubble through to more complex and heterogeneous substrates such as coral gardens e.g., octocorals, and cold-water coral reefs i.e., scleractinian corals. More than 8,000 individuals classed as macrofauna were sorted to putative species level arising from 16 phyla, which included 40 polychaete families, 26 families of isopods and 20 amphipod families. Whilst levels of diversity and community composition and similarity were explored, whilst functional traits were also investigated.

Combining community composition with diversity and functional traits allows us to provide a more holistic understanding of how changes in habitat characteristics arising from possible ferro-manganese mining, fishing and climate change may impact on biodiversity.

P1-6: Newly Discovered High Diversity of Cold-Water Corals along the Continental Shelf Margin of Northwestern South China Sea

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Scleractinian cold-water corals (CWCs) are one of the most important habitat engineers of the deep sea. Although the South China Sea (SCS) abuts the biodiversity center of scleractinian CWCs in the western Pacific, only a few sporadic records are available. We discovered new CWC sites by means of trawl sampling and video observation along the continental shelf in the northwestern SCS. All trawled scleractinian CWC specimens were identified to species level according to skeleton morphology and structure. The living CWCs and associated fauna recorded in the video were distinguished at a higher level of classification. Scleractinian corals were identified to genus level, while non-scleractinian CWCs were identified to family level and given generic names such as gorgonian corals, bamboo corals and black corals. Associate benthic dwellers were divided into major categories. A total of 28 scleractinian CWC species were identified to 7 families and 15 genera and 1 additional subgenus. Among them, 13 species were colonial, including important habitat-forming species in the genera *Eguchipsammia, Dendrophyllia and Cladopsammia*. Non-scleractinian CWCs were identified to 7 families, which consisted of 4 families gorgonian corals, 1 family bamboo corals and 2 families black corals. Gorgonian corals were the most abundant non-scleractinian CWCs in this region. Meanwhile, starfish, sea anemones, fish, gastropods, echinoderms and other associated benthic fauna were recorded in the CWC habitats, with starfish belonging to the order Brisingida being most commonly found. New scleractinian CWC assemblages were discovered along the continental seabed mounds in the northwestern SCS. This study summarizes remarkable diversity of cold-water scleractinian corals in the whole SCS, shows the potential widespread and conservation prospect of CWC habitats in this region.

P1-7: A New Genus of Ectoparasitic Myzostomida from the Pacific Abyss

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The Myzostomida von Graff, 1887 are a small order of parasitic marine annelids, with only around 170 species described to date. This specialised group is associated with echinoderms and anthozoans, with most species living on or inside crinoids, and very few on asteroids and ophiuroids. Co-evolutionary analyses have indicated a strong phylogenetic relationship between myzostomids and their hosts, however there is limited data available on the relationships been these parasites and asteroid hosts. There are currently seven described families within the order, of which two – Asteriomyzostomidae and Asteromyzostomidae – are characterised by being endo- and ectoparasitic on asteroids respectively. Here we describe a new genus and two new species of Asteriomyzostomidae, the first species' of Myzostomida described from abyssal depths. Specimens were found infecting the dorsal surface of the starfish *Styracaster paucispinus* Ludwig, 1907, at abyssal depths in the equatorial Pacific Ocean, and on the dorsal surface of the starfish *Eremicaster crassus* (Sladen, 1883) in the Aleutian Trench. An integrative taxonomic approach was undertaken, including microCT scanning of individual myzostomids, and specimens attached to a host, allowing for a complete understanding of the species morphology.

P1-8: Bathymetric Zonation and Speciation in Ocean Trenches: The Case of Northwestern Pacific Bivalves

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Trench is an oceanic topography encompassing the deepest points on Earth. Past trench explorations revealed highly endemic species assemblages and led researchers to distinguish the trench fauna from the shallower abyssal fauna and to name its distribution range the hadal zone. However, difficulty of sampling and low population density have hampered detailed understanding of their diversity, distributions and speciation. Here we focus on Bivalvia, an exceptionally abundant taxon in the Japan and Kuril–Kamchatka Trenches off northeastern Japan, to overcome these fundamental obstacles.

A total of over 16,800 bivalve specimens, collected from 32 stations below 5,000 m deep with beam trawls and an epibenthic sledge, were classified into 38 species based on combined morphological and genetic criteria. Species composition analysis showed a clear faunal difference between 16 shallower (5,013–6,562 m) and 13 deeper (6,646–8,014 m) stations, identifying the boarder of the abyssal and hadal zones for the first time with quantitative data at around 6,600 m. The community structure within each zone was also correlated with depth but not with other factors including latitude and topographic setting.

Two closely-related pairs of species exhibited vertical segregation (Neilonella spp.: 5,313–6,539 m and 6,669–8,014 m) or a slight overlap in the lowermost abyssal zone (Bathyspinula spp.: 5,110–6,562 m and 6,522–7,654 m). Most interestingly, the hadal ones of the species pairs did not show population genetic structuring despite their apparently discontinuous distributions as benthic adults with a shallow (6,280 m) gap between the Japan and Kuril–Kamchatka Trenches. Depth-driven ecological speciation in the face of gene flow seems to be prevalent among bivalves in trenches with ontogenetic vertical migration and dispersal as lecithotrophic swimming larvae.

P1-9: An Investigation into the Biodiversity of Deep-Sea Wood Falls in Montserrat

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Wood falls are large organic materials that provide a source of food, substrate and shelter to the deep-sea floor. The decomposition of wood falls is known to support a succession of, often novel, specialist, opportunistic and chemosynthetic fauna. However, due to the lack of deep-sea research capacity, knowledge of deep-sea habitats, within the Caribbean, including of wood falls, is limited. Montserrat is a tropical wooded island within the Caribbean that has been subjected to multiple volcanic eruptions and hurricanes impacting both shallow and deep-water ecosystems. It is thus highly likely that many wood falls not only exist but also contribute to the diversity and function of the deep sea. In this research, we assess ROV imagery of numerous naturally-occurring wood falls in Montserrat. Additionally, taxonomic and community analyses were undertaken on several of these wood falls and their inhabiting fauna, which were collected from Montserrat's deep sea. These diverse communities include previously undiscovered fauna and provide valuable and rare biological knowledge from the Caribbean deep sea.

[The present work was supported by the Pew Fellows Program in Marine Conservation at The Pew Charitable Trusts.]

P1-10: Geographical Subdivision of the Hydrothermal Vent Bythograeid Crabs in the Indian Ocean

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Brachyuran crabs of the genus *Austinograea* are the endemic species of the deep-sea hydrothermal vents with widespread distribution in the western Pacific and the Indian Ocean. To date, only one species was reported in the Indian Ocean, *Austinograea rodriguezensis*. In this study, we investigated the population connectivity of bythograeid crabs of the genus *Austinograea* in the Indian Ocean. Mitochondrial COI sequences were collected from the seven vent fields. The bythograeid crabs were separated geographically into northern and southern groups, which showed high level of genetic distance (>5% in COI gene) between them. Each group had a high sequence similarity (>99%) with *A. rodriguezensis* and undescribed *Austinograea* species reported in the Carlsberg ridge in the northern Indian Ocean, respectively. Interestingly, the two groups were observed to co-occur at the Onnuri vent field. This study suggests speciation of the brachyuran crabs of genus *Austinograea* in the Indian Ocean.

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P1-11: Filling in the Missing Pieces of the Global Phylogenetic and Biogeographic Puzzle of Deep-Sea *Amphisamytha* (Annelida, Ampharetidae): Insights from the Northwest Pacific

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Deep-sea ecosystems are threatened by the increasing human activities, but for most deep-sea animals, the diversity, divergence history and biogeographic patterns remain poorly known. Recent studies have shown members of the annelid genus *Amphisamytha* (Annelida: Ampharetidae) to be widely distributed in deep-sea chemosynthetic environments, yet to understand their global diversity and biogeographic patterns and evolutionary history requires the study of samples from the major world ocean basins. Here, we described four new species of *Amphisamytha* from the northwest Pacific (NWP) based on morphological and molecular analyses: *Amphisamytha izuensis* sp. nov. inhabits the hydrothermal vents of the Izu-Ogasawara Arc, *A. jiaolongensis* sp. nov. inhabits the Jiaolong methane seep in the South China Sea, *A. okinawensis* sp. nov. inhabits the sedimented vents of the Okinawa Trough, and *A. rousei* sp. nov. occurs on both cold seeps of Sagami Bay and hydrothermal vents of the Okinawa Trough. Our global molecular phylogenetic analysis supports the monophyly of the deep-sea *Amphisamytha*, revealing the split between the deep-sea clade with 11 species from its shallow-water clade in the Early Eocene, the divergence of the deep-sea Amphisamytha into three major clades in the Late Eocene to mid-Oligocene in the world oceans, and the most recent radiations in the Miocene, and highlight the importance of sedimented vents during the habitat shift in the evolution history of deep-sea fauna. The recent radiation of *Amphisamytha* from the Early Eocene adds to the list of chemosynthetic fauna that appear to have diversified after the Palaeocene/Eocene Thermal Maximum. Our ancestral area analyses inferred that the present *Amphisamytha* originated from the East Pacific, followed by vicariance speciation, allopatric speciation, and transoceanic dispersal. Our study reveals the complex speciation and distribution patterns of *Amphisamytha*, and illustrates how plate tectonics and local niche specialisation may have structured the faunal biogeographic patterns of t chemosynthetic habitats.

P1-12: Deep Pacific Relations: Towards a Phylogenetic Revision of the Isopod Genus *Nannoniscus* G.O Sars, 1870 Linking Morphology and Genetics

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The genus Nannoniscus G.O Sars, 1870, belonging to the deep-sea isopod family Nannoniscidae Hanse, 1916 (Isopoda, Asellota), is known for its worldwide distribution, especially in deep-sea environments, and includes over 30 described species with a high degree of morphological diversity. In fact, in a recent study, the genus was classified as polyphyletic, characterized by both ancestral characters (plesiomorphies) common to the Nannoniscidae and unique derived characters (synapomorphies) specific to a certain clade within the family - including Nannoniscus, Regabellator Siebenaller & Hessler, 1981 and Rapaniscus Siebenaller & Hessler, 1981 amongst others. Contrastingly to the well-supported monophyly of the Nannoniscidae, the marked diversity in morphological characteristics renders Nannoniscus a highly heterogeneous group, further complicating its classification and differentiation from other genera in the family. Therefore, a thorough assessment is required to elucidate phylogenetic relationships in the genus. We designed a (still ongoing) study aimed at unravelling the systematic and phylogenetic issues surrounding the genus Nannoniscus, with a particular focus on species from the Pacific Ocean, including newly collected specimens from North Pacific trenches. Our approach integrates morphological and genetic data, encompassing the description of new species and examination of type specimens, to provide evidence that refines the genus' definition. This research aims to enhance our understanding of Nannoniscus' evolutionary history and its systematic positioning within the Nannoniscidae.

P1-13: Seafloor Observation Using Underwater Drone in Torigakubi Spur, Japan Sea

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A survey of seafloor organisms was carried out on June 20, 2024, in the vicinity of methane upwelling sites in Torigakubi Spur, offshore Joetsu, Japan, using a FullDepth underwater drone at 570m water depth. The results of the survey are reported using video images taken by the underwater drone. Despite the absence of active methane ebullition, microbial mats provided evidence of elevated methane flux. Additionally, fresh exposures of gas hydrate were noted in disturbed areas of seafloor sediment.

With regard to the fauna observed on the seafloor, specimens of squid, snow crab, and shrimp were noted. Of particular interest were the defensive movements exhibited by several squids in response to the presence of the underwater drone. In addition, during the two drone deployments, a variety of invertebrate sea life was noted, including; tunicates, sea cucumbers, stem corals, and gastropods. A variety of fish species were also present, including deep-sea ocean pout (genge). The stem corals were present both individually and with several species attached as epibionts on each other. The FullDepth underwater drone was able to observe small coral polyps and other features on the seafloor without disturbing the seafloor sediment as would occur with larger ROV equipment.

Further research is required to characterize the complex ecosystems associated with gas seeps along the margins of the Japan Sea.

P1-14: Diversity of Demosponge Fauna in the Abyssal Nodule Fields of the Eastern Clarion-Clipperton Zone, Pacific Ocean

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There are more than 7000 demosponge species described globally but less than 2% are known from the deep-sea abyssal plains, which occupy 50% of the Earth's surface. The Clarion-Clipperton Zone (CCZ) in the Pacific Ocean, an area of interest for deep-sea mining, exemplifies this gap in knowledge. Over 1000 demosponge samples were collected using box core from 66 stations in the polymetallic nodule fields of the eastern CCZ. Morphological and molecular analyses identified 21 species across 13 genera, nine families, and seven orders, most of which are new to science. These demosponges are mostly small (less than 5 mm), with simple skeletons and poor spicule diversity. Notably, *Plenaster craigi*, the most common and abundant species in this region, averaging over 25 individuals per square meter, represents a new family, and possibly a new order. Interestingly, *P. craigi*, along with other filter-feeding species from the Polymastiidae and Hamacanthidae, are far more abundant in nodule fields than the carnivorous sponges (Cladorhizidae) which was widely known to be the most dominant demosponge group in the abyssal depths.

P1-15: Assessing the State of Knowledge and Charting a Path for Deep-Sea Scientific Research in Barbados

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For less economically developed countries and Small Island Developing States (SIDS), the deep sea remains a difficult ecosystem to study, given that the extreme conditions require expensive technology and there is often limited expertise at the national level. Many Caribbean SIDS have an Exclusive Economic Zone (EEZ) that is predominated by the deep sea, and without comprehensive baseline information on deep-sea ecosystems, there will be a lack of evidence-based decision-making. Barbados, the subject of this research, has within its EEZ a deep-sea environment ranging between 200 - 5,500 metres, which accounts for 99.8% of the area. This work assesses the state of knowledge of deep-sea science in Barbados' EEZ and proposes a path forward to fill the gaps in this area. A comprehensive review of species records from scientific literature, museum databases, fisheries reports, cruise reports, reference collections, and online databases was undertaken. Here we discuss trends in the limited existing knowledge and propose priority areas for future research, especially given past deep-sea studies undertaken in Barbados left little baseline information or capacity in country. This research is particularly critical as Barbados is presently in the initial phases of developing a comprehensive Marine Spatial Plan (MSP) for its EEZ. Closing remaining deep-sea scientific gaps will be a monumental task that will require clear direction, substantial resources, and robust coordination and collaboration. We therefore suggest a potential high-level road map of activities that could be taken.

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P1-16: Remarkable New Findings of Deep-Sea Bivalve Diversity in the Abyssal Pacific Ocean

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With a growing interest in extraction of resources from the deep sea such as bioprospecting of genetic diversity and metals, society is concerned with protection and conservation of deep-sea biodiversity. Most deep-sea species are undescribed and their distribution in general not well understood. Authorities such as the International Seabed authority and any new authority tasked with the new BBNJ legislation will need species registers and distribution maps to assess the risk of extinction and enforce conservation measures such as protected areas of representative ecosystem and species diversity. Since most species are small, cryptic and with low abundances sampling is challenging requiring dedicated ship time on long cruises to remote areas. Using molecular and morphological data we investigated a sample of 277 bivalves from the two exploration contract areas UK1 and NORI-D in the eastern part of the Clarion Clipperton Fracture Zone (CCZ) in the Central Pacific Ocean collected during seven scientific cruises between 2013 and 2023. All individuals but four were successfully sequenced for either one or both of the molecular markers 18S and COI. We had evidence to assign 88 specimens to the described species *Vesicomya galathea* (45), *Ledella knudseni* (2), *Bathyspinula calcar* (6), *Nucula profundorum* (32) and *Dacrydium panamense* (3). 36 individuals found attached to nodules were similar to *Bentharca asperula* but lack of data from the type locality in the western Atlantic provided no evidence in support of the hypothesis that they belonged to this species. Phylogenetic reconstructions based on molecular data from all the sequenced specimens suggested that the remaining 153 individuals were distributed among a little over 40 species new to science. The resulting trees also indicate that the sampled individuals, being just a few millimeters in size, represent most of the known phylogenetic diversity of Bivalvia including the subclasses Heteroconchia, Protobranchia and Pteriomorphia.

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P1-17: Molecular Diversity and Distribution of Tube-Dwelling Serpulid Worms in the Abyss

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Clarion Clipperton Fracture Zone (CCZ) in the Central Pacific Ocean is an area of interest for deep-sea mining of the polymetallic nodules that lie on the abyssal ocean floor. The deep-sea fauna that lives there and may be disturbed by mining is not yet very well documented although this work is in progress. Among the many annelid taxa living in the area, worms from the family Serpulidae might be more impacted than others as many of them live attached to the polymetallic nodules, and yet the deep-sea serpulid community in the area is poorly surveyed and recorded. In this study we have examined over 500 serpulid specimens from the eastern part of the CCZ collected at several scientific cruises between 2013 and 2023. The molecular results in our study shows that the deep-sea serpulid community in the area demonstrates substantial diversity, with all subdivisions of the Serpulidae family - Filograninae, Spirorbinae and Serpulinae - represented. Some of the species seem to have broad distribution ranges with molecular matches from e.g. Australian deep-sea communities.

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P1-18: Shape Matters: Application of Geometric Morphometric Techniques in Deep-Sea Isopod Taxonomy (Asellota: Macrostylidae)

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The deep-sea isopod family Macrostylidae consists of a single genus, *Macrostylis*, which exhibits morphological homogeneity despite significant genetic diversity. These isopods have a global distribution and span an extensive range of depths from approximately 30 m to 11,000 m. There are currently 87 described species of macrostylid isopods (WoRMS, 2024), though this is an underestimate of true species diversity as there are numerous new species pending description. Historically, taxonomic classification within Macrostylidae has relied on linear measurements and morphological variation to distinguish species. However, with the use of molecular genetic techniques, several species have been found to be synonymous: *M. ovata* with *M. grandis*, and *M. subinermis* with *M. longipes*. These taxonomic discrepancies are in part due to the striking morphological similarity observed in the genus and in part due to the varying degrees of sexual dimorphism observed. However, despite its advantages, molecular genetics isn’t always feasible and can be both time and cost intensive. More recently, geometric morphometrics has gained popularity in the taxonomic toolset. This technique is excellent at detecting subtle shape differences that get overlooked by traditional methods. This technique uses Cartesian coordinates and statistical analyses to capture and quantify shape variation. Geometric morphometrics has been successfully applied to delimit cryptic species, discover new species and explore other evolutionary questions across various taxa. However, this technique has not yet been used in macrostylid isopods. In our research, we use an integrative approach that combines geometric morphometrics, traditional morphometrics and molecular genetics to study macrostylid isopods. Our application of geometric morphometric techniques has resulted in the discovery of a new species and has provided further insight into the subtle shape differences that differentiate macrostylid isopods. Future analyses will continue to employ geometric morphometrics to identify diagnostically informative characters, investigate sexual dimorphism, study morphological variation and discover new species.

P1-19: Delving into the Depths: Investigating the Deep-Sea Biodiversity of the Tubbataha Reefs Natural Park, Philippines

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The Tubbataha Reefs Natural Park (TRNP), a UNESCO World Heritage Site in the Sulu Sea, Philippines, is renowned for its extraordinary marine biodiversity, yet its deep-sea ecosystems remain largely unexplored. Between May 31 and June 4, 2022, we conducted the first visual assessment of TRNP's deep-sea biodiversity employing innovative technology from the National Geographic Society Exploration Technology Lab. Using deep-sea camera systems, we documented biodiversity across five locations within TRNP at depths ranging from 1,037 m to 2,599 m, with most deployments on soft seabed substrates. A total of 14 species were documented, including invertebrates such as giant isopods, shrimp, sea cucumbers, sponges, and soft coral, along with demersal bony fishes and three species of elasmobranchs. The Leafscale gulper shark (*Centrophorus squamosus*) was observed on three occasions between 1,870 m and 2,588 m with a MaxN of three individuals. False catsharks (*Pseudotriakis microdon*) were encountered on two deployments at 2,255 m and 2,588 m. A third catshark species was also observed at 1,697 m, but due to the low quality of footage and subtle morphological differences, its identification is pending further confirmation. This expedition revealed the presence of Vulnerable Marine Ecosystem (VME) indicator species and species previously unrecorded in the area. Additionally, the presence of marine debris on the seafloor underscores the ecosystem's vulnerability to anthropogenic activities. Notably, observed *C. squamosus* species are exploited by a local fishery within the same municipal waters. These findings underscore the urgent need for their inclusion in conservation strategies. The study also emphasizes the necessity for local access to low-cost deep-sea technology and expertise to enhance understanding of deep-sea biodiversity within the region.

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P1-20: The Biodiversity of Hadal Holothurians in the Japan Trench and the Southern Kuril-Kamchatka Trench

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Hadal ecosystems occupy trench regions below 6000 m depth and are known for their high degree of endemism. Holothuroidea (Echinodermata) is the most dominant taxon in the hadal fauna in terms of both species richness and biomass. Izu-Ogasawara, Japan (JT), Kuril-Kamchatka (KKT) and Aleutian are four trenches in the Northwest Pacific that are classified as the Aleutian-Japan hadal biogeographical province. However, among these trenches, benthic biodiversity surveys have been conducted mainly in KKT, and to date, 23 and 6 hadal holothurian species are known from KKT and JT, respectively. At the junction of KKT and JT, the Erimo Seamount subducts and divides the hadal habitat into north and south, making it an ideal region to study the evolutionary and biogeographic effects of seamount subduction into trenches on trench faunal biodiversity. This study aims to update the understanding of the hadal holothurian fauna of the southern KKT and northern JT, based on more than 3000 individuals of hadal holothurians collected during two research cruises conducted by the R/V *Hakuho Maru* (JAMSTEC and the Atmosphere and Ocean Research Institute, the University of Tokyo; KH-22-8, September-October 2022; KH-23-5, September-October 2023). Surveys were conducted by beam trawls or an epi-benthic sledge. A total of 13 casts were conducted in KKT (depth range 6093-7288 m) and 16 casts in JT (6169-8018 m), resulting in the recognition of 18 and 23 species from southern KKT and JT, respectively. A comprehensive holothurian fauna in the hadal depths of the JT was revealed for the first time, and taxonomic and biogeographical information was updated for more than 10 holothurian taxa, including undescribed species. It suggested that the species richness of Holothuroidea in the JT has been underestimated and masked by survey bias. Most hadal holothurian species were shared between the southern KKT and the northern JT.

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P1-21: A Biogeographical Inventory of Benthic Macrofauna Based on Long-Term Observations in the Arctic Ocean

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As the Arctic undergoes unprecedented transformations due to climate change and anthropogenic pressures, a comprehensive understanding of deep-sea benthic biodiversity and its connectivity patterns is a priority for supporting conservation strategies and decision-making. The presented work inventories benthic macrofauna diversity based on 25 years of annual benthic sampling with diverse gears (Box Corer, Agassiz Trawl) in the long-term HAUSGARTEN observatory in the North Atlantic Gateway to the Arctic Ocean and is, thus, a profound and new baseline for monitoring future changes. The observatory is strategically located within the Fram Strait, the only deep passage to the Central Arctic Ocean, where the variety of water masses is mirrored in a biogeographic transition zone of faunal communities: a boreal community influenced by warm, saline North Atlantic water inflow is found in the eastern and a characteristic cold-water polar community in the western strait. Here, new taxonomic insights are presented after the second year of sampling with the Epibenthic Sledge as part of the ALONGate project (A LONG-term observatory of the North Atlantic Gateway to the Arctic Ocean, 2024/25 – 2029/30). To increase the consistency in the determination of species, this project aims to provide the first traditional (dichotomous) as well as an interactive digital identification key to selected groups (Cumacea, Isopoda Pycnogonida), filling a significant gap in the literature. The distribution data of occurring taxa is enriched with the latest status quo of various open source databases such as OBIS[1], GBIF[2], CRITTERBASE[3]. Additionally, genetic barcodes will be provided for ethanol preserved species and previously recorded geographical occurrences of these taxa will be visualized for the Fram Strait and the surrounding Arctic Ocean.

P1-22: Cold-Water Corals from the 2024 Western Pacific International Cruise for Digital DEPTH - Preliminary Findings and Research Visions

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Having successfully completed the 2024 Western Pacific International Cruise for “Digital Deep-sea Typical Habitats” (August 10th – September 23rd, 2024), we aim to summarise our preliminary findings on the collected and observed corals. Our goal is to encourage collaboration and dialogue on research priorities. The Western Pacific is one of the regions with the highest densities of seamounts on our planet and boasts an impressive diversity and density of cold-water corals, particularly within the class Octocorallia and the order Antipatharia (class Hexacorallia). The material collected (corals from 11 families, 5 orders, and 2 classes) during our expedition holds potential for various research avenues, including, but not limited to: i) species description and phylogenetic analysis using genomic data; ii) biogeographic distributions; iii) assessment of genetic connectivity with cold-water corals in other regions; iv) longevity and growth rate assessment; v) climate dynamics based on coral skeletal information; and more. Overall, these studies will enhance our understanding of the diversity and ecology of cold-water corals in the region. Furthermore, in conjunction with coral specimens collected from other areas and in collaboration with regional and international scientists, we can achieve a more comprehensive view of cold-water corals across the oceans.

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P1-23: A New Species of the Subgenus *Stephanocyathus (Stephanocyathus)* (Scleractinia: Stephanocyathidae): Morphology, Mitochondrial Genome, and Phylogenetic Relationship

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Stephanocyathus (Stephanocyathus) (Stephanocyathidae) is a subgenus of solitary cup coral with ten species recorded in the deep sea of the southern Pacific and the Atlantic. However, its diversity is poorly known in the northern Pacific, with *S. (S.) regius* as the sole recorded species. Here we described a new species of *Stephanocyathus (Stephanocyathus)* based on samples collected from a cold seep in the South China Sea, determined its molecular divergence from and relationship with its congeneric species, and described the features of its mitochondrial genome. Morphologically, this species can be distinguished from its congeneric species by its septal arrangement, paliform lobes, columella and costal arrangement. Sequence distance and phylogenetic analysis based on the 28S rRNA fragments and mitochondrial genomes supported the placement of the new species in *Stephanocyathus (Stephanocyathus)* and its recognition as a distinct species. Its mitochondrial genome is similar with those of its congeneric species in gene order arrangement and in having 13 protein-coding genes, 2 transfer RNA genes and 2 ribosomal RNA genes. Overall, our study contributes to a better understanding of the diversity and phylogenetic relationship of *Stephanocyathus (Stephanocyathus)*.

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P1-24: Genomics Reveal Evolutionary Surprises in Planktonic Ctenophores

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Most ctenophores, or comb jellies, were described ~100–200 years ago. More recently, based on morphology and amplifications of the conserved *18S rDNA* fragment, it seemed that many species had global distributions, some even occupying multiple ocean basins. To examine other more variable genes like mitochondrial *COI* requires amplification by primers, but the mitochondrial genomes of ctenophores are highly divergent from other animals. Most of the 'universal' primers do not produce *COI* fragments for a large portion of the species. The application of our newly designed ctenophore 'barcoding' primers enabled us to reveal the presence of unknown cryptic lineages and patterns of species partitioning that weren't otherwise clear. Interestingly, these patterns of speciation did not necessarily correlate with geography or other clear barriers to gene flow. Although genetic barriers are difficult to identify, especially in the deep-sea, the pelagic environment provides a unique opportunity to study evolution. Here, we focused our efforts on the family Pleurobrachiidae, which includes numerous species in the genera *Hormiphora* and *Pleurobrachia*. In order to understand the worldwide biodiversity and relationships of this family, we estimated molecular and morphological phylogenies. Our results showed that the genera require reorganization, as *H. californensis* should be classified as *Pleurobrachia*. We also used population genomics to understand connectivity within the different species. Our results showed discrepancies between very closely related species that inhabit the same geographic ranges. For example, *H. californensis* had high levels of gene flow from Alaska to Baja California, with little divergence amongst populations. In contrast, *P. bachei* had much higher levels of diversification, where populations from the eastern Pacific were clearly differentiated. The differences between *H. californensis* and *P. bachei* were surprising: not only do the species co-occur, but they are also morphologically and ecologically very similar and thus seemingly subject to the same oceanographic conditions that would suggest equal levels of dispersal. These results illustrate that the life histories of pelagic animals are an important component of species distributions and the processes of speciation in the open ocean.

P1-25: Meiobenthos Contribution to Bioturbation

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Bioturbation processes influence particulate (sediment reworking) and dissolved (bioirrigation) fluxes at the sediment-water interface. Recent works showed that benthic foraminifera largely contribute to sediment reworking in intertidal mudflats; yet their role in bioirrigation processes remains unknown. In a laboratory experiment, we showed that foraminifera motion-behavior increased the oxygen penetration depth and decreased the total organic content. Their activity in the top 5 mm of the sediment also affected prokaryotic community structure. Indeed, in bioturbated sediment, bacterial richness was reduced and sulfate reducing taxa abundance in deeper layers was also reduced, probably inhibited by the larger oxygen penetration depth. Since foraminifera can modify both particulate and dissolved fluxes, their role as bioturbators can no longer be neglected. They are further able to mediate the prokaryotic community, suggesting that they play a major role in the benthic ecosystem functioning and may be the first described single-celled eukaryotic ecosystem engineers.

Here we also introduce novel imagery techniques used to describe meiofaunal behaviour allowing for precise tracking of individual motion in artificial and natural sediments as well as manipulating pore-water chemical gradients.

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P1-26: Remarkable Diversity in a Polychaete Genus *Anguillosyllis* Day, 1963 (Annelida, Syllidae) from Polymetallic Nodule Exploration Areas, Eastern Clarion-Clipperton Zone, Abyssal NE Pacific

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The benthic annelid fauna of polymetallic nodule fields in the eastern Clarion-Clipperton Zone (CCZ), abyssal NE Pacific, has been the subject of recent taxonomic investigations aiming to document the biodiversity of this region, which is currently targeted for potential seabed mineral exploration. An accurate understanding of baseline biodiversity will be essential for projecting the extent of potential anthropogenic impacts and for assessing extinction risk and capacity for ecosystem recovery. While annelids are known be diverse within the CCZ, we present data showing remarkably high diversity discovered within the genus *Anguillosyllis* Day, 1963 (Annelida: Syllidae). Prior to work presented here, only 20 species of *Anguillosyllis* had been formally described globally, with only two recorded from the CCZ. Using an integrative taxonomic approach incorporating both molecular and morphological methods, 32-34 putative species were identified in just over 130 individuals from material collected over several environmental surveys across the eastern CCZ. With current sampling efforts only representing a fraction of the CCZ relative to the size of the region, these results suggest that the true diversity of this genus may still be greatly underestimated. In the context of curating an accurate species inventory for the CCZ, we also highlight the broader taxonomic challenges in formally describing abyssal annelid material, in addition to challenges in species delimitation, for example relating to cryptic species complexes.

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P1-27: Application of FAIR Data Principles to a Multidecadal Benthic Invertebrate Time Series

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The Porcupine Abyssal Plain Sustained Observatory time-series benthic invertebrate dataset is one of a small number of long-term deep-sea benthic data sources. We present our efforts to ensure those data are findable, accessible, interoperable, and reusable (FAIR). We use the ocean biodiversity information system (OBIS) as the data repository and access portal. The data are structured using the OBIS-ENV data standard (De Pooter et al., 2017, https://doi.org/10.3897/BDJ.5.e10989), supported by the ecological metadata language (EML) as the metadata standard, formal controlled vocabularies (e.g., the UK Natural Environment Research Council's vocabulary server, NVS), and the world register of marine species (WoRMS). The data are stored in three linked tables: (i) Event, capturing details of research cruises and sampler deployments; (ii) Occurrence, capturing biological specimen identities; and (iii) Extended Measurement or Facts, that variously captures environmental details (e.g., water depth), sampler details (e.g., physical sample size), and biological specimen details (e.g., morphometric measurements and biomass determinations). Currently, the dataset encompasses otter trawl catches collected between 1989 and 2022, representing 22 research cruises, 67 catches, more than 150000 specimens, and more than twice that number of unique data entries. The first tranche of data, 1989-2005, has been released to OBIS, covering the major prior publications based on these data (Thurston et al., 1994, https://doi.org/10.1016/0967-0637(94)90100-7; Billett et al., 2001, https://doi.org/10.1016/S0079-6611(01)00060-X; Billett et al., 2010, https://doi.org/10.1016/j.dsr2.2009.02.001). We will release the second tranche of data, 2011-2022, in due course. Our experience in producing this large dataset suggests that the OBIS-ENV data standard is effective in capturing the full range of data (survey design, sampling strategy, taxonomic hierarchy, associated environmental data, and broad sweep of biometric data) that is necessary to ensure the complete and effective reuse of these data in various ecological applications.)

P1-28: Description of a New Genus and Species of Deep-Sea Mysids (Malacostraca, Peracarida, Mysida) from the Caroline Ridge, Northwest Pacific, with a Systematic Analysis of the Order

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The order Mysida Boas, 1883 is a group of small, shrimp-like peracarid crustaceans with surprisingly high morphological and ecological diversity. In this study, a new genus and species of deep-sea mysids, *Muscamysis carolinensis* gen. et sp. n., is described based on a solitary specimen recently collected from the Caroline Ridge, Northwest Pacific. To determine the phylogenetic position of the new genus within Mysida, we reconstruct a comprehensive multi-gene phylogeny of the order, incorporating 45 species from 10 sub-families and two families. Our analysis reveals strong support for a close relationship between the new genus and Mysidellinae Czerniavsky, 1882, with both forming a clade nested within Heteromysinae Norman, 1892. Notably, our findings do not support the current delineation or monophyly of most mysid sub-families, emphasizing the necessity for further taxonomic revisions. Specifically, Palaumysinae Wittmann, 2013 is now synonymized with Erythropinae Hansen, 1910, while Heteromysinae is synonymized with Mysidellinae. Bayesian divergence time estimation uncovers, for the first time, multiple independent coastal subterranean colonizations of mysids during the Mesozoic. Ancestral state reconstruction analyses suggest that characters, such as the cleft telson and reduced male pleopods, are the results of parallel evolution, indicating that certain diagnostic characters may not be apomorphic, thereby necessitating more substantial revisions to the current higher-level classification of the order.

P1-29: The Paradox of Sameness: Morphological Variation in a Genetically Uniform Southern Ocean Isopod

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Understanding morphological variation is fundamental to unravelling evolutionary processes. While traditional research has largely focused on differences between species, a considerable amount of phenotypic diversity occurs within species. This study examines a newly described isopod species and genus within the family Paramunnidae Vanhöffen, 1914, collected from two geographically distant locations in the Weddell Sea, based on complete mitochondrial genomes (mitogenomes) and intraspecific morphological variation.

Our results reveal pronounced morphological differences, particularly in males, despite extremely limited mitogenomic genetic distances. Although polymorphisms in size, shape and colour are known in marine isopods, such extensive intraspecific morphological variation in external anatomical features has rarely been reported. We discuss how local environmental conditions and specific adaptive pressures may contribute to this morphological variation. By demonstrating that genetic uniformity can coexist with substantial phenotypic diversity, our study advances our understanding of the mechanisms driving adaptation and evolutionary change in polar ecosystems.

P1-30: Home Sweet Home: Coral-Associated Fauna in *Chrysogorgia* Duchassaing & Michelotti, 1864 Species

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This study investigates the coral-associated fauna of *Chrysogorgia* sp., employing a multidisciplinary approach that integrates molecular barcoding, morphological identification, and advanced imaging techniques. The genus *Chrysogorgia*, known for its complex morphology and diverse habitats, supports a variety of associated fauna. Yet, detailed knowledge of these associations and their taxonomic classifications remain limited. Morphological identification of *Chrysogorgia* corals from Mayotte (West Indian Ocean) was conducted through detailed examination of colony structures and polyps, supplemented by Scanning Electron Microscopy (SEM) imaging of sclerites. SEM analysis allowed us to capture high-resolution images of the sclerites, revealing intricate surface details which are critical for distinguishing between closely related species. By integrating SEM images with morphological assessments, we provide a robust framework for the taxonomic classification of *Chrysogorgia* species, ensuring the accuracy of morphological identification. We then applied DNA barcoding using the mitochondrial MutS and nuclear 28S ribosomal DNA markers to identify the *Chrysogorgia* species. Finally, we utilized the cytochrome c oxidase subunit I (COI) and additional markers to achieve accurate species delineation of the associated fauna. This integrative approach not only facilitates a deeper understanding of the taxonomic diversity within *Chrysogorgia* microhabitats, but results also underscored the ecological significance of these corals as hosts to a wide array of marine organisms. Documenting the diversity and associations contributes valuable insights into coral biodiversity, informing conservation strategies aimed at preserving these complex and Vulnerable Marine Ecosystems (VMEs).

P1-31: Same (Sea) Bed Different Dreams: Biological Community Structure of the Haima Seep Reveals Distinct Biogeographic Affinities

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Deep-sea chemosynthetic communities, including hydrothermal vents and cold seeps, harbour hundreds of endemic species threatened by human activities like deep-sea mining and hydrocarbon extraction. The South China Sea (SCS) offers an opportunity to study the biogeography of these ecosystems, with two well-investigated active seeps - Haima in the west and Site F in the east. Here, we conducted extensive field surveys using Remotely Operated Vehicles (ROVs) and collected specimens for morphological, molecular, phylogenetic, and stable isotope analyses. Cluster analyses revealed the community structure of vents and seeps in the Western Pacific and Northern Indian Ocean. The study identified 65 species from Haima, covering seven phyla and 14 classes - double the previously reported number. Among them, 35 of these species are currently known only from Haima. Stable isotope analysis confirmed a typical chemosynthesis-based biological community. Community structure analysis at the genus level clustered Haima with Site F, despite distinct species compositions and dominance patterns between the two SCS seeps. The higher species richness and endemism at Haima may be due to unique environmental factors and geographic isolation in the northwestern SCS. Similarities in genus-level community compositions between SCS and North Indian Ocean seeps suggest potential connections mediated by the Early Pliocene opening of the Indonesian islands and the strong westward Indonesia Throughflow. Given ongoing gas hydrate exploration in the SCS, these findings can inform the establishment of a global network of marine protected areas for chemosynthetic ecosystems. The rich and endemic biodiversity at Haima calls for conservation policies to protect this unique ecosystem.

P1-32: New Records and DNA Barcoding of the Deep-Sea Cusk Eels (Teleostei: Ophidiiformes) from the Brazilian Continental Slope (24°-27°S)

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Ophidiiformes are a diversified group of fishes with more than 500 valid species in four families, most of which occurs in the deep sea. So far, 45 species have been reported from the Brazilian EEZ. Recently, new collections were made onboard the Brazilian R/V Alpha Crucis focusing the continental slope off southeastern Brazil. The objectives are to report the diversity of Ophidiiformes species collected during the DEEP-OCEAN expeditions and share new molecular sequences. A total of 27 stations were performed between 24° and 27° S, at depths from 200 to 1,500 m, using bottom trawl. The tissues samples for molecular analyses were taken from the specimens soon after collection. A total of 249 specimens from 10 species were collected. The most species-rich family is Ophidiidae (7 species), followed by Bythitidae (2 species), and Carapidae (1 species). Two species represent new taxa, the recently described bythitid *Sciadonus alphacrucis* and the ophidiid *Bassozetus* sp., which is under investigation. The species richness in the area is characterized by the presence of four species shared with the North Atlantic, two with the western South Atlantic, one with the South Pacific, one circumglobally distributed, and two endemics. The ophidiiforms have a gradual bathymetric distribution along the slope, with three species from the upper slope (200–750 m) -- *Diplacanthopoma brachysoma, Genypterus brasiliensis,* and *Monomitopus americanus* --, one from the middle slope (750–1,000 m) -- *Echiodon cryomargarites* and *Sciadonus alphacrucis* --, and four from the lower slope (1,000–1,500 m) -- *Bassogigas gilli, Bassozetus trachibranchus*, *Bassozetus* sp., *Holcomycteronus squamosus*, and *Xyelacyba myersi*. The COI sequences were deposited in public databases and represent the first on-line data available for the western South Atlantic deep-sea fishes. The Brazilian deep-sea ichthyofauna remains largely unexplored, thus the number of known ophidiiforms tends to increase with additional expeditions and further taxonomic studies.

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P1-33: Consistency or Change in the Benthic Deep-Sea Macrofauna: An Update from the Central Arctic Ocean

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The deep Central Arctic Ocean (CAO) is one of the least studied regions on Earth due to its difficult accessibility. Biological observations of the deep-sea macrofauna are rare, resulting in missing baseline information. The CAO is predominantly ice-covered and has low primary production resulting in lower biomass and density of benthic macrofauna on the abyssal plains compared to the vast shelf areas. Changes in species community composition and density across spatial and temporal scales and responses to the rapidly changing Arctic are poorly understood. Here, we analyzed deep-sea macrofauna samples from 36 stations from over 2000 m depth from the Nansen and Amundsen Basins over a time frame of four decades from the years 1993, 2012 and 2023. We assessed the spatial and temporal distribution of macrofauna species richness, abundance, and biomass in relation to environmental parameters such as sea ice cover and sediment organic matter availability. In total, nine higher taxa were present with Annelida being the most abundant taxa followed by Crustacea. Stations with a year-round sea ice coverage exhibited lower species richness, abundances, and biomass compared to stations with seasonal ice cover. This pattern is mainly driven by higher organic matter availability, resulting from higher primary production and particle flux in seasonally ice-covered areas. Here we deliver a solid baseline of changes across different ice regimes together with organic matter availability at the seafloor. With the rapid decrease of sea ice thickness and sea ice cover predicted for the next decades shifts in the distribution of Central Arctic macrofauna are expected, with yet unknown consequences for benthic ecosystem functioning.

P1-34: Ribbon Worms from Hydrothermal Vent Fields and Seamounts

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Ribbon worms (phylum Nemertea) are diverse predators and scavengers found in marine, freshwater, and terrestrial ecosystems. The order Monostilifera, comprising around 594 species in 127 genera, is characterized by an eversible proboscis housed in a fluid-filled chamber called the rhynchocoel, typically used for capturing prey like polychaetes, molluscs, and small crustaceans. The proboscis in monostiliferans is often armed with a stylet apparatus featuring a single central stylet.

Nemerteans from hydrothermal vents and seeps are rarely reported, with only four known genera: *Alvinonemertes* Sagorny et al., 2022, *Chernyshevia Sagorny* et al., 2022, Ovicides Shields, 2001, and *Thermanemertes* Rogers et al., 1996. None of these genera have been documented in Japanese waters.

In 2023–2024, we collected several monostiliferous nemerteans from chemosynthesis-based ecosystems and seamounts around Japan. Each species exhibited granule-like structures within the submuscular layer, similar to a unique character previously observed only in *Thermanemertes.* We performed ultrastructural analysis using electron microscopy and energy-dispersive spectroscopy for the submuscular accumulation. Furthermore, multi-locus phylogenetic analyses were performed to explore the adaptive evolution of these nemerteans to chemosynthesis-based environments.

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P2-1: Rapid Emergence and Evolution of Cold Seep Ecosystem at The Hydrate-Bearing Seafloor

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Marine cold seeps are ‘windows to deep geosphere’, through which a vast amount of the deeply sourced methane discharge at seafloor, sustaining chemosynthetic biota that prevent further release of methane to hydrosphere. To date, the formation process and timescale of cold seep ecosystem remain enigmatic, due to challenges in tracking its emergence and evolution on the vast seafloor. Here we report the birth of a methane seep ecosystem at hydrate-bearing seafloor of the South China Sea, recorded during the yearly geological surveys from 2018-2023. There a unique seep community assembled in ~2 years since the onset of methane seepage, with dense microbial populations (up to 10^{11} cells g^{-1}) dominated by previously undescribed strains affiliated to aerobic (*Methyloprofundus*) and anaerobic methanotrophs (ANME-3), and faunal community (up to ~80,000 individuals m^{-2}) predominated by polychaete worms and copepods. Those dense worm tubes enhanced the downward transports of high-energy electron acceptors (O_2, NO_3^-) from seawater, fueling highly active methane and nitrogen cycling in the surface seafloor. Metagenomic and transcriptomic analyses combined with isotopic labeling experiments further revealed the occurrence of dissimilatory nitrate reduction in the newborn seep, at the highest rates reported in marine ecosystems (>50 mM m^{-2} h^{-1}), and its potential coupling with methane oxidation to efficiently consume the discharged methane. Together our results demonstrate faster-than-expected formation of cold seep ecosystem in response to methane discharge, suggesting that intrinsic potential of seafloor biota exists for instantly mitigating the release of methane from hydrate-bearing seafloor to ocean.

P2-2: Adaptation to the Cold Seep: Sulfide Induces the Different Distribution of Squat Lobsters

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The squat lobsters *Shinkaia crosnieri* and *Munidopsis verrilli* are both dominant species at the cold seep Site F in the South China Sea. However, they exhibit different distributions and feeding behaviors. *S. crosnieri* forms impressive aggregations around the core regions of Site F and utilizes the abundant epibiotic bacteria that adhere to the setae to obtain nutrients. In contrast, *M. verrilli* exhibits a relatively random pattern of distribution and displays a potential beneficial relationship with its epibiotic bacteria. A comparative analysis of the epibiotic bacterial communities on squat lobsters was conducted to investigate the relationships between epibiotic bacteria and host lifestyle factors. The results showed that the epibiotic bacteria on *S. crosnieri* displayed markedly elevated higher density and diversity, with a multi-layer configuration, in comparison to those on *M. verrilli*. Furthermore, the relative abundance of amplicon sequence variant 3 (unknown species in order *Thiotrichales*), which was associated with sulfide oxidation, was significantly higher in *S. crosnieri* than in *M. verrilli*. Given the higher concentration of reductive materials in the core regions of Site F, we postulated that the aggregations of *S. crosnieri* facilitated their utilization of sulfide ensuring a stable supply of nutrients. In light of the aforementioned findings, we hypothesized that chemical cues, such as hydrogen sulfide, might induce the congregating of *Shinkaia crosnieri* in cold seeps. Subsequently, behavioral experiments were conducted using a Y-maze system to investigate the preference for hydrogen sulfide of *S. crosnieri* and *M. verrilli*. The result demonstrated that sulfide exerts a strong attraction for *S. crosnieri* yet exhibits no comparable effect on *M. verrilli*. Further analysis indicated that the ionotropic receptors IR8a, IR93a and IR25a on the antennules of *S. crosnieri* were involved in this chemosensory process. In conclusion, our results deepen the understanding of adaptive mechanisms of crustacean in deep-sea chemosynthetic environments.

P2-3: Variation of Microbial Nitrate Reduction Processes Across a Wide Range of Benthic Habitats in Continental Margins

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Nitrate reduction is a key pathway of benthic microbial respiration in continental margins, largely controlled by inputs of bioavailable organic matter (OM) from the deposition of oceanic photodetritus and terrestrial matters, as well as the upward transport of subsurface geofluids. A lack of systematic examination on microbial nitrate reduction processes across seafloor habitats with varied OM inputs limits our understanding on the flux and pathway of nitrate reduction in continental margins. Here, by integrating quantification of reaction rates through ^{15}N isotope pairing technique, geochemical analysis, metagenomics, and metatranscriptomics, we investigated the potential rates, pathways, and their driving factors of microbial nitrate reduction in 291 sediment samples retrieved from a variety of sites in continental margins of the west Pacific Ocean, including the East China Sea (ECS), South China Sea (SCS), and several cold seep sites in the SCS. Following an attenuated flux of OM deposited to the seafloor, potential nitrate reduction activities dominated by denitrification generally decline with increasing water depth, from 28.4-102.1 nmol cm^{-2} h^{-1} in continental shelfs to 1.6-3.7 nmol cm^{-2} h^{-1} in continental slopes. Nitrate reduction rates are 1-2 orders of magnitude higher at cold seeps than those in continental slopes without the input of methane-rich geofluids. Exceedingly high rates of nitrate reduction moreover, were detected at cold seep in its early developing stage (125.4–487.0 nmol cm^{-2} h^{-1}), and greatly dominated by the activity of dissimilatory nitrate reduction to ammonium (DNRA, 79–91%). By extrapolating the measured potential rates to a regional scale, fluxes of denitrification and DNRA are 0.02 and 0.08 Tg yr^{-1} at cold seeps, respectively, accounting for 0.6 and 67.2% of those total fluxes in the SCS continental slopes. Phylogenetically divergent microbial lineages with significantly varied gene-specific rates (ratios of rates to funtional gene abundnces) appear closely linked to the varied fluxes of nitrate cycling across the geochemically distinct habitats in continental margins. Together our data depict the general pattern of microbial nitrate cycling varied with OM inputs, emphasizing the previously overlooked role of geological processes in sustaining nitrogen-cycling hotspots in continental margins.

P2-4: Biotransformations of Arsenic in Marine Sediments Across Marginal Slope to Hadal Zone

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Arsenic compounds from natural and anthropogenic emissions are accumulating in deep ocean, but their ecological impacts on deep-sea ecosystem remain elusive. Here, we studied 32 sediment cores (101 layers for metagenomes, along with 41 global reference sediment metagenomes) collected from the South China Sea (SCS), the Mariana Trench (MT) and the Challenger Deep (CD), characterized with high arsenic accumulation in MT and CD. In these metagenomes we revealed a significantly positive correlation between relative abundance of arsenite methyltransferase gene (*arsM*) and sampling depth, which suggests that methylated arsenic compounds including arsenobetaine were potential osmolytes critical for adaptation to the high pressure as indicated previously. Lower relative abundance of arsenic efflux genes *acr3* and *arsB* and organoarsenical efflux permease *arsP* and *arsK* gene, compared with *arsM*, indicates that microbes in deep-sea sediments were prone to further methylate arsenite and retain it for utilization rather than efflux arsenite and organic arsenic from the cell. Phylogenetic relationships of the ArsM proteins revealed seven clades comprising at least two novel ones that are frequently shared among the microbes to cope with common stresses in the deep-sea sediments. Five metagenome-assembled genomes (MAGs) containing *aioA* for arsenite oxidation also harbor carbon fixation genes in the sediment layers across marginal slope to hadal zone, suggesting previously unnoticed contribution of arsenite oxidizing autotrophic bacteria to the carbon cycle. Therefore, the arsenic compounds were differently transformed for detoxification and adaptation in deep-sea sediments, which renews our understanding of arsenic in their ecological impacts and potential contribution in deep ocean.

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P2-5: *In Situ* Sampling Uncovers Seasonal Variability in Community Structure and Metabolism of Deep-Sea Microbes

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Learning about the metabolic activities and adaptations of deep-sea microbes is a challenging task, because the collection and retrieval of samples from the deep ocean can cause RNA degradation and alteration of microbial communities. Here, we employed a novel *in situ* DNA/RNA co-extraction device to collect 18 time-course nucleotide acid samples for winter and summer seasons in the South China Sea to generate metatranscriptomes and metagenomes with the minimal possible sampling perturbation. Between the two seasons, the prokaryotic microbiota showed seasonal variations in species composition, yet dominant active species remained largely consistent as shown in the metatranscriptomes. The most active eukaryotic microbes were Ciliophora, whereas the most abundant but inactive eukaryotic microbes were Retaria. In the winter, autotrophic microorganisms contributed to organic matter production by CO_2 fixation associated with nitrification. In the summer, the primary source of energy originated from heterotrophic microorganisms that can utilize alkanes, aromatic compounds and carbohydrates, partially relying on anaerobic respiration. This may relate with nutrient source variations as reflected by the different levels of microbial network complexity between two seasons. Altogether, we uncovered the metabolic activities and adaptations of active microbial groups in two seasons with *in situ* metatranscriptomes, precluding bias associated with deep ocean sampling, and paving the way to identification of the real microbial contributors to element cycles in the deep ocean.

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P2-6: Bioluminescence in Mesopelagic Fish: The Microbiome Connection

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Bioluminescence is pervasive across the tree of life, from bacteria to vertebrates, and different habitats of the Planet. In deep-sea ecosystems, more than 75% of creatures can produce light for multiple purposes including communication, camouflage, attracting prey, and mating. Particularly, the twilight zone (200-1000 m depth) has been reported as the major realm of bioluminescence.

Most bioluminescent fish are believed to have endogenous luciferases intrinsically produced by their luminous organs. However, information on the actual origin of bioluminescence in mesopelagic fishes remains vague. In addition, luciferase genes and proteins in these fishes have not yet been found. In the present study, we investigated the role of microbiota associated with luminous organs in *Argyropelecus hemigymnus* and *Maurolicus muelleri,* two species of mesopelagic fishes belonging to the *Sternoptychidae* family, which live from the surface down to > 1000 m depth. We used a multiomics approach (based on 16S rDNA metabarcoding, metagenomics, metabolomics and metaproteomics) combined with microscopy-based techniques to assess the taxonomic and functional specificities of the microbiome in different organs of the fishes, including photophores. The results obtained will provide new insights into the knowledge of the bioluminescence mechanism in the dark ocean and the potential role of microbiota in such a process.

P2-7: Genetic Arsenal of a Coral Endosymbiotic *Ruegeria* Lineage Being Targeted as the Next-Generation Coral Probiotics

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The application of probiotic bacteria to help maintain or restore coral health has shown promising potential. However, the current approach of selecting coral probiotics based on predefined beneficial traits overlooks the difficulty of manipulating these probiotics in such a complex and dynamic wildlife setting. Our recent study has identified a coral holobiont-associated *Ruegeria* population (MC10) as a compelling candidate for next-generation coral probiotics due to its facultative endosymbiotic nature, which potentially enables efficient delivery and prolonged retention of probiotics. In this study, we conduct a comparative genomic analysis to explore genetic differences between MC10 and co-occurring but likely non-endosymbiont *Ruegeria* populations. Our findings reveal that although MC10 differs from other populations by as low as 0.55% at the 16S rRNA gene sequence, its genome content differs from others' by nearly 50%. Notably, MC10 harbors a complete gene cluster responsible for producing enterobactin, which is a high affinity siderophore for iron acquisition. MC10 also carries a gene cluster encoding a cytochrome bd oxidase which may contribute to the elimination of reactive oxygen species (ROS). These unique metabolic traits may help MC10 evade host immune responses and facilitate its colonization in the coral tissue. Our results are relevant to our ongoing efforts to apply MC10 as one of the next-generation probiotics for coral conservation.

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P2-8: Microbial Communities and Metagenomes in Methane-Rich Deep Coastal Sediments

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Coastal sediments are rich in embedded recalcitrant organic carbons that are biotransformed into methane. In this study, gas composition (carbon dioxide, methane and nitrogen) and chemical indicators (total nitrogen, total carbon, and total sulfate) were examined in five deep sediment cores (up to 130 m in length) obtained from the Hangzhou Bay. The V3-V4 region of the 16S rRNA gene amplicons was amplified and sequenced for the prokaryotic community analysis. The species composition, along with the physicochemical factors of the sediments, revealed a strong correlation with methane content in one of the sediment cores. We then obtained metagenomes of the two sediment samples selected for their high methane content and enrichment of methanogenic Bathyarchaeota with phylogenetic evidence. A total of 27 draft genomes were retrieved through metagenomic binning methodologies and were classified into Bathyarchaeota, Asgard archaea, Planctomycetes, and other microbial groups. The data provided are valuable for understanding the relationship between methane generation and microbial community composition in deep sediment core samples from coastal to marine environments.

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P2-9: Impact of Funnel Accumulation on the Community Structure and Ecological Functions of Hadal Microorganisms

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Hadal trenches, with depths exceeding 6,000 m, are the deepest oceanic regions on Earth. The unique funnel-shaped topography of hadal trenches accelerates the collection of organic matter at the trench bottom, making them organic depocenters. Correspondingly, diverse heterotrophic microorganisms are present in the hadal realm and may contain unique catabolic capacities to utilize unpalatable compounds that escape from surface degradation. However, our understanding of how these enigmatic microbial ecosystems are fueled is still limited. Through combined culture-dependent and culture-independent methods, we investigated the microbial community compositions, metabolic capabilities and evolutionary trajectories in the hadal waters and sediments of the Mariana Trench. The hadal waters harbored distinct microbial communities capable of degrading hydrocarbon and cell-wall derived polysaccharides under physiologically relevant conditions, suggesting the accumulation of structurally complex organic “leftovers” that may serve as significant carbon sources for these microorganisms. Additionally, high-rate episodic sedimentation events triggered by earthquakes introduced large amounts of "old carbon" and microbial cells into the hadal bottom sediments, significantly altering the subseafoor microbiosphere by promoting the growth and extracellular enzymatic activity of in situ microbial communities. Furthermore, significant adaptive evolution occurred in microorganisms transported to the hadal ocean. Using ammonia-oxidizing archaea as an example, we provided evidence for a direct niche expansion into the hadal realm from the coastal/surface ocean rather than from the mesopelagic/bathypelagic waters that are spatially closer to the hadal zone. Ammonia-oxidizing archaea exhibited clear niche separation between hadal water and sediments through intraspecific genomic variation. These findings are crucial for understanding the microbial ecology and evolution in the extreme hadal environments and the biogeochemical processes they drive.

P2-10: Functional and Adaptive Study of the Sulfurovaceae Bacteria in the Gut of Polychaetes from Hydrothermal Vents and Whale Falls

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The gut microbiota plays a significant role in a variety of physiological and biochemical processes for organisms. For polychaetes, which lack well-development gills, gut microbiota is crucial for those living in hydrothermal vent areas characterized by high temperatures, low nutrients, and high concentrations of H_2S. This study is based on high-throughput sequencing of 16S rRNA, metagenomics, and metaproteomics to study the community structure of gut microbiota in polychaetes from hydrothermal vents and whale falls, as well as the functional adaptability and evolution of dominant bacteria. We found that compared to environmental microbes, the differential characteristic bacteria in the gut of polychaetes are mainly sulfur-oxidizing bacteria of the Sulfurovaceae family, and they belong to different genera classifications. The Sulfurovaceae bacteria of family mainly rely on different types of sqr genes in the polychaete gut to oxidize hydrogen sulfide into non-toxic elemental sulfur for detoxification and preservation, while also encoding the denitrification pathway of nitrate reductase, which is beneficial for the sulfur-oxidizing bacteria to transfer electrons in the anaerobic environment of the gut. To adapt to the host's gut environment, the Sulfurovaceae bacteria can additionally utilize substances such as glucose, polysaccharides, and amino acids to provide nutrition. In the long-term evolution, genes related to bacterial adhesion have also been expanded, and genes related to movement have been lost, suggesting that these sulfur-oxidizing bacteria are gradually evolving towards colonization. In addition, the Sulfurovaceae bacteria in hydrothermal vents regulate the host's methionine content through Metk enzyme to help it avoid damage from high temperatures. Through multi-omics research, we have studied the gut microbiota community of polychaetes in two deep-sea environments with high levels of hydrogen sulfide from multiple angles, revealing the adaptability, ecological functions, and evolutionary direction of sulfur-oxidizing bacteria of the Sulfurovaceae family in the host's gut, providing basic data for the symbiosis of deep-sea microbes and their hosts.

P2-11: The Co-Occurrence Patterns and Assembly Mechanisms of Microbial Communities in Haima Cold Seep

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The Haima cold seep locating in South China sea, is the largest deep-sea cold seep in China. The microorganisms in this typical chemosynthetic ecosystem are important for ecological and medical researches. However, there has been a bias in the investigation of microbial diversity in different habitats and microhabitats, resulting in the mechanism which maintain the stability of ecosystem and biodiversity remain unknown. In this study, the water column and sediment samples from 5 different microhabitats (mussel, sea anemone, blank seabed, dead clam and clam) were collected. The species interactions and mechanisms for community assembly of prokaryotes and microeukaryotes were explored. The results showed that more complex species interactions of microorganisms in water column than that of sediment. And the network of microorganisms from sea anemone has most complex species interactions while the the network of microorganisms from mussel has the lowest complex species interactions. Furthermore, both the deterministic processes and stochastic processes structuring the microbial community assembly. The deterministic processes play more important role in structuring both the prokaryotic and microeukaryotic communities from water column and the deterministic processes play more important role in structuring prokaryotic communities from sediment. However, the undominated has the highest relative importance in structuring microeukaryotic communities. Additionally, the deterministic processes play more important role in structuring microbial community assembly in the biotic microhabitats (mussel, sea anemone and clam) while the stochastic and undominated processes play more important role in structuring microbial community assembly in the abiotic microhabitats (blank seabed and dead clam).

P2-12: Diet and Gut Microbiome of Parrotfish in the South China Sea

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Coral reefs are vital ecosystems facing threats from human activities and climate change, leading to a decline in biodiversity. Parrotfish (Scaridae), characterized by their robust beak-like jaws, play a key role in reef accretion by scraping algae and contributing to sediment production, particularly through the consumption of coral skeletons, which are subsequently ground up and excreted as sand. Due to the absence of a stomach and the presence of a short intestine, questions arise regarding the mechanisms of nutrient absorption and the role of gut microbes in their ecological functions. In this study, we collected 200 parrotfish from the South China Sea and analyzed their food composition and trophic niche using 18S rRNA sequencing and stable isotopes analysis. Additionally, metagenomic analysis was performed to characterize the bacterial community composition and functional potential of their gut microbiomes. We found that parrotfish primarily feed on algae, mostly red, brown, and green algae. Due to the raking feeding style of scraper parrotfishes, their diets were more diverse and trophic niche are broader. However, excavator species ingest significantly more coral than scraper species. Pseudomonadota was prevalent in their gut microbiomes. The combined analysis of functional annotation against KEGG and COG databases revealed a clear dominance with carbohydrate metabolism. The enzymatic activities primarily involved in the metabolism of algae and the degradation of toxins. Environmental, habitat, diet, and host species factors influence the fish microbiota. These findings underscore the importance of gut microbes in the ecological functions of parrotfish and their adaptive strategies to different habitats, providing insights for the conservation of parrotfish biodiversity and the maintenance of coral reef stability. Understanding the response of parrotfish and their microbiota to environmental changes is essential for protecting these valuable ecosystems.

P2-13: Microbial Biodiversity and Their Metabolic Potential in Marine Sediments

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Two thirds of the Earth's surface was covered by the ocean, thus the ocean floor, where particulate organic matter from the water column settles, contains the largest pool of organic carbon on the planet. Sediment-inhabiting microorganisms represent great abundance and phylogenetically diverse communities. The inhabitants in marine sediments process organic carbon while cycling other nutrients, e.g., nitrogen, sulfur, and iron. Single-gene surveys in sediments have revealed a diversity of deeply-branched, uncultured bacterial and archaeal phyla. We have employed metagenomics to study these microbial communities. Assembling and binning resulted in more than 10,000 prokaryotic genomes (>50% completeness, <10% contamination) from over 50 sediments samples collected from coastal sea to deep oceans. Phylogenomic analyses of these genomes revealed they comprise more than 100 bacterial and archaeal phyla, including over 20 new candidate phyla that have never been described. Comparison of their rRNA genes with public databases reveals that several of these novel phyla are globally distributed in different habitats, including marine, freshwater, and terrestrial environments. Genomic analyses suggest these organisms are capable of mediating key steps in sedimentary biogeochemistry, including anaerobic degradation of polysaccharides and proteins, and respiration of sulfur and nitrogen. Interestingly, these genomes code for an unusually high proportion (~9% on average, up to 20% per genome) of protein families lacking representatives in public databases. Genes encoding hundreds of these protein families colocalize with genes predicted to be involved in sulfur reduction, nitrogen cycling, energy conservation, and degradation of organic compounds. This large dataset of marine genomes provides an opportunity to understand how carbon, nitrogen, and sulfur are processed in marine sediments. We further applied metatranscriptomics and the testing of sulfide, thiosulfate, and sulfide oxidation in sediment samples to figure out how sulfide is oxidized in the sediments. Surprisingly, sulfur oxidation is wide-spread in the microbial community (>85.8%) of mostly heterotrophic prokaryotes across 67 phyla, dominated by Proteobacteria. Our findings advance our understanding of bacterial diversity, the ecological roles of these bacteria, and potential links between novel gene families and metabolic processes in the oceans.

P2-14: Unlocking Virus Diversity and Virus-mediated Microbial Mortality in Atlantis II Deep Brine Pool in Red Sea

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The Atlantis II Deep Brine Pool (ABP), located at >2 km depth in the Red Sea rift valley, is a hydrothermally active brine pool characterized by elevated temperature (~68 °C), high salinity (~250 psu), anoxic conditions, and high metal concentrations. Despite being one of the most studied of all the Red Sea brine pools, little is known about the virus composition and ecology of microbial lysis in this unique and extreme environment. Here, we profiled virus communities and estimated taxon-specific microbial cell lysis from four layers of the ABP (overlying, brine-water interface, middle, and bottom layers). We discovered 6759 species-level DNA viral populations (vOTUs) from >15 viral families. The vast majority of vOTUs are specific to the ABP, and share little to no similarity to other viral metagenomic datasets and reference virus databases, indicating the unique viral landscape in ABP. The virus communities detected in the ABP are as diverse as those found at the sea surface and appear to be active, as >95% of vOTUs were predicted to have a lytic lifestyle. The ABP viruses primarily infect prokaryotes, with the predicted hosts derived from six archaeal and 16 bacterial phyla. By sequencing extracellular 16S rRNA in the ABP stratified layers, cell lysis was detected in taxa from nine out of 22 prokaryotic phyla: *Actinobacteria, Bacteroidota, Bdellovibrionota, Cyanobacteria, Campilobacterota, Firmicutes, Proteobacteria, Crenarchaeota, and Thermoplasmatota*, implying that viral lysis contributes to biogeochemical cycling in the ABP. In addition, viruses in the ABP possess a variety of auxiliary metabolic genes (AMGs), which may aid in the promotion of host metabolism and adaptation in response to harsh environmental conditions. This study unveiled the hidden diversity of viruses in the Red Sea's deep, hypersaline, anoxic, and hot brine pools, and contributed to our understanding of viral diversity and cell lysis in extreme marine environments.

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P3-1: A Transition from Generalist to Specialist Denitrifying *Ruegeria* in Corals Along Elevated Nitrate Gradients In Hong Kong Reefs

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Anthropogenic activity-induced mass coral bleaching, which refers to the physical whitening of coral tissue due to the depletion of endosymbiotic algae, poses a significant danger to the continuing existence of coral reefs. Nitrogen eutrophication is one of the significant factors that threaten coral fitness in highly urbanized Hong Kong reefs, given the nitrate levels far exceed the global average by orders of magnitude. Denitrifying bacteria, i.e., prokaryotes that can covert nitrate and nitrite into dinitrogen gas, are considered key players to support coral fitness in general and especially in highly eutrophicated reefs. Harnessing the naturally increasing nitrate gradients in Hong Kong reefs from east to west, we hypothesized that corals in western Hong Kong were enriched with a group of specialist denitrifying *Ruegeria*. By employing denitrifying *nirS* gene and *Ruegeria* population-resolving gene (*ATP5B* and *parC*) amplicon sequencing, *Ruegeria* genome sequencing, and 15N-labelling based denitrification activity measurements, we identified five specific specialist denitrifying *Ruegeria* populations that were found only enriched in the western Hong Kong reefs. Further investigation revealed that all western specialist denitrifying *Ruegeria* possessed genes capable of completing the denitrification process. The denitrification gene clusters were found to be located together on the chromosomes. Remarkably, our preliminary data has shown that western specialist denitrifying *Ruegeria* also exhibited superior denitrification activities, as proxy by higher dinitrogen gas outputs, albeit with negligible nitrogen dioxide levels compared to their counterparts. The existence of western specialist denitrifying *Ruegeria* suggests that microbial evolution in corals may enhance the host's ability to adapt to the stressful circumstances. Specialist denitrifying *Ruegeria* can potentially act as probiotics to enhance the fitness of coral holobionts in eutrophication reefs.

P3-2: Insight into the Adaptation Mechanisms of High Hydrostatic Pressure in Physiology and Metabolism of Hadal Fungi from the Deepest Ocean Sediment

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The deep sea is one of the least explored extreme environments on Earth. Most of the existing research on deep-sea fungi focuses on the screening of secondary metabolites for activity and the development of novel drugs. High hydrostatic pressure (HHP) influences the life processes of organisms living at depth in the oceans. While filamentous fungi are one of the essential members of deep-sea microorganisms, few works have explored their piezotolerance to HHP. In this study, 113 deep-sea fungi were successfully isolated from seawater and sediment samples of the Mariana Trench through a combination of traditional plate separation and culture techniques, in-situ culture simulation techniques and high-throughput screening techniques. High hydrostatic pressure affected the phenotypes, gene expression and secondary metabolite activities of hadal fungi. To explore the pressure-adaptive mechanism of hadal filamentous fungi, we obtained three homogeneous *Aspergillus sydowii* from terrestrial, shallow, and hadal areas, respectively, to compare their pressure-resistance. A set of all-around evaluation methods including determination of growth rate, metabolic activity, and microscopic staining observation was established and indicated that *A. sydowii* DM1 from the hadal area displayed significant piezotolerance. Global analysis of transcriptome data under elevated HP revealed that *A. sydowii* DM1 proactively modulated cell membrane permeability, hyphae morphology, and septal quantities for seeking a better livelihood under mild pressure. Besides, differentially expressed genes were mainly enriched in the biosynthesis of amino acids, carbohydrate metabolism, and cell process, etc., implying how the filamentous fungi respond to elevated pressure at the molecular level. We speculated that *A. sydowii* DM1 could acclimatize itself to HHP by adopting several strategies, including environmental response pathway HOG-MAPK, stress proteins, and cellular metabolisms.

P3-3: DeepSeaDB: An Integrated Functional and Evolutionary Genomic Database for Deep-Sea Organisms

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The deep-sea is the largest habitat on earth, spanning across cold seeps, hydrothermal vents and rugged seamounts. It covers 71% of the world's surface and remains largely unexplored. Living in extreme environments, such as high pressure, limited light, and high temperatures, deep-sea organisms present some of the most striking adaptations. Emerging genomic resources have recently provided promising insights into our advanced understanding of deep-sea ecosystems and evolution. To better access and utilize these resources, we integrated comprehensive genomic and transcriptomic resources from deep-sea organisms. We provided functional support toolkits for multi-dimensional integrated and comparative genomic analyses. We also offered a systematic view of genomic information, including genome assembly, single-cell and symbiont information, genome phylogenies, gene family, KEGG pathway, expression profiles, core pathway information, pan-geneset, candidate horizontal transfer genes (HGTs), and gene tree. Furthermore, we also provided constructed co-expression networks in species with expression views across different tissues and developmental stages, and macrosynteny analysis for genomic evolution. Finally, we constructed an integrated functional and evolutionary genomic database for deep-sea organisms, named DeepSeaDB (http://143.89.25.9/DeepSeaDB). It aims to help the deep-sea community cope with continuously expanding genomic resources and offers insights into the understanding of biology and adaptive evolution of deep-sea species under extreme conditions.

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P3-4: Metabolic Constraints on Symbiotic Relationships in the Abyss

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Symbiotic relationships alter the dynamics and function of ecosystems and their inhabitants, but these relationships have been underexplored in the deep sea outside hydrothermal vent systems. Epibiota impact their hosts by increasing their drag during movement and increasing their energy use, a tax on host metabolism. A recently-presented scaling theory for parasitism in terrestrial organisms, based on measured body size, temperature and derived metabolic rate, provides a framework for assessing the energetic constraints shaping symbiotic relationships in abyssal plains megafauna. The scaling of epibiota with their hosts was tested in 50 trawl-caught specimens of holothurians *Molpadiodemas villosus* and *Paroriza prouhoi* with epibiotic *Englandactis commensalis* at the Porcupine Abyssal Plain Sustained Observatory. Two important constraints were revealed: first, epibiont load (as total biomass and energy flux) scaled with host body size; and second, the theory predicted that epibiont load was constrained by surface area rather than host energetics. These findings provide a new framework for assessing relationships between symbiotic abyssal fauna, and extend our understanding of the influence of body size scaling in the deep sea.

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P3-5: 3D Analysis of Bacteriocytes in the Deep-sea Mussel *Gigantidas platifrons*

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Deep-sea mussels thrive in extreme environments such as hydrothermal vents and cold seeps through stable symbiotic relationships with chemosynthetic bacteria. This study utilized Volume Electron Microscopy (vEM) technology to perform subcellular-resolution 3D modeling of bacteriocytes from various tissues of deep-sea mussel *Gigantidas platifrons*. The aim was to reveal the structural mechanisms that sustain long-term symbiotic relationships. Key findings include:

Methanotrophic bacteria (MOB) are located within an interconnected network of membrane channels, enhancing interconnectivity and promoting a modular distribution of symbionts within bacteriocytes, enabling survival in diverse microenvironments.

Two functionally distinct symbiont morphotypes were identified within bacteriocytes: MOBhd (bacteria with abundant high-density granules) and MOBld (bacteria with few low-density granules). The MOBhd can provide nutrients through autolysis, while MOBld maintains symbiont population stability through cell division.

Compared to gill bacteriocytes, epithelial cells in non-gill tissues cannot sustain symbiotic relationships over the long term. In non-gill bacteriocytes, the spatial modularity of symbionts is weaker, with random autolysis of different morphotypes and a lower rate of symbiont division.

The findings indicate that the spatial modularity of symbionts and the orderly process of autolysis within bacteriocytes are key structural foundations for maintaining long-term symbiotic relationships. These results not only deepen our cellular-level understanding of symbiotic maintenance mechanisms in deep-sea bivalves but also provide new perspectives on survival strategies in extreme environments.

P3-6: Function and Development of Deep-Sea Mussel Bacteriocytes Revealed by Integrated Analysis of snRNA-seq and ST-seq

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The deep-sea chemosynthetic ecosystem represents one of the most unusual ecosystems on the earth, where majority of megafauna formed close symbiotic associations with chemosynthetic microbes to obtain nutrition and shelter from toxic environment. Despite the diverse forms of symbiotic organs in these deep-sea holobionts, the function and development of bacteriocytes, host cell harboring symbionts, are yet largely uncharacterized. Here, we have conducted the *in situ* decolonization assay and state-of-the-art single-nucleus and spatial transcriptomics to reveal the function and development of deep-sea mussel bacteriocytes. Mussel bacteriocytes appear to optimize immune processes to facilitate recognition, engulfment, and elimination of endosymbionts, and interacted with them directly in carbohydrate, and ammonia metabolism by exchanging metabolic intermediates via transporters such as SLC37A2 and RHBG-A. Arisen from three different proliferation cells, we for the first time reveal that the bacteriocytes are still able to proliferate. Moreover, the molecular functions and developmental process of bacteriocytes are guided by the same set of mollusk-conserved transcription factors and may be influenced by endosymbionts via sterol metabolism. The coordination in the functions and development of bacteriocytes and between the host and symbionts highlights the development plasticity of symbiotic organs, and underlies the interdependency of symbiosis in adaptation to deep-sea.

P3-7: Insights into Symbiotic Interactions and Adaptation of a Deep-sea Seep Mussel through In-Situ Transplant Experiments and Omics Analyses

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Methane seeps are extreme deep-sea ecosystems that rely on chemosynthesis to sustain benthic communities. Deep-sea mussels are key subjects in methane seep fauna research due to their wide distribution, high abundance, and diverse symbiotic relationships. As the dominant species in Haima methane seep, *Gigantidas haimaensis* has established methanotrophic oxidizing bacteria (MOB) inside gill epithelial cells to maintain long-term energy supply. However, the specific molecular mechanisms underlying their endosymbiotic relationships with MOB and their adaptive strategies remain poorly understood. We conducted a deep-sea transplantation and cultivation experiment on *G. haimaensis*, integrating *in-situ* sampling fixation techniques and various omics analyses to minimize systematic errors from laboratory conditions and sampling processes. Here, we report the genome of *G. haimaensis* with a completeness of 96.6% and a size of 1.95 Gb, annotated with a gene model completeness of 93.7%. Compared to non-symbiotic organs, gills exhibited 4,200 highly expressed genes, including complex signaling pathways， immune recognition, and apoptosis, highlighting their significance in endosymbiotic bacteria recognition, maintenance and population control. After 6 days of transplantation, the abundance of endosymbiotic bacteria decreased by 50%, with 870 differentially expressed genes identified in MOB, which upregulated pmmo gene to enhance methane oxidation efficiency. In *G. haimaensis*, 9,000 differentially expressed genes were detected, showing significant upregulation of those involved in immune regulation related pathways including MAPK signaling, Toll-like receptor signaling, and Imd signaling. Additionally, genes associated with the cytoskeleton and filter-feeding increased, suggesting that the mussels are adapting in low-methane areas by enhancing the methane flux to their endosymbiotic bacteria and possibly increasing filter-feeding to obtain energy. Furthermore, downregulation of genes related to lysosomes and apoptosis suggests a shift from relying on digesting endosymbiotic bacteria for energy to protecting them. This research significantly advances our understanding of the symbiotic relationships and adaptive strategies of organisms in methane seep ecosystems.

P3-8: Molecular Adaptation of Two Hot-Vent Chemosymbiotic *Alviniconcha* Snails Revealed by Multiple-Omics Analyses

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Deep-sea hydrothermal vents represent an 'extreme' environment with highly fluctuating and stressful physicochemical conditions for animals, where specially adapted animals form dense aggregations, mostly those relying on chemosymbionts. The molecular cross-talking between the host animal and their symbionts at vents has evolutionary significance that favor the survival of the holobiont to take advantage of such environment. A major example of such holobiont is the hairy snail genus *Alviniconcha* which enlarged gills which house Gammaproteobacterial or Campylobacterota symbionts at the intermediate phase between intracellular and extracelluar, but the molecular mechanisms allowing the host animal to carry out this symbiosis remained unclear. In this study, we assembled two high-quality *Alviniconcha* genomes, one harboring Gammaproteobacteria (*A. adamantis*) and the other harboring Campylobacterota (*A. marisindica*), to explore the adaptive strategies shared by these two species. From the gene family analyses, we show that the solute carrier gene families which can transport various nutrients are significantly expanded. We also found that the *Alviniconcha* snails have incomplete methionine biosynthesis pathways, but this is complemented by the capacity of both symbionts; indicating nutrient transportation and complement between host and symbiont. In the gill of *Alviniconcha* we detected high protein and gene expression of myoglobin as opposed to previously suggested hemoglobin, suggesting a strategy of storing oxygen in myoglobin as an adaptation to highly fluctuating oxygen availability in the environment. Comparing the gene expression level in the bacteriocytes versus other parts in the gill filaments highlighted that the host likely obtain nutrients from the symbionts predominantly by digestion via phagocytosis, but the milking without digestion was also present. Overall, our results provide a holistic view of host-symbiont interactions, revealing key adaptations of *Alviniconcha* snails to the deep-sea hydrothermal vent.

P3-9: Evolutionary Dynamics Exist Between Deep-Sea Mussels and Their Chemosynthetic Symbionts in Global Hydrothermal Vents

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The deep-sea environment is an extreme ecosystem characterized by high biomass, primarily driven by symbiotic relationships between animals and chemosynthetic microorganisms. Deep-sea mussels acquire their chemosynthetic symbionts from the environment during their early life stages and exhibit a global distribution in patchy habitats such as hydrothermal vents. These mussels are considered foundation species that create habitats for other organisms to colonize and supply essential nutrients, making them an invaluable model for investigating evolution and adaptation in the deep sea. Despite their importance, the establishment of symbiotic associations and local adaptation to variable environmental conditions remain poorly understood. To address this knowledge gap, this study employed metagenomic analysis of symbiont genomes to investigate the core metabolic capability for symbiosis in true Bathymodioline mussels, symbiont population diversification in response to environmental and host genetic factors, and the co-evolutionary dynamics between host and symbiont for local adaptation. Our hypothesis posits that globally distributed vent mussels display consistent symbiotic mechanisms, in tandem with locally adaptive features, and that the extent of symbiont reliance on host genetics varies across populations, underscoring the dynamic interplay between the host and its symbiont.

P3-10: The Origin and Evolution of Host Association of Bdellovibrionota in Marine Ecosystems

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Members of Bdellovibrionota phylum have been identified as symbionts in marine ecosystems and were primarily associated with sponge hosts. However, the origins and adaptations to sponge associations remain largely unknown. In this study, we reconstructed eight metagenome-assembled genomes (MAGs) of sponge-associated Bdellovibrionota, six of which are from the deep sea. We employed the phylogenetic analysis on the 423 Bdellovibrionota MAGs, which revealed sponge-specific clades such as f_Bin106 and f_JACOND01. Comparative genomics between sponge-associated and free-living Bdellovibrionota showed significant enrichment of genes in the sponge-associated group, including those encoding glycine cleavage systems. Additionally, the symbiotic Bdellovibrionota lack mobility systems (flagellum) compared to their free-living counterparts, highlighting their unique adaptations to a symbiotic relationship with sponges. This research enhances our understanding of evolutionary adaptation of Bdellovibrionota to the sponge association and underscores their crucial interactions in marine ecosystems, particularly in deep-sea environments where they impact host-symbiont dynamics.

P4-1: New Pacific Records of the Abyssopelagic Annelid *Buskiella abyssorum* (Flabelligeridae) and Synonymy of *B. flabelligera*

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Buskiella McIntosh, 1885 comprises three species of abyssopelagic annelids (Flabelligeridae): *B. abyssorum* McIntosh, 1885 from the central Atlantic, *B. flabelligera* (Hartman, 1967) from southern Chile (formerly *Flota flabelligera*), and *B. vitjasi* (Buzhinskaya, 1977) from the northwestern Pacific (formerly *Flota vitjasi*). Typically occurring at 2,800-6,500 m depth, these worms are characterized by an oligomeric body and long chaetae protruding from a gelatinous sheath. Morphological comparisons are challenging due to the damaged condition of type material and the frequent distortion of these animals during collection and preservation. The three species are morphologically distinguished only by the number and shape of gonopodial lobes, and genetic data have been lacking for specimens from the type localities. We report a trans-oceanic range extension of *B. abyssorum* from the Mid-Atlantic Ridge to the Clarion-Clipperton Zone in the eastern Pacific, based on 99.8-100.0% identical COI sequences of submersible-collected specimens from both localities. The morphology of the eastern Pacific specimens matches the description of *B. flabelligera* and the genetic connectivity implies overlap with the reported range of this species (southern Chile to Cape Horn). We therefore synonymize *B. flabelligera* as a junior synonym of *B. abyssorum*. Additional genetic records with >97% COI identity extend the Pacific range of *B. abyssorum* to the Gulf of California and Monterey Bay.

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P4-2: Examination of an Ecological Triple Junction: Mesopelagic Interactions with Surface and Bottom Faunas at the Oceanic Rim

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The unprecedented 2010 *Deepwater Horizon (DWH)* oil spill substantially impacted Gulf of Mexico (GOM) ecosystems and injured untold numbers of deep-sea taxa and the habitats they rely upon. In 2016, the DWH Trustees finalized their damage assessment and restoration plan, which called for a comprehensive, integrated ecosystem approach to restoration and robust monitoring and adaptive management throughout implementation. This requires identifying and filling data gaps. A project entitled *Deep-Sea Benefits (DSB): Outcomes of Mesophotic and Deep Benthic Restoration* (https://www.gulfspillrestoration.noaa.gov/project?id=350) will help fill these needs by identifying and quantifying the water column interactions with multiple deep-sea faunal groups. Building off prior GOM research, the DSB project will use multiple approaches to quantify mesopelagic nekton, marine mammal, and sea turtle interactions with upper bathyal benthic communities. Mesopelagic faunal composition, abundance, and distribution will be assessed with net sampling, active acoustics, and eDNA collection. Marine mammals will be assessed using passive acoustic monitoring and passive acoustic tracking; the latter can triangulate odontocete water-column locations and their interactions with mesopelagic prey fields observed by paired active acoustics monitoring. Sea turtle distribution will be assessed via eDNA monitoring. The information gleaned from the DSB project will increase our understanding of critical ecological connections in this and other oceanic rim ecosystems. This information will directly contribute to DWH-associated restoration planning and assessment as well as broader resource management within the GOM.

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P4-3: Interannual Variability of Local Cephalopod Community off Terceira Island Using Environmental DNA

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Understanding the food web dynamics of oceanic systems is crucial for predicting ecosystem responses to environmental changes, such as those driven by climate change. Cephalopods are key players in most oceanic food webs, serving not only as predators but also as important prey for larger marine nekton, such as sharks and cetaceans, thereby connecting higher and lower trophic levels. Despite their ecological significance, cephalopods, particularly those inhabiting the deep sea, remain largely understudied due to their tendency to evade common sampling methods like camera observation or nets, and their sometimes fragile nature. Environmental DNA (eDNA) offers a promising approach to filling this knowledge gap by enabling the detection of organisms based solely on the genetic material they leave behind. We analyzed 387 eDNA samples from 11 stations off Terceira Island, Azores, a hotspot for cephalopod biodiversity and foraging habitat for several deep-diving cetaceans, such as *Ziphius cavirostris*. Using eDNA metabarcoding with cephalopod-specific primers targeting the 18S and 16S rRNA gene, we assessed cephalopod community composition and its interannual variability in 2018, 2019, and 2020, expecting consistency over the years. Samples were collected in summer/fall each year from surface to bottom waters (down to 1600 m) at 100 m intervals, creating a unique, high-resolution deep pelagic eDNA cephalopod time series. We detected 57 taxa, with 68% belonging to the families *Mastigoteuthidae*, *Octopoteuthidae*, *Onychoteuthidae*, *Loliginidae*, *Chtenopterygidae*, *Chiroteuthidae*, *Enoploteuthidae*, *Histioteuthidae*, *Sepiolidae*, and *Cranchiidae* – many key components of local cetacean diets – which were present across all years. Additional notable findings comprise single-year detections of *Haliphron atlanticus* and *Vampyroteuthis infernalis*, as well as repeating detections of the giant squid *Architeuthis*. Our findings indicate that the cephalopod community off Terceira Island has remained stable over time, highlighting eDNA as a valuable tool for future community analyses, especially as databases become more comprehensive.

P4-4: Investigating Evolutionary Adaptation and Metabolic Interaction Between Deep-sea Host and Their Symbionts Through Genome-Scaled Metabolic Modelling

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Symbiosis in the deep sea has enabled many deep-sea organisms to thrive at extreme environments, such as cold seeps, hydrothermal vents and seamounts. While some studies have employed various methodologies to explore host-symbiotic relationships and distinctive adaptations to extreme deep-sea environments in clams, mussels, tubeworms and snails, there remains a gap regarding a systematic investigation of evolutionary adaptation and metabolic interaction between deep-sea host and their respective symbionts across a wide range of deep-sea organisms. In this study, we performed the reconstruction of high-quality genome-scale metabolic models (GSMMs) and evolutionary models based on annotated genomes. Our preliminary results suggested that the final metabolic model in host (*Archivesica marissinica*) and respective symbiont species comprised 1,557/457 genes, 2,576/1,436 reactions and 2,038/1,274 metabolites across three compartments, respectively. Comparative analysis will be conducted on metabolites on phylogenetic trees between hosts and their symbionts based on evolutionary model. Our study provides a systematic overview of the metabolites and metabolic pathways between deep-sea hosts and their symbionts from an evolutionary perspective.

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P4-5: Using Low Volume eDNA Methods to Sample Pelagic and Deep-Pelagic Marine Animal Assemblages

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Environmental DNA (eDNA) is an increasingly useful method for detecting pelagic animals in the ocean but typically requires large water volumes to sample diverse assemblages. Ship-based sampling programs that could implement eDNA methods generally have restrictive water budgets. Studies that quantify how eDNA methods perform on low water volumes in the ocean are limited, especially in deep-sea habitats with low animal biomass and poorly described species assemblages. Using 12S rRNA and COI gene primers, we quantified assemblages comprised of micronekton, coastal forage fishes, and zooplankton from low volume eDNA seawater samples (n = 436, 380–1,800 mL) collected at depths of 0–2,200 m in the southern California Current. We compared diversity in eDNA samples to concurrently collected trawl samples (n = 27), detecting a higher diversity of vertebrate and invertebrate groups in the eDNA samples. Differences in assemblage composition could be explained by variability in size-selectivity among methods and DNA primer suitability across taxonomic groups. Using hierarchical clustering, we resolved horizontal and vertical variability in marine animal assemblages from samples characterized by a relatively low diversity of ecologically important species. The number of reads and amplicon sequences variants (ASVs) per mL of seawater did not vary substantially among shallow (<200 m) and deep samples (>600 m). However, the proportion of invertebrate ASVs that could be assigned a species-level identification decreased with increasing sampling depth, reflecting underrepresentation of deep-sea taxa in reference sequence libraries. Low volume eDNA samples will quantify greater taxonomic diversity as libraries continue to expand, especially for deep-pelagic invertebrate species. To contribute to this effort, we are working to characterize the faunal diversity of poorly known but biomass-dominant crustaceans (Decapoda, Lophogastrida, Mysida) across epipelagic, mesopelagic, and upper bathypelagic habitats. This work will increase taxonomic familiarity with deep-pelagic crustacean biodiversity and expand verified reference libraries for deep-sea ecosystems.

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P4-6: Quantification of Gelatinous Zooplankton Community Structures in Two Contrasting Ocean Regions

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Zooplankton biomass and diversity is an essential ocean variable. However, biomasses and diversities of gelatinous zooplankton are not well quantified for most ocean regions and the deep sea. We used two in situ camera systems in two contrasting ocean regions to quantify pelagic gelatinous communities from 0 to 1000 m. In the eastern tropical North Atlantic, we performed pelagic horizontal video transects with a stereo camera mounted on the towed platform XOFOS along a sea surface productivity gradient from east to west. From the video transects, we inferred diversity and abundance, measured the size and calculated the biomass of 200 gelatinous individuals from 10 different taxa. In the oligotrophic eastern and central Mediterranean Sea, we performed towed horizontal video transects in the water column using the pelagic in situ observation system (PELAGIOS). Following video segmentation using a sliding background extractor and object tracking to avoid duplicates, we clustered objects larger than 1 cm and identified organisms to the lowest possible taxonomic level. Our preliminary results show that gelatinous taxa in the eastern Mediterranean Sea were significantly lower in diversity and abundance compared to the eastern tropical North Atlantic. These results fit with our hypothesis that energy availability is a major driver for shaping deep-sea gelatinous zooplankton community structure. Abundance and distribution in both systems had strongest correlation to sea surface productivity, which is affected by water column stratification and available energy. Most dominant groups were Hydromedusae and calycophoran siphonophores. In both systems, their abundances were highest at the deep chlorophyll maximum and at the most eutrophic stations. Our efforts pioneer in situ size and volume measurements of gelatinous taxa, and show how segmentation of pelagic transect videos may improve annotation efficiency and reduce observer variability. This will improve our understanding of poorly explored deep-sea pelagic environments.

P4-7: Trait Based Biodiversity Patterns in India's Deep Sea

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Decades ago, the deep sea biodiversity was a mystery to science and society. But, the curiosity of the pioneering researchers like William Beebe had unveiled such mystery through his curiosity driven journey of deep sea biodiversity exploration using a metal bathysphere. Since then, several hundreds of manned and unmanned submersibles are developed across the globe, which revealing the hidden deep sea life as well as paved way to discovery of tonnage of nodules present on the seabed, including Indian subcontinent. However, little is known about the diverse micro and macro-organisms with unexplored phenotypic and genotypic traits that play vital roles in deep-sea ecosystems and biogeochemical cycles. Thus, monitoring and conservation of deep sea biodiversity have become global interests in view of seabed mining and climate change scenarios. Indian subcontinent has a vast deep seabed area, whose biodiversity remains potentially undocumented and understudied from the aphotic zone. So far, the deep sea fish and shrimp resources have been widely exploited and studied. However, other deep sea biota has not been much documented like coastal resources. Here, we present the data of deep sea biodiversity based on traits such as bioluminescence, fluorescence, iridescence, and pigments. Additionally, the possible risks and threats to deep-sea biodiversity in the form of habitat disturbance, damage, water pollution, and substrate substitution, posed from bathypelagic trawlers and seabed mining will be presented. Further research is focused on to explore the deep sea biodiversity from the nodule forming locations to better understand the seasonal diversity dynamics and manage their conservation for future generations through important deep sea living resources security policies.

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P5-1: Glowing in the Depths: Unraveling the Bioluminescent Origins of Deep-Sea Shrimps (Dendrobranchiata, Caridea)

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Bioluminescence is estimated to have 94 independent origins across the metazoan tree of life, with representatives from nearly every phylum, underscoring the ecological significance of this adaptation as a universal language of light. Understanding the evolutionary pathways of bioluminescent modes is crucial for elucidating the adaptive significance and diversification of bioluminescent traits in marine environments. In decapod crustaceans, autogenic bioluminescence, the self-production of light in living organisms, has thus far only been positively documented in 157 shrimp species from 12 families spanning Dendrobranchiata and Caridea, but not in any other decapod groups. Despite this, the evolutionary history of bioluminescence across decapods remains unknown. Bioluminescence in shrimps may occur through a combination of modes, including specialized light-producing organs called photophores and/or defensive luminous secretions. Remarkably, all known bioluminescent modes are reported in both Dendrobranchiata and Caridea, groups estimated to have diverged approximately 400 million years ago. Several instances of lensed photophores with unique structural morphologies restricted to species of the same family suggest multiple independent origins of bioluminescence. This study combines existing genetic data from 20 previous molecular phylogenies with newly generated sequences to construct the most robust molecular shrimp phylogeny to date comprising 19 genes from over 700 taxa. Using a combination of Sanger sequencing and genome-skimming approaches with dense taxon sampling, this comprehensive effort aims to clarify family-level relationships across all shrimp groups. Additionally, this study seeks to investigate the evolutionary history of bioluminescent modes across shrimps using ancestral state reconstruction, providing insight and shedding light on the mechanisms and evolutionary pressures that shaped these adaptations.

P5-2: Ontogenetic Variation in Sensory Detection in Hydrothermal Shrimp Alvinocarididae

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Several species of shrimp in the Alvinocarididae family are known to occur in hydrothermal environments along the Mid-Atlantic Ridge (e.g. *Alvinocaris markensis, Rimicaris exoculata, Rimicaris chacei and Mirocaris fortunata*). In these species, the mechanisms involved in perceiving the environment in aphotic habitats are not completely understood. Recent studies have demonstrated a role for temperature in the localization of hydrothermal sites in adult individuals, whereas olfaction probably does not play an important a role as previously suggested (Ravaux et al. 2020). However, these two sensory modalities have never been studied at other life stages in our model species, notably in larvae. Being the dispersive phase, and traveling in the water column far from the hydrothermal emissions, their sensory modalities probably differ from those of adults. A study of the morphology of the sensory organs and receptors involved between life stages would provide a better understanding of how these species perceive their environment. In order to describe the processes involved in sensory detection by these species, we are examining both their sensory system (i.e. morphology of sensory organs, identification of receptors involved) and their central nervous system (i.e. brain areas). This presentation will focus on : 1/ the diversity and localization of receptors/co-receptors involved in two sensory modalities (i.e. thermodetection and olfaction), by a transcriptomic analysis of our four adult model species; 2/ the morphology of antennal appendages and central nervous system, throughout the development of these species using scanning and transmission-electron microscopy, as well as the structure of the brain using X-ray tomography (i.e. µCT-scan).

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P6-1: A Tale of Two Shrimp - Speciation and Demography of Two Sympatric *Rimicaris* Species from Vents of the Izu-Bonin-Mariana Volcanic Arcs

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The insular nature, typically with considerable distances between nearest sites and disrupting geographic barriers between them, makes deep-sea hydrothermal vents suitable as natural laboratories to study speciation processes especially given its highly specialized and endemic fauna. Two sympatric species of *Rimicaris* shrimp occur at vents from the Izu-Bonin-Mariana arcs: *Rimicaris* (formerly *Opaepele*) *loihi* and the recently described *Rimicaris cambonae*. Both species have very wide geographic distributions with the range of *R. loihi* further extending to Loihi Seamount near Hawaii and *R. cambonae* also occurring at West Mata volcano close to Tonga. These shrimp are genetically close with less than 2% genetic divergence in the COI gene, raising the question of how they can remain separate while co-occurring in the same habitat. Here, we use DNA barcoding and shotgun whole-genome sequencing to investigate whether the two species are indeed completely isolated or if gene flow with some hybridization still exist between them. For some vent fields, we also evaluated their population demography over several years with video transects and samplings to assess shrimp population densities and sex ratios. Our results show that *R. cambonae* and *R. loihi* are recently diverged but form two clearly distinct genetic groups, although with some hybrid individuals detected. We also observe that shrimp population densities fluctuate alongside their genetic diversities, according to variations in venting activities over the years. In addition, the two species differ by their sex ratio equilibria, largely biased toward females for *R. loihi* and equilibrated for *R. cambonae*, possibly suggesting distinct mating strategies in each. Finally, we discuss plausible scenarios that could have led to a recent speciation of these two shrimps despite their current sympatry, some level of ongoing gene flow, and very wide distribution ranges across the Pacific Ocean.

P6-2: Trophic Support in The High Antarctic Megafauna at Methane Seeps: Uncovering the Role of Chemosynthetic Production

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Chemosynthetic production from methane seep habitats can provide a food subsidy to non-seep endemic taxa. One place where this may be critical and analogous to deepsea habitats is the high Antarctic, where five months of darkness preclude photosynthetic production from fueling the abundant benthic community. Through a directed study of the only known, active Antarctic methane seep, we have found taxa that are not unique to the seep but instead abundant members of the Antarctic seafloor community that also inhabit seepage areas. Here, we identify the role of chemosynthetic production to the dominant megafaunal community: the sea star *Odontaster validus*, urchin *Sterechinus neumayeri*, and the nemertean *Parborlasia corrugata*. We sampled these taxa at the Cinder Cones seep and "control" sites just after the end of the Antarctic winter. 16S rRNA gene analysis indicated the presence of methanotrophic taxa in the megafauna's gut content (<1% of total sequences). The presence of *Methylococcales* (Type I methanotroph) and *Methanomicrobiales* (methanogen) were found within the guts of the *O.validus*(4.5% of individuals), *P.corrugata*(8.3%), and of *S.neumayeri*(11.1%); however, these were not limited to areas of known seepage. The potential widespread consumption of the methanotroph was supported by Fatty Acid (FA) analysis that resolved C16:1(n-7) and C18:2(n-6)c biomarkers, which are indicative, but not exclusive to, methanotrophic bacteria. These data support seasonal and widespread use of methane-fueled microbes as a food subsidy by the megafaunal community, however this is not their only source of nutrition. The presence of photosynthetic FA biomarkers (C20:4(n-6) and C20:5(n-3)), further support a diverse diet for these taxa. These key findings provide the first evidence of the potential ecological impact of Antarctic seepage on higher trophic levels and point to a seasonal importance of chemosynthetic production, adding a temporal component to the concept of a sphere of influence of seepage on marine habitats.

P6-3: Using eDNA to Map the Distribution of Deep-Sea Coral Epifaunal Associates on Seamounts in the Phoenix Islands Protected Area

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The deep sea exists as one of the most extreme and remote biomes on Earth, yet organisms thrive and form diverse communities by building unique relationships and symbioses with one another. Similar to their shallow-water counterparts, deep-sea coral form vital habitat for diverse assemblages of organisms that use the coral for protection, food, egg-laying substrate, and other ecological services. Coral-associated deep-sea invertebrates can be seen utilizing coral across the full diversity of interspecies relationships (mutualistic, facultative, predatory, etc.) and often with high fidelity between the epifauna and its host. Studying these associate species is important to accurately gauge the complexity and diversity of these deep-sea ecosystems and can improve our understanding of how they influence major processes of organic material decomposition, nutrient cycling, and carbon sequestration in the deep sea.

While environmental DNA (eDNA) is considered a powerful and cost-effective tool to measure regional species diversity, it has yet to be used to detect the presence of coral-associated invertebrate species in the deep sea. In this project, samples and metadata from a 2017 cruise by the NOAA vessel *Okeanos Explorer* and a 2021 cruise by the R/V *Falkor* to the seamounts of the Phoenix Islands Protected Area (PIPA) were analyzed to construct a genetic barcode database of coral-associated invertebrate species, including newly discovered species. These barcodes were used to analyze eDNA aliquots to determine if associate DNA is detectable in the surrounding water column. The results of this ongoing study have the potential to inform new applications of eDNA in the deep sea targeted at mapping the distribution patterns and association mechanisms of corals and their associate invertebrates.

P6-4: The Biomineralization Toolkit as Revealed by Genomic and Shell Matrix Proteomic Analyses of a Deep-Sea Vesicomyid Clam

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The solubility of calcium carbonate gradually increases with depth and hydrostatic pressure, which are basic characteristics of the deep sea. However, there are still a large number of bivalves whose shells mainly consist of calcium carbonate and shell matrix proteins in this environment. The shells of Archivesica marissinica (Mollusca, Bivalvia, Vesicomyidae) are directly exposed to ambient seawater, indicating a unique shell formation mechanism in this organism but remain poorly understood. In this study, a multi-omics analysis method combining genomics and proteomics is used to investigate the molecular characteristics of shell formation in the clams. We reported an updated A. marissinica genome with a size of 2.38 Gb, 18,788 predicted protein-coding genes and 96.5% completeness. This provides a basis for the following analysis. The shell matrix proteomic analysis revealed 191 proteins in the clam shells. These SMPs can be assigned into six broad groups, calcium-biding including 13 SMPs (6.8%) such as ISMPs, polysaccharide interaction during shell formation including 20 SMPs (10.5%) like chitin and other insoluble polysaccharides, 18 enzymes containing a total of 45 proteins (23.5%), extracellular matrix-related proteins including collagen, EGF, VWA and muclin-2-like proteins and more, and a total of proteins (52.4%) with blast homology but no predicted functions, as well as 13 proteins (6.8%) with no blast homology indicating some protein products may have been independently recruited into the biomineralization context and function in specific lineages. This study will support various follow-up studies to better understand the functions of these SMPs with biomineralization in the deep sea.

P6-5: Environmental DNA Metabarcoding Reveals Spatial Variation in Eukaryotic Communities at Hydrothermal Vents of the Central Indian Ridge

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Hydrothermal vents are unique deep-sea ecosystems characterized by extreme environmental conditions and high biodiversity, playing a crucial role in supporting complex ecological interactions. Growing concerns about the potential impacts of anthropogenic activities, such as resource exploitation and climate change, underscore the need for effective monitoring tools to manage and conserve these ecosystems by establishing environmental baseline data. In this study, we applied environmental DNA (eDNA) metabarcoding as a less-invasive and cost-effective tool to analyze the eukaryotic community structures of hydrothermal vents in the Central Indian Ridge, a large and hard-to-access ecosystem. Seawater samples, totaling four liters each, were collected from eight hydrothermal vent sites and one control site in the adjacent abyssal plain using Niskin bottles attached to a remotely operated vehicle (ROV). High-throughput sequencing targeting the 18S rRNA gene on the Illumina MiSeq platform yielded 907 amplicon sequence variants (ASVs) from 794,255 eukaryotic merged reads, which were assigned to 29 phyla and 62 classes. The majority of ASVs belonged to "Unknown", showing less than 90% sequence identity to currently deposited databases, indicating a high level of unexplored biodiversity. Among the identified ASVs, the phyla Radiozoa, Ascomycota, Euglenozoa, and Mollusca were most prevalent. Similarity analysis revealed that each eukaryotic community had its distinct structures and clustered into three groups at a 40% similarity cut-off, showing more related to latitudinal location rather than vent activity. Our results demonstrate the effectiveness of eDNA metabarcoding as a monitoring tool for hydrothermal vent ecosystems, providing valuable insights into community structures and their spatial variation without environmental disturbance. Continued efforts in expanding sequence databases are essential to enhance our understanding of hydrothermal vent ecosystems and establish tailored conservation strategies.

P6-6: Water Volume, Biological and PCR Replicates Influence the Environmental DNA (eDNA) Characterization of Deep-sea Pelagic Fish Communities

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The pelagic deep sea is challenging to investigate due to logistical constraints regarding access and collection of samples, however environmental DNA (eDNA) can potentially revolutionize our understanding of this ecosystem. Although advancements are being made regarding technology and eDNA samplers, many countries and research groups still do not have access to modern equipment. At the same time, no investigation has been performed to assess the impact of different experimental designs using common gear found on research vessels (i.e., CTD mounted with Niskin bottles). Here, we investigated the effects of sampled water volume, biological and PCR replicates in characterizing deep-sea pelagic biodiversity. Samples were collected at 450m depth at night in the northern Gulf of Mexico using Niskin bottles, and we targeted the fish community using the MiFish primer (12S rRNA). Our results show that 1L is insufficient to characterize deep-sea pelagic fish communities. The treatments 5L and 10L detected similar communities and numbers of species, but 10L detected more exact sequence variants (ESVs). Five biological replicates can detect up to 80% of the species detected in the water collected in both 5L and 10L treatments. Extrapolation analysis indicates that 10 replicates would also potentially recover 100% of the species. More biological replicates would be necessary to detect all ESVs. PCR replicates also had an important role in taxa and ESV detection, being the best strategy to perform more replicates if you filter less water (optimal number inversely proportional to the water volume filtered). We suggest that future studies collect at least 5L, 5 field replicates, and 5-10 PCR replicates to adequately investigate deep-sea pelagic biodiversity using eDNA, considering the limitations we mention. Our study provides guidance for future eDNA studies and a potential route to democratize eDNA studies at a global scale.

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P6-7: Proteomic Analyses Reveal the Key Role of Gene Co-Option in the Evolution of the Scaly-Foot Snail Scleritome

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Biomineralization as a key driving force behind the dramatic morphological diversity, is a process widely adopted by metazoans to incorporate inorganic minerals into organic matrices. The Scaly-foot Snail *Chrysomallon squamiferum* uniquely possesses hundreds of sclerites on the foot in addition to a coiled shell, which provides an exclusive case study to examine the formation of evolutionarily novel hard parts. Here, we identify matrix proteins present in sclerite and shells of *C. squamiferum* and *Gigantopelta aegis*, a confamilial species from the same vent habitat yet lacking sclerites to uncover the components presumably involved in the sclerite formation processes. Comparative multi-omics analysis suggests *C. squamiferum* co-opted a diverse range of metazoan bio-calcifying proteins through sclerite formation in a likely deep homology scenario, and up-regulated biomineralization-related genes in non-biomineralizing tissues implies alternative sources of sclerite proteins. Sclerite-secreting epithelium was revealed with employment and utilization of genes considerably older than those in mantle, supporting the predominant contribution of co-option in *C. squamiferum* sclerite formation. Our results highlight the significance of gene co-option in shaping novel hard parts in animals and indicate the incorporation of lineage-specific genes is likely a key factor leading to the great diversity of hard parts seen among molluscs.

P6-8: A New Species of *Acharax* (Bivalvia, Solemyida, Solemyidae) from the Haima Cold Seep, with New Insights into the Mitogenome Characteristics of Solemyidae Bivalves

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Solemyidae is an ancient group of protobranch bivalves that typically inhabit unusual environments, such as deep-sea chemosynthetic environments, and are symbiotic with chemoautotrophic and gill-hosted bacteria. In May 2018, a living solemyid bivalve was collected using a remotely operated vehicle at a depth of 1,390 m from the Haima cold seep in the northwestern slope of the South China Sea. Through a comprehensive taxonomic approach combining morphological observations and molecular phylogeny reconstruction of concatenated mitochondrial COI,16S rRNA and 18S rRNA gene sequences, a new species, *Acharax haimaensis* **sp. nov.** is identified and described. Then the complete mitogenome of *A. haimaensis* was determined and compared with other available mitogenomes of solemyids. The mitogenome of Acharax sp. is 18 970 bp in length and consists of 13 protein-coding genes, 2 ribosomal RNA genes, and 22 transfer RNA genes. The gene arrangement was identical to those of other sequenced solemyids. The Ka/Ks ratio analyses indicated that 13 protein-coding genes of present five Solemyidae mitogenomes suffered strong purifying selection. Compared to 45 existing shallow water equivalents, the 18 available mitogenomes from the deep-sea, including the *A. haimaensis* in this study, show significantly more nonpolar amino acids in the 13 protein-coding genes, which indicates the adaptation to the deep-sea environment. The phylogenetic tree based on 48 Bivalvia complete mitogenomes provided further information to support the scientific classification of protobranchs. The relationships among Solemyidae were assessed based on 2 mitochondrial (16S rRNA and COX1) and 3 nuclear (18S rRNA, 28S rRNA, and histone H3) gene sequences from 17 in-group species. The two genera *Acharax* and *Solemya* formed a monophyletic clade each, and *A. haimaensis* clustered with previously reported Acharax bivalves with high support values.

P6-9: Population Genetic Structure and Diversity of the Sharpchin Slickhead, *Bajacalifornia burragei*

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The sharpchin slickhead, *Bajacalifornia burragei*, is a deep-sea fish endemic to the eastern North Pacific Ocean. While the phylogenetic placement of its order, Alepocephaliformes, has been examined previously, the population genetics of *B. burragei* remain unexplored. This study aims to characterize the genetic structure and diversity of this species within the Carmen Basin, Gulf of California, by analyzing mitochondrial genome sequences. Four individuals of *B. burragei* were collected in a single trawl at 1,300 meters in the Carmen Basin, Gulf of California in May, 2024 from the R/V *Sally Ride.* This specimen underwent whole genome sequencing, and a high-quality reference genome was generated using PacBio long reads for one specimen, while the remaining three genomes were assembled using Illumina PE150 data. By comparing mitochondrial genome sequences, we assess nucleotide diversity, calculate Fst values, and infer maternal lineages.

P6-10: Population Structure of Deep-Sea Octocoral *Acanella Arbuscula* (Isididae) Across the North Atlantic, Using Snps Generated from UCE Sequencing

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Large gardens of *Acanella arbuscula* growing in soft sediments are uprooted and destroyed when contact with fishing gear occurs. These octocorals are ecologically important, because *A. arbuscula* are known to host species of ophiuroid sea star, polychaete, nematode, copepod, anemones, barnacle, and crinoid feather star. They are often found in association with commercially important redfish (*Sebastes* spp.). To investigate population connectivity of *A. arbuscula* across the North Atlantic, specimens were collected at multiple depth bands from nearly its entire geographic range from Newfoundland and Labrador (Canada), Greenland, Scotland, Ireland, and Spain. Population structure was inferred from the analysis of single nucleotide polymorphisms (SNPs) generated through high throughput sequencing of ultra-conserved elements (UCEs). Furthermore, the 5,783 SNPs were used to test the depth differentiation hypothesis across the North Atlantic which proposes that there is greater genetic differentiation across depth ranges as opposed to geographical distance. Sites within all depth bands in Canada and Greenland were well connected and exhibited high relative levels of gene flow to the deepest sites in Scotland, Ireland, and Spain. Shallower sites in Scotland and Ireland were well connected to each other but isolated from the rest of the study sites with nearly zero gene flow to the Canadian and deeper European sites. The shallowest site in Spain formed a genetically distinct population with very little geneflow to the other European sites and Canada. An investigation into the possibility of cryptic species forming the genetically distinct isolated populations is being conducted. Additionally, local adaptation to temperature, phosphate, nitrate, pH, oxygenation, chlorophyll concentration, and salinity was tested against UCE marker allelic frequency. Twelve UCE loci showed significant evidence of local adaptation in *A. arbuscula* populations in response to sea floor temperature. The main driver of local adaptation in *Acanella* across the environmental variables tested was sea floor temperature.

P6-11: Metagenomic Analysis of Deep-sea Mussels Revealed a Mosaic Evolution Pattern of Endosymbionts Driven by Heterogeneous Environments

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The within-species diversity of symbiotic bacteria represents an important genetic resource for their environmental adaptation, especially for horizontally transmitted endosymbionts. Although strain-level intraspecies variation has recently been detected in many deep-sea endosymbionts, their ecological role in environmental adaptation, their genome evolution pattern under heterogeneous geochemical environments, and the underlying molecular forces remain unclear.

Here, we conducted a fine-scale metagenomic analysis of the deep-sea mussel *Gigantidas platifrons* bacterial endosymbiont collected from distinct habitats: hydrothermal vent and methane seep. Endosymbiont genomes were assembled using a pipeline that distinguishes within-species variation and revealed highly heterogeneous compositions in mussels from different habitats. Phylogenetic analysis separated the assemblies into three distinct environment-linked clades. Their functional differentiation follows a mosaic evolutionary pattern. Core genes, essential for central metabolic function and symbiosis, were conserved across all clades. Clade-specific genes associated with heavy metal resistance, pH homeostasis, and nitrate utilization exhibited signals of accelerated evolution. Notably, transposable elements and plasmids contributed to the genetic reshuffling of the symbiont genomes and likely accelerated adaptive evolution through pseudogenization and the introduction of new genes.

The current study uncovers the environment-driven evolution of deep-sea symbionts mediated by mobile genetic elements. Its findings highlight a potentially common and critical role of within-species diversity in animal-microbiome symbioses.

P6-12: Genomic Features and Distribution Patterns of Viruses That Infect Cyanobacteria in the Deep Dark Ocean

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As the smallest phototroph with biological rhythms, the unicellular cyanobacterium *Prochlorococcus* is a key contributor to marine primary productivity and ocean carbon cycling. The infection process of cyanobacteria by viruses (cyanophages) can be regulated by the light level, with some cyanophages being able to infect host cells only in the light while others can even infect host cells in total darkness. However, the genomic features and distribution patterns of viruses with different dark infection traits are not fully understood. Here, we isolated and sequenced multiple cyanopodoviruses in the South China Sea near the Yongxing Island. These phages displayed unique and diverse genomic structures. Using qPCR, we identified three distinct dark infection traits in 21 cyanopodoviruses: NN (no adsorption, no replication), AN (adsorption, no replication), and AR (adsorption and replication). Spatial and temporal distribution patterns of these cyanophages in the ocean are revealed by metagenomic analysis. The abundances of the three viral groups vary from surface to 500 meters below sea level. We reveal that NN and AN cyanophages are more prevalent in surface waters and less abundant in mid/deep waters, whereas AR cyanophages gain a competitive advantage in deeper waters due to less light dependency. Notably, the global distribution of the three groups was closely related to the abundance of *Prochlorococcus*. This work generates in situ insights into cyanophage rhythms, highlighting the environmental drivers shaping their spatiotemporal distribution and interaction with *Prochlorococcus* hosts.

P6-13: Comparative Transcriptomics for Mollusc Neuron Cell Type Identification

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Molluscs are the second most specious phylum, this is accompanied by great diversity in morphology, ecological role and cognitive ability. While many molluscs, such as many gastropods or bivalves, have reduced or otherwise simple nervous systems, the coleoid cephalopods possess a highly centralised nervous system and are capable of certain complex tasks. However, the relationship between structure and function of the mollusc is poorly understood. Hence, we will analyse the neuron transcriptomes of molluscs across the phylum including cephalopods, gastropods and polyplacophora in order to identify the different cell types present across molluscs. This has already been done in some species such as the gastropod *Berghia stephanieae* but no comparative study has been done between species. The evolutionary relationship of these cells will then be investigated, allowing for the identification of novel cell types and unique genes within groups. Following this, the structure of mollusc neuronal systems can then be studied through the use of in-situ hybridisation, highlighting the interaction of these different cell types in the brain. This information would allow for a greater understanding of how these structures affect cognitive ability and the development of greater cognitive abilities.

P7-1: A Species Trait-Based Database for the Entire Offshore Pacific Bioregion, Canada

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Offshore areas present specific challenges for their understanding and management due to their remoteness, limited knowledge of species and habitat distributions, and poorly understanding of change rates and scales. The Offshore Pacific Bioregion (OPB), Canada, is a vast area which covers unique shallow and deep ecosystems, seafloor features such as seamounts and hydrothermal vents, and several marine protected areas. The Trait Offshore Research Synthesis (TraitORS) project aims to collaborate with knowledge holders, scientists, and managers to build a trait-based database for the species inhabiting the OPB. This includes all animal species from the meio- to megafauna size fractions from benthic and pelagic environments, that is, from zooplankton to seabirds and whales, and from the deep sea all the way up to shallow waters. Ultimately, the species trait database will underpin the development of key Essential Biodiversity Variables, or indicators, for monitoring and reporting against conservation objectives and internationally agreed conventions and treaties.

P7-2: Baseline Assessment of Deep-Sea Biodiversity in Trinidad and Tobago: Implications for Conservation and Resource Management

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The deep sea encompasses nearly 70% of Trinidad and Tobago's' Exclusive Economic Zone, with depths ranging between 200 to 3500 metres. Despite it being the largest ecosystem in Trinidad and Tobago, biological knowledge remains extremely limited, with only a handful of studies conducted. Robust baseline knowledge is critical for effective decision-making regarding Trinidad and Tobago's deep ocean, particularly as deepwater oil and gas extraction is on the horizon. This study assesses the current state of knowledge of deep-sea biodiversity in Trinidad and Tobago. Following an in-depth examination of existing deep-sea species records from scientific literature, museum databases, fisheries reports, cruise reports, reference collections, and online databases, we present a comprehensive inventory of invertebrate and fish fauna found in Trinidad and Tobago's deep sea. Here we discuss trends in the limited existing knowledge and propose priority areas for future research, given the substantial knowledge gaps that remain. For example, depths below 2200m are completely unknown, and observed species richness continues to increase with sampling effort, suggesting a high potential for undiscovered biodiversity. This study reveals helpful insights and underscores the urgent need for expanded deep-sea exploration, systematic data collection, and increased capacity building with local scientists.

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P7-3: Variation and Diversity of Deep Seabed Macrofaunal Communities in the Rockall Trough

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The Extended Ellett Line is a long-running repeat hydrographic section in the North East Atlantic that begins off the sound of Mull and crosses the Rockall Trough before ending off Iceland. The Rockall Trough has been a specific area of economic and scientific interest for decades. Benthic samples from one of the fixed stations within the trough have been collected from the mid-1970s until 2016 at 2200m depth. During my PhD project, I will use these samples to assess how the benthic community has responded to changes in surface parameters, (temperature, salinity and plankton dynamics) over time.

Long-running deep-sea time series, such as the Ellett Line, are rare and very important in identifying baseline changes in habitats. By identifying faunal diversity over long timescales, I aim to identify variations in benthic community structure, functional group dominance and abundance from year to year and over multiple decades. It is predicted that almost every plankton group will decrease in abundance in the North East Atlantic over the coming decades, meaning less carbon sinking to the deep sea. Will changes in the North East Atlantic system and particle flux, due to climate change and ocean warming, significantly affect these deep seabed ecosystems? And to what extent have they changed already?

P7-4: Benthic Habitat Distribution and Diversity on the Slopes of Madeira

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Baseline data on biodiversity and spatial distribution of deep-sea benthic habitats is critical to enable measurements of the impacts of anthropogenic stressors. However, such data is missing for many regions in the world. This is why it is essential to describe and map benthic habitats to allow future targeted research and monitoring efforts. The Madeira archipelago is part of the Macaronesia bioregion and is located in the North-East Atlantic. The steep volcanic slopes of Madeira reach the deep sea close to the island, making it a comparatively accessible study region for deep-sea biology and ecology. In this context, during the research cruise MSM126 in February/March 2024 we collected benthic video and image transects of Madeira's slopes between 70 and 1800 m of depth with the remotely operated vehicle (ROV) "PHOCA" as well as with the towed camera system XOFOS. Additionally, we collected bathymetry and backscatter data with two ship-based multibeam echosounders, a Kongsberg EM712 and EM122. The expedition resulted in a total of six benthic ROV and seven benthic XOFOS dives on the southern flanks of Madeira and over 270 km2 of mapped seafloor with multibeam echosounders, which we present and discuss here. A clear depth zonation of benthic habitats on the slopes of Madeira was observed and several habitats with vulnerable marine ecosystem (VME) indicator taxa were identified. These include mesophotic black coral forests, deep-sea xenophyophore fields, as well as deep-sea coral and sponge aggregations. Additionally, we will highlight observations of habitat-associated sessile and mobile fauna. Finally, we report clear signs of anthropogenic pressure through marine litter including lost fishing longlines. We will discuss our findings in the broader framework of benthic biodiversity and distribution off oceanic islands in the North-East Atlantic.

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P7-5: Examining Abundance and Condition Changes in Northeast Pacific Seamount Foundation Species Using High-Resolution Photogrammetry Mosaics

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The Northeast Pacific Ocean is distinctive, containing some of the lowest oxygen levels in the global ocean and losing oxygen rapidly. These changing conditions threaten the abundant, long-lived foundation species (i.e., cold-water corals and sponges) on at least 38 seamounts in Canadian waters. Within Canada, many Marine Protected Areas (MPAs) aim to maintain and restore cold-water corals and sponges given a backdrop of rapid ocean change. However, our current understanding of how these species are responding to ocean change is lacking. Long-term monitoring sites were established in 2018 on seamounts within the MPAs at depths identified as vulnerable to further oxygen depletion. Several of these sites have been resurveyed for the first time, between 3and 5-years post establishment. 3D reconstructions were created for each of the resurveyed sites and compared to baseline reconstructions to 1) examine changes in the abundance and condition (i.e., health) of foundation species and 2) provide advice for future monitoring efforts as different tools (e.g., remotely operated vehicles, drop-camera) are used year to year. We observed changes in abundance and condition of cold-water corals and sponges for all 13 monitoring sites. We find that while abundance and condition changes for foundation species are apparent and measurable, especially for sites within the oxygen minimum zone, the magnitude of these changes varied greatly between sites. Further, we find that drop-cameras are sufficient to capture abundance information for large, conspicuous species; however, condition metrics and small, cryptic species are often indiscernible. Variations in changes between sites highlights the importance of further ecological studies to identify drivers of foundation species biodiversity within the Northeast Pacific. Moreover, our study provides necessary information to report on the current status and trends, guide future monitoring efforts, and facilitate adaptive MPA management by the Federal Government and co-managing First Nations.

P7-6: Expanding the Red List for Global Hydrothermal Vent Endemic Species

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The IUCN global Red List of threatened species is the most well recognized conservation communication tool in the world, providing an extinction risk assessment for individual species. Although the IUCN Red List method can be applied to any (macroscopic) organism, it is largely under-used for marine species, and especially for the deep sea. Under the newly-formed IUCN Marine Invertebrate Red List Authority, we have set a goal to assess all species endemic to hydrothermal vents for the global Red List. Red List assessments for vent molluscs were published in 2021, under a project that developed a method for applying IUCN Red List criteria to hydrothermal vent endemics. The time has come to assess all other known vent endemic macrofaunal taxa. An initial taxon list of 499 species containing annelids, cnidarians, echinoderms, nematodes, nemerteans, porifera, arthropods, and a few added molluscs is currently being investigated, and a team including experienced researchers and volunteers has begun assessing the selected species. Hydrothermal vents face significant threats from deep sea mining, prompting the protection of some vents within Exclusive Economic Zones (EEZs) under national regulations against mining or a part of MPAs. However, vents in Areas Beyond National Jurisdiction (ABNJ) remain less protected, though a general decision regarding mining in ABNJs is expected from the International Seabed Authority (ISA) soon. It is crucial to assess the vent-endemic species before extensive mining activities begin. The Red List category for each vent species—ranging from “Least Concern” to “Critically Endangered”—is primarily determined by a combination of geographical range and the potential for mining or Marine Protected Areas (MPAs). A global map of extinction risk across many phyla will provide an important tool to communicate the vulnerability of these unique habitats and the potential effectiveness of deep sea MPAs.

This project is funded by a generous philanthropic donation that supports the Senckenberg Ocean Species Alliance (SOSA) with additional support from the International Union for the Conservation of Nature (IUCN).]

P7-7: Macroinvertebrate Communities Inhabiting Hard Substrates at Southern California Methane Seeps

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Methane seeps are distinct deep-sea ecosystems characterized by the release of methane and other hydrocarbons, recognized for hosting diverse invertebrate communities and playing a crucial role in global carbon cycling. As part of the Challenger 150 program under the UN Ocean Decade initiative, this study aims to characterize macroinvertebrate communities at methane seeps along the southern California margin, addressing questions about their distribution and response to environmental gradients. Utilizing samples collected by the submersible ALVIN from the RV Atlantis during cruise AT50-12, carbonate rock samples from six seep sites were analyzed for macrofaunal density, diversity, and composition. Preliminary observations indicate varied densities across sites, with shallower and oxygenated sites exhibiting higher densities compared to deeper and low-oxygenated sites. Depth and oxygen concentrations influenced community structure, but seepage activity did not, highlighting the complex dynamics of methane seep ecosystems. Comparison of macrofaunal community structures on colonization experiments and transplant rocks is currently underway and will provide insights into the resilience and adaptability of seep communities under changing seepage. Continuing the study of methane seeps is imperative to deepen the understanding of these ecosystems and implement effective conservation and management strategies, aligning with the goals of the UN Decade of Ocean Science.

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P7-8: Restoring Deep-Sea Habitats to Rebuild European Seas: the REDRESS project

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The REDRESS project aims to provide a key contribution to the EU commitments towards restoring degraded deep-sea ecosystems. This is the first EU funded project entirely devoted to the restoration of deep-sea ecosystems. REDRESS will provide solutions to prioritize future restoration actions, expand deep-sea restoration approaches to novel (previously neglected) deep-sea habitats, and demonstrate the feasibility, potential, and value for success of deep-sea ecosystem restoration. The project will focus on habitats that have great potential to contribute to carbon sequestration and climate mitigation. Most of these have been degraded by deep-sea fishing, especially trawling, and by the development of deep-sea infrastructures and extraction activities. The project will focus on vulnerable marine ecosystems, including sea pens and bamboo corals on soft sediments, coral gardens, cold-water coral reefs, sponge fields, and cold seeps. The project will map degraded deep-sea habitats and identify habitat refugia to prioritize restoration efforts that will adapt to future scenarios of climate change. The development of cutting-edge solutions in REDRESS will make a significant technological investment and will benefit from a relevant ship time by in-kind contribution (136 days of fieldwork). REDRESS will offer nature-based solutions to public authorities and operators to advance ecosystem restoration in the deep sea. Building on the previous experience, REDRESS will go beyond the state of art, either developing new methodologies, using sophisticated technologies, defining success indicators, and expanding the target habitats also to cold seeps. Finally, REDRESS will provide novel insights into the advantages and limits of active vs passive deep-sea restoration, and related cost-benefit analysis of restoration in different deep-sea habitats. The results will enable a significant advancement in the EU's marine restoration strategy supporting policies and decision makers in the future application of the Nature Restoration Law.

P7-9: Does Larval Behaviour Affect Dispersal? Using Larval Dispersal Modelling to Investigate Deep Sea Coral Connectivity in the Scotia Sea, Southern Ocean

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The Scotia Sea (Southern Ocean) is home to many species of deep-sea coral that are key to creating habitats for other deep-sea organisms. Despite their ecological importance, we still have much to learn about their biological properties (e.g. reproduction), and the connectivity and resilience of known populations.

There are many intersecting challenges (seasonal sea-ice, ocean conditions etc) when it comes to collecting samples or observing these organisms *in-situ*, so larval dispersal modelling offers a method for investigating the potential connectivity of populations of species', and testing whether different larval behaviour impacts species' dispersal and connectivity.

We have used a generalised set of larval behaviours - not associated with any one species, but to cover a range of options that could be possible for coral in that region - and modelled dispersal from around the geological features of the Scotia sea (Scotia ridge, islands etc) and the open ocean to investigate whether the behaviour of the larvae impacts it's dispersal potential in the region.

We hope to share our preliminary results of this investigation, along with our plans for ground truthing these results with our population genomic dataset.

P7-10: Science-Policy Gap Analysis for Mesopelagic Fishes, Fisheries and Ecosystems

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Mesopelagic ecosystems are a global feature, hosting diverse and abundant communities of animals whose collective movements and roles in food webs and biogeochemical cycling connect ocean midwaters to surface ecosystems above and deep-ocean environments below. While scientific advances abound, considerable geographic and scientific gaps still prevent a comprehensive assessment of how mesopelagic communities may be impacted by future anthropogenic threats (e.g., fisheries, deep-sea mining, oil spills). This hinders the ability of policymakers to implement science-based policy decisions to conserve mesopelagic ecosystems, and oceanic ecosystems more broadly. In this study, we detail the process and preliminary outcomes of a survey targeting the collective knowledge of a diverse range of stakeholders with mesopelagic expertise, including scientists, policymakers, industry representatives, and non-governmental organizations. We will analyze expert opinion-based data through thematic coding, content analysis, and statistical techniques to identify key themes, patterns, and priorities. We will pinpoint current and potential knowledge gaps and spatial disparities that hinder effective management and conservation efforts in the global mesopelagic zone across three thematic areas (basic science, anthropogenic threats, and policy/management). These insights aim to evaluate the integration of recent scientific discoveries into existing policies governing the mesopelagic zone and inform future research priorities and regions to enhance the management and conservation of the deep-pelagic ocean.

P7-11: Subseafloor Life at Hydrothermal Vents: Macrofauna Diversity and Trait-Analyses

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During an expedition with *RV Falkor to*o and ROV *SuBastian* to hydrothermal vents at the 9°North East Pacific Rise (9NEPR) at 2500 meters depth in July 2023, animal life was discovered for the first time in shallow subseafloor cavities. The project SUBLIFE aims to elucidate the nature and extent of connectivity between the seafloor surface and subseafloor vent habitats, by determining which meio- and macrofaunal species can use the vent subseafloor as a permanent or transient habitat.

Meio- and macrofauna were sampled with the suction sampler and grabs of the ROV from 6 vent surface patches and subseafloor cavities at the vent site Fava Flow Suburbs, as well as from nearby bare-basalt locations. The specimens were identified to species level whenever possible. Community composition on each habitat (surface and subseafloor) was compared based on trait analyses aiming to investigate the variation and distribution of morphologies, functions and life histories of the over 50 macrofaunal species reported. Meiofauna was also present in the subseafloor but has not been analyzed yet. Juveniles and adults of vent endemic gastropods and polychaetes such as (e.g. *Eulepetopsis vitrea* J. H. McLean, 1990; *Amphisamytha galapagensis* Zottoli, 1983; *Archinome rosacea* (Blake, 1985)) were discovered in subseafloor cavities. These species are known to reproduce via larvae, suggesting the potential role of the subseafloor habitat as connectivity corridors during larval dispersal and early life stages. The characterization of subseafloor communities will transform our understanding of the ecology at deep-sea hydrothermal vents, particularly regarding animal recruitment and connectivity.

[The project SUBLIFE is funded by NWO (OCENW.M.22.080) to Sabine Gollner (PI), as well as SOI (Subsurface life – from viruses to animals – at deep-sea hydrothermal vents, 2023) and Austrian Science (FWF 31543) to Monika Bright (PI; Chief Scientist).]

P7-12: Microplastic Concentration in Mussels and Snails Living in Deep-Sea Hydrothermal Vents of the Southwest Pacific and Indian Oceans

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Plastic pollution, driven by various human activities, significantly impacts water environments, ecosystems, and potentially human health. However, the effects of microplastics on organisms in deep-sea hydrothermal vents remain poorly understood. In this study, we investigated plastic concentration in two deep-sea mussel species (*Bathymodiolus*) and two hairy snail species (*Alviniconcha*), living in hydrothermal vents in the Southwest Pacific and Indian Oceans. The identified microplastics consisted primarily of polystyrene (56.10%), acrylic nitrile (19.51%), polyethylene (17.07%), with smaller amounts of other polymers. Most detected particles were fragments (92.68%), with the remainder being fibers (7.32%). The composition of microplastics varied by sampling site and species, with levels in the Indian Ocean approximately 1.9 times higher than in the Pacific. Previous studies estimate that around 15% of the world's marine plastic enters the Indian Ocean, contributing to the presence of microplastics in near-shore and oceanic areas. These findings underscore the extensive impact of plastic pollution in deep-sea environments and the potential risks it poses to marine life.

P7-13: The Natural History Museum Deep-Sea Research Lab: Advancing Knowledge in Biodiversity, Taxonomy, Ecology and Evolution

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The Natural History Museum in London has a long history of deep-sea research alongside a vast collection of deep-sea specimens and samples. Over 10,000 samples from the HMS Challenger voyage are housed in the collection, and for the last 150 years the NHM has been actively leading deep-sea research as well building up an unparalleled collection of reference materials. For the last twenty years, the NHM has operated a Deep-Sea Research Lab focused on an end-to-end approach to deep-sea discovery, biodiversity science, taxonomy, evolutionary ecology that includes all aspects of research from leading oceanographic cruises to archiving specimens for future generations. Increasing societal discussion on debate on the potential for deep-sea resources such as minerals has made these data more relevant than ever before. Funded by a range of stakeholders including government, industry and philanthropy we synthesise evidence to improve our understanding of the ecology, biodiversity, conservation, population connectivity and evolutionary biology of deep-sea and Antarctic invertebrate animals. Underpinning all our work is sound taxonomy using the latest DNA methods and a commitment to open, transparent publication in the peer-reviewed literature alongside archiving materials for future generations.

We are always looking for new collaborations and opportunities. To enquire about our services please email georgina.glaser@nhm.ac.uk or visit our website www.nhm.ac.uk/deep-sea.

P7-14: Seabed Heterogeneity Regulates Megabenthic Community Patterns in Abyssal Nodule Fields

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Polymetallic nodule fields, between 3000-6000m water depth, harbour some of the most diverse seabed communities in the abyss. In these habitats, nodules and rock patches are keystone structures to many sessile species that depend on these hard substrata for growth. Polymetallic nodule patches can vary in size, shape and seabed coverage pattern; however, the effect of these variations on benthic communities remains largely unclear. Understanding the influence of nodule type on spatial patterns of biodiversity is urgently needed to accurately assess the impacts of potential nodule removal in areas like the Clarion-Clipperton Zone, a region targeted for deep-sea mining. Here, we explored variations in invertebrate megafauna (animals >10 mm) across space and nodule types within an abyssal seascape. We quantified changes in density, diversity and community composition using quantitative seabed imagery in 4 study areas. We reveal that different nodule types harboured distinct assemblages, with certain taxa being significantly more abundant in areas with particular nodule types. Study areas also exhibited varying levels of seabed heterogeneity, defined by the proportions of different nodule types present in each study area. The most heterogenous study area, which had multiple nodule types and sediment-only patches, had higher species richness and distinct community composition. This suggests both nodule type and seabed heterogeneity are an important driver of local benthic biodiversity patterns in abyssal nodule fields. By establishing a conditions baseline prior to any human disturbance, our study provides essential insights that should inform future monitoring programmes, regulations of mining activities, and biodiversity conservation in abyssal nodule field areas.

P7-15: MEER: Extraordinary Flourishing Ecosystem in the Deepest Ocean

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Here, we introduce the Mariana Trench Environment and Ecology Research (MEER) project, which provides the first panoramic view of life in the deepest ocean.

The full ocean-depth rated manned submersible Fendouzhe (placed in active service in 2021) provided new opportunities for systematic hadal investigation. During our TS21 expedition from August to November in 2021, we carried out 33 Fendouzhe dives, successfully collected hadal microorganism samples from 227 push-cores (~1,700 stratified sediment samples), 12 in-situ filtered seawater samples and typical hadal macroorganism samples (including both amphipods and fishes) covering the depth from 6000 to 10900 m. Sampling sites covered the Mariana Trench, Yap Trench and Philippine Basin. These precious and sufficient hadal samples laid the foundation for achieving a detailed description of the ecosystems in the deepest ocean regions.

MEER results provide a systematic picture of the amazing hadal ecosystems, especially the abnormal flourishing of microorganisms under ultra-high pressure in the deepest ocean. We specifically answer the following questions: (i) Why does the hadal microbiome have extremely high novelty and diversity? (ii) How do hadal microorganisms adapt to the hadal? (iii) How do hadal macrofauna adapt to the extreme hadal conditions, invertebrates vs. vertebrates?

P7-16: A Hidden Skatepark: Discovery of a Skate Egg-Case Nursery on a Costa Rican Seamount

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Nursery areas are crucial for the development and survival of vulnerable deep-water batoid species, yet research on these essential habitats remains limited. Here we report the discovery of a large aggregation of skate egg cases at the summit (1900 m depth) on Tengosed Seamount off Costa Rica in the 'Pampa Submarina' region during two expeditions aboard the Schmidt Ocean Institute's R/V *Falkor (too)* in 2023. We also recorded the presence of several adult Pacific White skates (*Bathyraja spinosissima*), leading us to propose and characterize this site as an egg-case nursery, hence the proposed name of 'The Skatepark.' Eight egg cases were collected, with three containing embryos and five hatched and degraded. Ongoing genetic analysis will confirm the species, while ROV image analysis of the site is assessing the scale of the nursery. Environmental data is also being analyzed to understand why this site is used by skates. The high density of egg cases suggests that skates are specifically targeting this site for egg-laying, highlighting the Skatepark's critical role as a nursery. These findings are crucial for understanding the life-history traits of slow-growing deep-water skates and highlight the urgent need for tailored conservation efforts to identify and protect these vulnerable habitats.

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P7-17: Widespread Chemosynthesis in Seeps and Background Communities Through the Lens of Infauna in McMurdo Sound, Antarctica

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The challenge of accessing chemosynthetic habitats in the deep sea inhibits our ability to study temporal and spatial dynamics of seep systems. Analogous or model habitats provide one option to advance our understanding of the role of chemosynthesis in ocean ecosystems. The discovery of seepage at only 10 m water depth in the High Antarctic, at a latitude that experiences 5 months of darkness, and at a site where we know that seepage began in 2011, allows us to observe shifts in trophic support as the seep ages. Here we quantified the dietary support and community dynamics of the infaunal community at this seep, 10 years after it began seeping. Macrofauna community dynamics coupled with 16S gene gut content analysis, and Fatty Acid Methyl Ester (FAME) methods were conducted at 4 locations around the McMurdo Sound, two of which have seepage, and two that do not. In the most intense areas of seepage, the infauna were dominated by mobile epibenthic organisms (isopods, ostracods, amphipods), whereas at areas of reduced seepage the communities were analogous to background communities, dominated by tube-dwelling polychaetes and burrowing anemones (*Edwardsia sp.*). Surprisingly, independent of seepage being present, the 16S gut content analysis revealed a diversity of chemoautotrophic taxa with the guts of *Edwardsia*, including taxa involved in the methane cycle. This ubiquity of chemoautotrophic microbes supports widespread chemosynthetic potential throughout the Sound with a potential role of trophic support to the infaunal community. This is not to imply that there was a uniform diet at sites as FAME analysis highlighted different fatty acid signatures between seep and non-seep sites, indicating different sources of trophic support. This highlights the importance of chemosynthesis to marine systems, both at areas of active methane release as well as to the overall benthic ecosystem.

P7-18：Understanding a Unique Larval Form: A Study of the Warén's Larva

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Ifremeria nautilei is a hydrothermal vent snail with symbiotic chemoautotrophic bacteria and a unique larval form. The "Warén's larva" develops within a brood pouch located in the foot of adult *I. nautilei* snails before its release. In spring 2022, *I. nautilei* were collected from seven vent sites in the Lau Back-Arc Basin near Tonga. Warén's larvae were extracted from the snails and a series of culturing, temperature, and energetics experiments were performed. In all, we maintained over 155 cultures at 4 and 14°C, allowing us to use scanning electron and brightfield microscopy to describe a 9-stage developmental timeline for embryonic and larval growth. Larvae extracted from the brood at later stages had a better chance of survival, suggesting they are likely to be naturally released from the adult as Warén's larvae. We also conducted two temperature experiments—one assessing survival of 4 stages at 5 temperatures and the second using only embryos and Warén's larvae at 4 and 14°C. Larvae reared at cooler temperatures lived longer but did not develop, whereas those in warmer temperatures did not live long but developed rapidly. Finally, we assessed the energetics of development by performing micro-bomb calorimetry on newly-released Warén's larvae and monitoring their oxygen consumption at 4°C. The extremely energy-rich Waren's larvae had very low metabolic rates suggesting they could live for a long time without feeding. This study clarifies our understanding of the embryonic and larval development of the only new larval form described in over 100 years.

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P7-19: Population Connectivity of Corals

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Corals associate not only with dinoflagellates, which are their algal endosymbionts, but also with a diversity of other microbes including the archaea, viruses, eukaryotic microorganism, fungi and bacteria and evidence is mounting that the microbiome within a host has a pivotal role in coral biology.

Despite the abundant marine biodiversity in the China's Greater Bay Area, particularly of scleractinian coral, research concentrating on the coral microbiome within this region is still restricted in scope regarding the diversity of host species. As oceans continue to warm, understanding the compositions, abundances and diversity of key microbial partners in the coral holobiont may hold the key to effective reef restoration and it is necessary to conduct a more comprehensive characterization of the bacterial communities associated with corals in the area aiming to enhance our understanding of the crucial role that microbes play within the coral holobiont.

Using the 16S rRNA amplicon sequencing analysis, we compare the microbiome of *Acropora digitifera* and *Montipora peltiformis* from representative localities in the Greater Bay Area, ranging from Hong Kong, Shenzhen, Huizhou, and Zhuhai. Our objective is to examine and compare the microbiome compositions, relative abundances and diversity across different species and locations identify the core microbiome specific to each coral host species, and subsequently discover a shared core microbiome among those two species. The data can serve as a baseline for monitoring changes and facilitating the identification of microbes that might be crucial for coral and the reef ecosystems they build, faced with on-going global declines.

P7-20: Vertical Reefs of the GalÁPagos: Preliminary Results from the Fkt230918 Expedition

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Shipboard multibeam echosounders provide a smoothed representation of rough topography, particularly in deeper waters, and as such fail to adequately characterize the vertical dimension of complex 3D seafloor structures. Trawls or towed-camera systems are similarly ineffective in characterizing highly rugged environments. Consequently, it was not until the 1990's that vertical deep-sea habitats started being discovered. However, for the most part, these striking deep-sea landscapes have remained unexplored, even though cliffs provide markedly different environmental conditions from the surrounding terrain, and often host rich communities of fragile suspension feeders, including corals and sponges. As environmental conditions likely affect the life cycle of these habitats distinctly from other cold-water coral (CWC) environments, in September 2023, a Schmidt Ocean Institute-funded expedition onboard the research vessel *Falkor (too)* focused on the exploration of vertical CWC cliff ecosystems in the Galápagos Archipelago using the remotely operated vehicle (ROV) *SuBastian*. During the expedition, multiple *Madrepora occulata* dominated reefs were discovered and mapped in ultra-high resolution using a Voyis MicroInsight laser scanner and a Norbit WMBS multibeam echosounder. Visualisation of 3D point clouds revealed that the laser data produced fine-scape quantification of habitat complexity that could be used to examine its influence on the diversity of associated organisms. In total 494 biological, 70 geological and 102 fossilized coral samples were recovered from 25 ROV dives across a depth range of 120 m to 1,600 m. Over 100 CTD casts were completed to characterize internal tides and the oxygen minimum zone to assess their influence on the benthic communities. This expedition shed light on the incredible diversity of cold-water corals and associated species which inhabit the waters of the Galápagos National Park.

P7-21: Possible Effects of Deposition from Deep-Sea Sulfide Mining on Benthic Microbial Communities

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The first excavation tests of deep-sea seafloor massive sulfides took place in 2017 under the auspices of the Japan Organization for Metals and Energy Security (JOGMEC). Initial work has focused on infaunal metazoan communities and found several possible impacts of sediment redeposition on both meiofaunal and macrofaunal communities. This study builds on past work by analyzing microbial communities from these same sediment samples. Core samples were collected at six locations within ~10-60 m of the disturbance site before and up to 3 years after the excavation test. Levels of deposition for each coring location were identified using current data, topography, and concentrations of several metals found to have elevated concentrations in the water column sediment plume during the test. Microbial OTUs were identified by sequencing PCR-targeted regions of the 16S rRNA gene of both bacteria and archaea while PICRUSt2 was used to examine functional aspects of the microbial community using these OTUs. All sample locations that experienced heavy or moderate deposition showed shifts in communities 2 weeks after the excavation test compared with before; however, all but the most heavily impacted station appeared to recover within 6 months. Microbial changes included a large increase in the proportion of the bacterial community comprised of chemosynthetic taxa, primarily driven by Epsilonproteobacteria, in impacted samples while the proportion of Archaea doubled. However, changes in gene functions represented in the community were less clear. More research is required, but these findings suggest that chemosynthetic habitat may be created from deep-sea mining itself, albeit briefly. Hydrothermal vents form unique communities, and there is concern these habitats may be lost due to activities such as mining. If deep-sea mining does create or expand the area where chemosynthetic communities can occur, the mining periphery may provide a short-term refuge for animals at the excavation sites.

P7-22: Marine Mammal Communities and Human Activities Including DSM in the North-Eastern Tropical Pacific: Conservation and Management Strategies

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Marine mammals could be impacted by deep-sea mining activities because of their physiological and behavioural characteristics, their migration patterns and their ecology, although there are knowledge gaps concerning them for the Clarion Clipperton Zone (CCZ). The present paper aims at reviewing the current state of marine mammal populations and their associated ecosystems in the water column of the tropical north-eastern Pacific. Specifically, we assess their vulnerability to natural and anthropogenic impacts, in particular to deep-sea mining in the mineral-rich CCZ. As there is growing evidence that marine mammal communities and other apex predators play a critical role in ecosystem structures and functions, we outline their vulnerability and the existing conservation measures for marine mammals in the Pacific. We then propose to enhance knowledge in different domains of research linked to marine mammals and to adapt conservation strategies to ensure their well-being and the continuity of the ecosystem services they provide to the oceans and human societies in integration with other fields of ocean management.

P7-23: Biodiversity and Community Structure of Benthic and Demersal Scavengers at Inactive and Active Hydrothermal Areas on the Central and Southeastern Indian Ridge

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Before seafloor mining at hydrothermal SMS deposits can occur, comprehensive baseline studies are necessary to census the seafloor and pelagic biodiversity and ecosystem processes taking place here. While there have been extensive studies of hydrothermal vent ecosystems in multiple ocean basins, very few have catalogued the biodiversity, community structure and feeding dynamics of benthic and demersal scavengers close to active sites and compared them to the fauna found at inactive locations. We carried out eight 24-hr benthic camera lander deployments along a >600km transect of the southern Central Indian Ridge and the northern Southeast Indian Ridge to quantify the biodiversity and community structure of benthic and demersal scavengers close to active vent sites (n=4) as well as inactive areas (n=4). The benthic camera landers were deployed with mackerel bait. We documented >9000 individual scavengers in >3000 images but found no difference in species richness nor Pielou's evenness based on MaxN data. Estimated species richness at both habitat types was high (15), and extrapolated curves showed that species were rapidly accumulating beyond 100 individuals. Multivariate analysis showed no difference in community structure between inactive sites and areas close to active vent areas. A negative but not significant relationship between the number of shared species and distance between sites was observed. Community structure similarity between habitat types did, however, decrease from 80% at the NW end of the transect to 55% at the SE location indicating, that community overlap between inactive sites and sites located close to vents may decrease towards the SE part of the ridge. This study provides the first baseline dataset of benthic and demersal scavenger biodiversity, community structure, and scavenger feeding ecology on the Central and Southeast Indian Ridge.

P7-24: Re-visiting 1994-1997 Megafauna Data from IOM BIE Site (CCFZ, NE Pacific): A Work in Progress

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In 1995, the INTEROCEANMETAL Joint Organization (IOM), an ISA contractor in the NE Pacific's Clarion-Clipperton Fracture Zone (CCFZ) polymetallic nodule field, carried a small-scale field experiment (Benthic Impact Experiment, BIE) aimed at assessing effects of nodule removal from the seafloor, using a device producing disturbances mimicking those resulting from actual nodule mining. The suite of disturbance indicators included the composition and abundance of the megafauna, assessed from seafloor photographs taken before the experiment (1994), immediately in its aftermath (1995) and during a follow-up cruise (1997). The data collected revealed significant spatial (nodule-covered vs. nodule free bottom) and temporal differences in the megafauna abundance and composition. However, the data were obtained by examining black-and-white NEGATIVES of still photographs taken during the seafloor surveys. In view of a considerable technological progress in seafloor photographing resulting in acquisition of high-resolution, technically excellent images of the seafloor and its associated fauna, we decided to re-analyse the data by converting the frames of the 1994-1997 surveys to regular black-and-white POSITIVES, scanning them to computer-viewable images (also black-and-white), and examining and annotating them from the computer screen rather than from under a stereomicroscope as in the initial study. Both a manual annotation and a machine-learning algorithm are being applied. As this is the work in progress, reporting of the results is pending the project completion.

P7-25: Deep Sea Biotic Responses to the Neogene Indonesian Throughflow Dynamics

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As a current transporting moisture and heat from the equatorial western Pacific Ocean to the eastern Indian Ocean, Indonesian Throughflow (ITF) and its dynamics could impact ecosystems. The existence of a restricted ITF in the Neogene is supported by paleontological evidence from planktonic foraminifera and benthic foraminifera in nearby regions. However, the precise timeframe of the restriction and recovery of the ITF and its impact on marine biodiversity and the ecosystem remains unclear. We used the IODP Expedition 363 materials and microfossil Ostracoda (Crustacea) as a model system to better understand the deep-sea biodiversity and biotic response to ITF dynamics in this region. Our result shows that the biotic response of deep-sea ostracods to the ITF restriction event could be regarded as a three-stepped process, including the ITF restriction initial phase (~10 to 7 Ma, *Zabythocypris* and *Argilloecia* dominated), ITF restriction core phase (7 to 4 Ma, *Legitimocythere* dominated), and Post ITF restriction phase (after 4 Ma, *Henryhowella*, *Poseidonamicus*, *Anebocythereis* dominated). The taxonomic assemblage shifted from “pre-restriction” to “restriction” mode and then partially recovered after the restriction event ended. Our study showed the critical role of the ITF in affecting deep-sea ecosystem in the equatorial western Pacific Ocean for the past 10 Myr.

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P7-26: The Potential Mechanisms of the Slowdown of Host Cell Lysis after *Prochlorococcus* is Infected by Cyanopodoviruses

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As the most abundant photosynthetic organisms on Earth, the unicellular cyanobacteria *Prochlorococcus* and *Synechococcus* are responsible for as much as 50% of carbon fixation in oligotrophic oceans. Viruses (cyanophages) can lyse cyanobacterial cells and inhibit their carbon fixation, serving as critical components of the marine carbon cycle. Previously, we have successfully built mathematical models to describe the distinct life history traits of cyanophages P-HM2 and P-SSP7, showing that the adsorption rate and latent period of P-HM2 are affected by dark whereas those of P-SSP7 are not. However, the host abundances predicted by the initial models were much lower than experimental observations for both phages, suggesting potential mechanisms for the slowdown of host cell lysis. Here, we proposed five potential mechanisms for the slowdown of *Prochlorococcus* lysis after infection by P-HM2 or P-SSP7 and assessed them by experiments, respectively. The results showed that among the five candidate mechanisms the different eclipse and latent periods, successful adsorption rate as well as the percentage of resistant cells might contribute to this slowdown. We will add these infection parameters assessed by experiments to the initial models so that we can quantitatively describe the population dynamics of P-HM2 and P-SSP7 during competitions under light-dark cycles in a much more precise manner. Altogether, our findings revealed novel mechanisms by which cyanophages regulate cyanobacterial population dynamics and deepen our understanding of cyanobacteria-controlled marine food webs.

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P7-27: Chemosynthetic Alphaproteobacterial Diazotrophs Reside in Deep-Sea Cold-Seep Bottom Waters

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Nitrogen (N)-fixing organisms, also known as diazotrophs, play a crucial role in N-limited ecosystems by controlling the production of bioavailable N. The carbon-dominated cold-seep ecosystems are inherently N-limited, making them hotspots of N fixation. However, the knowledge of diazotrophs in cold-seep ecosystems is limited compared to other marine ecosystems. In this study, we used multi-omics to investigate the diversity and catabolism of diazotrophs in deep-sea cold-seep bottom waters. Our findings showed that the relative abundance of diazotrophs in the bacterial community reached its highest level in the cold-seep bottom waters compared to the cold-seep upper waters and non-seep bottom waters. Remarkably, more than 98% of metatranscriptomic reads aligned on diazotrophs in cold-seep bottom waters belonged to the genus *Sagittula*, an Alphaproteobacterium. Its metagenome-assembled genome, named Seep-BW-D1, contained catalytic genes (*nifHDK*) for nitrogen fixation, and the *nifH* gene was actively transcribed in situ. Seep-BW-D1 also exhibited chemosynthetic capability to oxidize C1 compounds (methanol, formaldehyde, and formate) and thiosulfate. Additionally, we observed abundant transcripts mapped to genes involved in the transport systems for acetate, spermidine/putrescine, and pectin oligomers, suggesting that Seep-BW-D1 can utilize organics from the intermediates synthesized by methane-oxidizing microorganisms, decaying tissues from cold-seep benthic animals, and refractory pectin derived from upper photosynthetic ecosystems. Overall, our study corroborates that carbon-dominated cold-seep bottom waters select for diazotrophs and reveals the catabolism of a novel chemosynthetic Alphaproteobacterial diazotroph in cold-seep bottom waters.

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P8-1: Biomarkers Discovery for Risk Assessment in the Deep Sea

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The cost-benefit of deep-sea mining (DSM) need to accurately account for the scale of environmental impact, the ecosystem services that might be compromised and the potential mitigation measures that can be implemented. DSM will creat localized plumes by mining collectors at the seafloor and dewatering ore slurry produced by the mining support vessel that may introduce complex mixtures of potentially toxic elements in the water column. While species resilience to impact will be conditioned by their capacity to resist exposure to toxic elements at present it is not possible to predict, in advance of DSM operations, the absolute toxicity thresholds. It is thus important to develop novel methodologies and indicators for ecotoxicological evaluation of risks of metal exposure for deep-sea organisms. This study aims to assess the ecotoxicological impacts using transcriptomics and proteomics approaches and to identify potentially new biomarkers. *In situ* sulfides/sediments exposure experiments with local fauna from deep-sea hydrothermal vents and cold seeps were performed. Mussel samples (*Bathymodiolus azoricus* and *Gigantidas haimaensis*) were collected from the Lucky Strike hydrothermal vent field (1700m depth), Mid-Atlantic Ridge and from the Haima seep (1385m depth), South China Sea, respectively. In the present study, we compare the potential biomarkers in both species that were modified under these exposure scenarios. The validation of candidate biomarkers will help to identify which are the most reliable. Results will help to define future threshold values for plume / metal concentrations, information seen as essential to be incorporated in regulations by policy makers to minimize the environmental impact of DSM activities.

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P8-2: Effects of Long-Term Disturbance on Food Quality and Fauna in the Clarion Clipperton Zone

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Deep-sea mining for polymetallic nodules will likely significantly impact abyssal ecosystems such as the Clarion Clipperton Zone. Understanding the long-term effects of nodule removal is key for comprehensive management of the nodule mining industry. Furthermore, we still lack basic biogeochemical and ecological knowledge about the deep-sea communities living on nodule plains. Deep-sea communities on nodule plains are largely sustained by the sinking flux of particulate organic material (POM) from primary production in the euphotic zone. Thus, POM has a central role in structuring deep-sea communities and food webs. Essential micronutrients e.g. lipids in POM are especially important in the biochemistry, life history, and population dynamics of deep-sea fauna. Here we determined food quantity (total organic carbon and nitrogen) and quality (lipid biomarkers) in sediments at the seafloor following nodule removal by the Ocean Minerals Company in 1979. We show that total organic carbon and nitrogen concentrations were lower within the mining track compared to the plume area and control site. Lipid concentrations were variable but labile and semi-labile lipids were higher in the control site compared to the mining track. Additionally, we show how food quantity and quality impacts faunal biochemistry at the Clarion Clipperton Zone. Our data provide the first long-term evidence of the effects of nodule removal on the quantity and quality of food available to deep-sea communities and demonstrates the impact of this on faunal biochemistry. We discuss the implications of our findings for recolonization of nodule mining sites.

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P8-3: Long-term Impacts of a Mining Disturbance Event on Abyssal Megafauna

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Polymetallic abyssal nodule fields are unique habitats that may experience large-scale anthropogenic disturbance in the near future as a result of deep-sea mining. The extent to which mining disturbance (nodule removal and sediment redeposition) impacts biodiversity patterns over multi-decadal timescales remains poorly understood. We revisited the site of the OMCO mining collector test, in the Clarion-Clipperton Zone, 44 years after it was conducted in 1979. This is significantly longer post-disturbance than previous impact studies. We used seafloor imagery to assess the direct and indirect impacts of mining disturbance on megafauna (animals >10mm) communities. We focus in detail on changes in key megafauna taxa, diversity and community structure not covered elsewhere. Photo transects were collected within the tracks (fully disturbed), immediately next to the tracks (plume impacted area) and at an unimpacted control site. Images collected in 1978 were also available, giving us the unique opportunity to also study natural variability in this area and explore the implications this has for monitoring impacts. Fully disturbed areas had significantly lower megafauna densities, diversity and distinctly different community composition compared to both plume and control areas. Sessile suspension feeders were largely absent in the areas where nodules were removed despite being dominant in surrounding areas. The plume impacted area showed no visible evidence of sediment cover. Surprisingly, the plume area hosted significantly higher densities than the control area although diversity (both richness and evenness) was similar across both areas. We show that the direct effects of mining on megafaunal communities are severe and long lasting, although the impact of the sediment plume was less evident. This study considerably extends our understanding of the long-term impacts of mining disturbance and has implications for future management of mining activities and conservation in this area.

P8-4: Body Size-feeding Niche Relationships Vary Temporally in the Abyss

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The key food source sustaining abyssal plain ecosystems (4000-6000m) is particulate organic matter (POM) produced in the surface ocean; the quantity and quality of which varies over intra- and inter-annual timescales. Most abyssal taxa are deposit feeders which consume settled POM and sediment. Their feeding niche is determined by body size – smaller organisms being reliant on fresh POM – however the quantity of POM is anticipated to decrease due to climate change. Therefore, we need to understand how the feeding niche of abyssal deposit feeders varies in response to interannual variation in food supply to better understand the impacts of climate-related changes. We used carbon and nitrogen stable isotope ratios to assess the trophic position-body size relationship of deposit-feeding megafauna (325 individuals; 5 species) from the Porcupine Abyssal Plain (north-east Atlantic) across three years. Quantity and quality of POM flux was determined each year. Overall, deposit feeders were smaller in the year with least POM flux and there was no variation in mean organismal $\delta^{15}N$ across the three years. Subsurface deposit feeders displayed a positive trophic position-body size relationship, which was consistent interannually, while surface deposit feeders displayed a similar relationship which varied interannually. Analyses of POM isotopes and the inclusion of carbon isotopic values will allow us to determine if the variations in organismal trophic position are related to variations in the amount or quality of POM each year. Our current results indicate that abyssal deposit feeder trophic position-body size relationships persist over time, and that surface deposit feeders are susceptible to variations in food supply. Identifying interannual variations in feeding niche is required to accurately estimate the impacts of long-term changes in food supply on abyssal ecosystems, and thus determine the impacts of climate change on the megafaunal community.

P8-5: Deep-Sea Mining Disturbance Effects on Benthic Ecosystem Function and Macro-Infaunal Community Structure on The Chatham Rise, Southwest Pacific

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Expansion of extractive industries to deep-sea environments will lead to increased stresses on seafloor ecosystems. We examined changes in environmental parameters following an in situ benthic disturbance at ~450 m water depth on the Chatham Rise, Aotearoa New Zealand. Measurements included sediment community oxygen consumption (SCOC), nutrient fluxes, macro-infauna community composition, and sediment organic carbon (C) and nitrogen (N) content. We observed an increase in SCOC immediately after the disturbance, alongside a decrease in infauna abundance, biomass, species richness, and diversity, and an increase in sediment C:N. One-year after the disturbance, SCOC and sediment C:N were similar to that of pre-disturbance levels, while infauna abundance and biomass were greater. We observed a shift in the community structure at directly disturbed sites one-year post-disturbance with decreased biomass of Polychaeta and increased biomass of Ophiuroidea. No changes were observed in sediment nutrient fluxes as a result of the disturbance. Our study indicates the benthic ecosystem was negatively affected by the disturbance, but the observed recovery of many parameters after one-year shows the potential resilience of the Chatham Rise benthic ecosystem. Compared to many proposed deep-sea resource extraction sites in high seas regions and at much deeper (abyssal) depths, the Chatham Rise experiences a relatively high-level of anthropogenic and natural disturbance (i.e., subject to frequent bottom trawling and strong bottom currents, respectively). Seafloor ecosystem resilience to such operations and potential recovery from their impacts will depend on local environmental conditions that need to be evaluated in any environmental impact assessments.

P8-6: Natural vs. Anthropogenic: Variability of Benthic Megafauna Communities in the Clarion-Clipperton Zone, Pacific Ocean

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The increasing demand for mineral resources has led to increased efforts towards extraction of polymetallic nodules on abyssal plains. Regions with large aggregations of polymetallic nodules can be found for example on abyssal plains in the Clarion-Clipperton Zone (CCZ, eastern equatorial Pacific Ocean). During the extraction process, nodules will be removed, surficial sediment layers will be disturbed and sediment particles will be redeposited. As a result, seafloor integrity loss and potentially long-term impacts on benthic communities are inevitable. An integral part of benthic communities are megafauna organisms, some of which are associated with nodules or dependent on low sedimentation rates. In a deep-sea mining scenario, megafauna organisms are therefore likely to be impacted and may exhibit strong variations in density and diversity.

In 2021, two areas within the CCZ were subjected to an industrial polymetallic nodule collector trial using the pre-prototype vehicle Patania II. One year before and after the trial, in 2019 and 2022, camera transects were carried out covering the collector trial sites as well as undisturbed reference sites. Image data from both areas, from the collector trial site and the reference site, will be analysed by annotating the present benthic megafauna along with the different disturbance degrees (i.e. collector impact, plume impact, reference) and seafloor characteristics (i.e. nodule size). Corresponding functional traits will be assigned to the megafauna organisms and compared between sites and years.

This image dataset provides a unique opportunity to study the variability of benthic megafauna community composition before and after the collector trial compared to the natural variability observed at the reference sites. The results will significantly contribute to our understanding of megafauna communities in deep-sea ecosystems and help to effectively assess potential impacts of deep-sea mining.

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P8-7: A Retrospective Analysis of Microplastic Pollution Using Deep-Sea Natural History Collection Holothurians Specimens of the Indo-Pacific

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Plastic production has risen exponentially since the early 1950s. Microplastics (below 5 mm) represent the vast majority of total marine litter in terms of number of particles. Microplastics can sink onto the seafloor either due to their density, biofouling or marine snow, and can consequently accumulate in the sediments, turning the deep-seafloor into a major microplastic sink. Microplastics are easily ingested by a broad range of organisms and display a wide variety of toxicity, including to benthic organisms. Holothurians are benthic organisms found at all depths and latitudes. A vast majority of holothurian species are deposit-feeders, with high bioturbation and sediment-filtering rates between 9 and 82 kg per individual per year. Hence, we hypothesise that holothurians could be a relevant organism to study microplastic benthic pollution. Research in shallow water ecosystems has already demonstrated the presence of microplastics in internal tissues and their associated toxicity for several families of holothurians. In the BackPlast project, we investigate a temporal trend of microplastic pollution, using a time-series of deep-sea holothurians from the Indo-Pacific Natural History Collections of the Paris Muséum National d'Histoire Naturelle (New Caledonia, Papua New-Guinea and Taiwan). Using an integrative taxonomy workflow, we managed to identify two candidate species that can be used as time-series, sampled between 1985 to today (see XXX abstract). Here, we show the method development to extract and quantify microplastics from holothurian intestines using Pyrolysis-Gas Chromatography/Mass Spectrometry. Of the 6 individuals analysed to develop the assay method, plastic was detected in all of them. Concentrations were in the µg/g (dry weight) range. Polyethylene and polyethylene terephthalate are highly represented. Through this project, we aim to shed light on the evolution of microplastic pollution, especially in understudied regions that yet harbour one of the highest biodiversity on Earth.

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P8-8: Economic Cost-Benefit Analysis Incorporating Environmental Impacts for Polymetallic Nodule Extraction in the Clarion-Clipperton Zone

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While the financial value of extracting polymetallic nodules from the Clarion-Clipperton Zone has been defined, the economic costs of likely environmental impacts have not previously been quantified in comparable economic terms. Valuing this loss is critical for assessing the overall societal benefit of deep-sea mining. We have undertaken a cost-benefit analysis that establishes four benefit transfers to define environmental harm: (i) ecosystem service damage; (ii) habitat equivalency analysis; (iii) carbon offset; and (iv) unplanned oil spills. We have applied the results of these transfers in the MIT cashflow model used by the International Seabed Authority for economic modelling of nodule extraction. The net present value of a best-case environmental cost scenario is estimated at 1999.40 million US$2023, which is substantially greater than the proposed environmental levy for nodule mining (305.60 million US$2023). Including private contractor profits and internalised environmental damage, the MIT model generates a net benefit or cost between 1561.4 and -4547.9 million US$2023. Initial calculations indicate that atmospheric carbon reduction via electric vehicle battery creation from the metals in CCZ polymetallic nodules may be less than the carbon emitted from mining them, highlighting a need for life-cycle regulation of critical minerals such as compulsory recycling. However, informed operational decisions such as opting for renewable-based processing of extracted nodules could reduce carbon-emission related costs by 2788.2 million US$2023. Calculating deep-sea mining economic viability and environmental cost-benefit transfers is restricted by the currently limited understanding of the CCZ ecosystem and observational data of nodule extraction impacts, and uncertainty in the nature of deep-sea mining operations and future commodity markets. However, this study demonstrates how internalising environmental damage into economic models is a useful step in assessing environmental loss and economic benefits together, necessary for policymakers to make equitable decisions and consider trade-offs to achieve a social optimum.

P8-9: Probabilistic Tools to Improve Environmental Risk Assessments for Human Activities in the Deep Sea

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Human activities such as fishing and mining can and could have significant impacts on deep seafloor ecosystems. The complexity of these ecosystems and the lack of comprehensive data make predicting the potential impacts of these activities challenging. Bayesian networks (BNs), a type of probabilistic model, provide a framework to address these challenges and can aid in the development of robust predictions of the effects of human activities on deep-seafloor ecosystems. In this presentation, we give an overview of the use of BNs as a modelling framework to enhance the development of robust quantitative predictions concerning the effects of human activities on deep-seafloor ecosystems, and provide an example of the approach for potential phosphorite nodule mining on the Chatham Rise, Aotearoa/New Zealand. The developed model describes causal connections between pressures arising from potential mining activities and the affected benthic ecosystem components. Using both field data and expert assessments, we incorporate knowledge from multiple sources into a quantitative risk assessment to estimate the probability of a range of ecosystem responses and recovery. The results illustrate that BNs can provide valuable insights into the potential impacts of human activities and inform decision-making for marine conservation and management. By using such tools, policymakers, researchers, and stakeholders can work together to minimise ecological harm from human activities and ensure the conservation of deep-sea environments.

P8-10: Deep-Sea Benthic Biodiversity and Function in a Changing Arctic Ocean

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The Arctic Ocean is rapidly changing, with repercussions on the entire ecosystem from the surface to the deep sea. Despite their pivotal role in the biogeochemical cycling of carbon and nutrients, very little is known about the structure and function of Arctic benthic deep-sea communities in general, and how they respond to environmental changes and other anthropogenic pressures. Here we present an overview of a decadal comparison of benthic communities and processes on the abyssal plains of the Eurasian Central Arctic Ocean in two contrasting years, one decade apart (2012 vs. 2023). As part of a larger consortium studying the impact of sea ice retreat on the entire ocean system, the Benthos team investigates the diversity and function of deep-sea communities and assesses their spatial and temporal distribution in relation to different sea-ice cover, primary production, carbon flux, and sediment biogeochemical parameters and processes. The comprehensive benthic dataset includes biogeochemical measurements (e.g. sediment phytopigments, total organic carbon, bacterial cell numbers, extracellular enzymatic activities, benthic oxygen uptake) and biological community samples across all sizes classes (microbes, meiofauna, macrofauna, megafauna). First comparisons between the two years indicate marked differences in sea ice properties and primary producer composition, resulting in the absence of large algal falls at the seafloor, as observed in 2012. Despite the absence of these larger algal deposits, sediment phytopigment content was higher in 2023. This was accompanied by higher extracellular enzymatic activities (e.g. beta-glucosidase, chitobiase), but at first glance not by higher oxygen consumption rates, indicating a rather moderate response of the benthic community. With a combination of image data analysis, taxonomic studies, additional biogeochemical measurements, and contextual ecosystem information, the work will provide novel insights into the biodiversity of understudied Arctic deep-sea communities and elucidate environmental drivers of benthic diversity and ecosystem functioning in the changing Arctic Ocean.

P8-11: DEEP REST: A Trans-Disciplinary European Project About the Conservation and Restoration of Marine Ecosystems in the Context of Deep-Sea Mining

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DEEP REST (2022-2025) is a trans-disciplinary European project financed by the BiodivRestore ERA-NET cofund (GA N°101003777). It connects experienced environmental and social scientists from 8 European countries and 15 research institutions/universities. It aims at developing a novel approach to improve our capacities for science-based spatial planning and management of two ecosystems threatened by deep-sea mining: nodule fields and hydrothermal vents. By combining data from large areas and across several disciplines, our project (1) investigates and compares the biodiversity, functioning and connectivity of biological communities within and across ecosystems, linking to environmental conditions, (2) evaluates the recovery potential and resilience of deep-sea communities at different degrees of disturbance, (3) tests, through experimentation, the effectiveness of different restoration actions on community recovery, (4) evaluates conservation/restoration outcomes -ecosystem services- and identifies the governance arrangements needed for efficient actions in association with stakeholders, (5) provides scientific guidance and recommendations to stakeholders and policy-makers to support deep-sea governance, ensuring a sustainable management of resources and conservation of ecosystems and (6) raises stakeholder awareness on issues linked to the exploitation of deep-sea mineral resources. The proposed baseline studies are essential to fill knowledge gaps and better understand the natural dynamics of deep-sea ecosystems. Only with fundamental knowledge will we be able to propose relevant hypotheses concerning recovery trajectories and restoration actions. This project is extremely timely, as it directly addresses the concerns of policy-makers in a moment when seabed mining and its associated regulations are rapidly evolving from exploration to exploitation. The DSBS represents a superb opportunity to present the most recent results and recommendations of the project.

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P8-12: Methane Use by Macrofauna at Methane Seeps off the Aleutian Margin of Alaska

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Methane seeps play an important role in global biogeochemical cycling, being an important carbon reservoir, sequestering methane and carbon dioxide (CO2) (Levin, Mendoza, & Grupe, 2016). Methane seeps have been reported from the Aleutian continental margin off Alaska including Edge (4900 m), Shumagin (4850 m), and Sanak (2020 m) seeps. This research project aimed to characterize the macrofauna communities on carbonates at Sanak seep and to identify which organisms use methane by analyzing stable isotopes from natural abundance and enrichment experiments. Macrofaunal animals (>0.3 mm) were taken from the Sanak site with twelve carbonate rocks and preserved in ethanol. In the lab, the associated macrofauna were sorted, identified at the phylum level, and counted. It was found that the densities of macrofauna varied on each rock and across clusters taken from a 1.5 km radius. Arthropods dominated the community composition on Sanak carbonates, and there was variability across each rock. With insight from Alaska Native researchers and community members, the Two-Eyed Seeing approach (one eye with Traditional Ecological Knowledge and the other with Western science practices) can be implemented in strengthening the research methods of deep ocean science. The conservation of benthic floor habitats is vital in ensuring the sequestration of methane to prevent the formation of CO2 causing warming in the polar regions.

P8-13: Ocean Warming Effects across Life History Stages of the Cold-Water Octocoral *Dentomuricea* aff. *meteor*: from Parental Spawning Time to Embryonic, Larval Development and Settlement

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While the impacts of ocean warming on adult cold-water corals (CWCs) are increasingly well documented, the impacts on its early life stages are poorly studied. This is especially concerning, because the early life stages are crucial for ensuring dispersal and connectivity between populations that supports species persistence in a changing ocean.

In this study, we investigated the effects of increased seawater temperature on the timing of natural spawning of parental colonies, and on the embryonic development from fertilization to the planula stage of the octocoral *Dentomuricea* aff. *meteor*. We exposed parental colonies and produced embryos and larvae to three temperature regimes: 14°C and 16°C, corresponding to the species' natural temperature range, and 19°C, representing the IPCC RCP8.5 prediction scenario (+3°C above the species' maximum natural temperature).

Additionally, we also explored substrate preferences for the larval settlement of D. meteor under the different temperatures tested against four different substrates: basalt rock, biogenic rock, green nylon lost fishing lines, and dead coral framework. The early life stages were monitored several times a week tracking the development through larva and young recruit polyp stages, with mortality rates assessed over time.

Although the data analysis is still ongoing, preliminary results suggest higher mortality at 19°C, with no significant differences at temperatures within the species' natural range. We also suspect that elevated temperatures will accelerate metabolic processes, leading to faster development and earlier metamorphosis into polyps. Additionally, larvae are likely to preferentially settle on basalt or biogenic substrates, which are commonly found in their natural environment.

Results of this innovative study, will improve our understanding of how ocean warming may influence key life history developmental processes and substrate interactions, potentially impacting species recruitment and survival. The findings of this research are also expected to enhance our understanding of the species' adaptability to climate change and help develop conservation and restoration strategies to protect the deep-sea coral ecosystems of the Azores.

P8-14: Adaptive Governance for Intertidal Sustainability Under Climate Change

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Marine heatwaves and ocean acidification pose significant threats to intertidal species and the communities that depend on them. Developing social-ecological models that account for the complex dynamics between ecological and social systems will be critical for supporting transformative change towards sustainability.Here we propose an integrative framework for constructing such models. We argue that models should account for 1) biophysical impacts on habitat and target species, including changes in ocean temperature, acidity, and other relevant abiotic factors; 2) ecological impacts on population dynamics, distributions, and interspecific relationships; 3) socioeconomic impacts on relevant stakeholders, including fishers, tourism operators, indigenous communities, and regulatory agencies; 4) governance mechanisms shaping resource access and management responses across scales; and 5) feedbacks between social and ecological systems that may dampen or amplify the system response. We provide examples of promising modeling approaches and highlight key challenges and uncertainties. Testing and refining this framework through empirical models codeveloped with resource users and managers will allow identification of leverage points and evaluation of alternative scenarios, supporting proactive, equity-focused adaptation for long-term sustainability of intertidal fisheries and ecosystems.

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P8-15: Sea Surface Salinity Change Since 1950: Internal Variability Versus Anthropogenic Forcing

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Using an eastern tropical Pacific pacemaker experiment called the Pacific Ocean–Global Atmosphere (POGA) run, this study investigated the internal variability in sea surface salinity (SSS) and its impacts on the assessment of long-term trends. By constraining the eastern tropical Pacific sea surface temperature variability with observations, the POGA experiment successfully simulated the observed variability of SSS. The long-term trend in POGA SSS shows a general pattern of salty regions becoming saltier (e.g., the northern Atlantic) and fresh regions becoming fresher, which agrees with previous studies. The 1950-2012 long-term trend in SSS is modulated by the internal variability associated with the Interdecadal Pacific Oscillation (IPO). Due to this variability, there are some regional discrepancies in the SSS 1950–2012 long-term change between POGA and the free-running simulation forced with historical radiative forcing, especially for the western tropical Pacific and southeastern Indian Ocean. Our analysis shows that the tropical Pacific cooling and intensified Walker Circulation caused the SSS to increase in the western tropical Pacific and decrease in the southeastern Indian Ocean during the 20-year period of 1993–2012. This decadal variability has led to large uncertainties in the estimation of radiative-forced trends on a regional scale. For the 63-year period of 1950–2012, the IPO caused an offset of ~40% in the radiative-forced SSS trend in the western tropical Pacific and ~170% enhancement in the trend in the southeastern Indian Ocean. Understanding and quantifying the contribution of internal variability to SSS trends help improve the skill for estimates and prediction of salinity/water cycle changes.

P8-16: Juvenile Apple Snails as New Biomonitors: Insight into Copper and Lead Toxicity and Underlying Molecular Mechanisms

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Environmental pollutants, such as heavy metals, affect organisms across different trophic levels in the aquatic environment. Although the effects of heavy metals has been extensively studied in a limited number of model organisms, their toxicity and underlying mechanisms remain poorly understood in numerous aquatic invertebrates. Here, we propose the potential of the apple snail *Pomacea canaliculata*, a currently widely distributed and new candidate biomonitor species, to assess the toxicity of two common heavy metals (Cu and Pb) on its juvenile stage through monitoring their heart rates, enzymatic activities and profiling their transcriptomic and proteomic responses. Our results demonstrated that *P. canaliculata* is more sensitive to two heavy metals compared with other aquatic invertebrates. The heart rate can monitor physiological status, with heart rate decreases more to Cu than to Pb. The antioxidant enzyme activity tended to increase at low concentrations but decrease at high concentrations under Pb exposure, while Cu suppressed the activity even at a low concentration. A total of 467 and 267 differentially expressed genes and 629 and 204 differentially expressed proteins were identified in the juveniles exposed to sublethal concentrations of Cu (40 μg/L) and Pb (1500 μg/L) for 72h, respectively. Functional analysis further revealed distinct molecular toxicity in *P. canaliculata*. Under Pb exposure, key pathways related to cellular oxidant detoxification, transmembrane transporter activity, ATP hydrolysis activity were enriched, while Cu significantly activated chitin binding, oxidoreductase activity and extracellular region. Overall, our findings demonstrate the exceptional ability of *P. canaliculata* juveniles to differentiate the toxicity and toxic mechanisms of Cu and Pb, positioning this species as a highly sensitive and informative biomonitor for comprehensive assessment of freshwater heavy metal pollution and its underlying toxicological impacts.

P8-17: Epigenetic-Assisted Rapid Adaptation of Oysters in Response to Ocean Acidification

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Excessive anthropogenic CO_2 emissions are absorbed by seawater, leading to a decrease of seawater pH, and such process is called ocean acidification (OA). OA has been proven to seriously affect many marine organisms, especially the growth, survival and mineralization of calcifiers. However, some highly polymorphic animals, such as oysters, exhibit plasticity and adaptability to the environmental changes. In previous studies, we found that DNA methylation can quickly respond to OA and participate in the phenotypic plasticity and carry-over effect of oysters at different life stages within the same generation. However, it is still unclear how and to what extent OA will affect the physiological phenotype of oysters across generations. Therefore, we designed a transgenerational experiment, starting with the F0 generation, two consecutive generations of F1 and F2 were exposed to low pH (pH 7.4) or control situation (pH 8.0). After three months, the F2 generation showed higher resistance to OA compared to F1 generation. We then performed molecular analysis on these two generations at the genomic, epigenomic (i.e., DNA methylation), and transcriptomic levels, and found that after one generation of continuous exposure, the genotype of F2 generation preferentially clustered with their parents (F1), regardless of exposure history. Moreover, multiple highly differentiated sites were identified in F2 generation coming from OA-treated parents compared to control. Many methylation sites appeared in both F1 and F2 generations, among which F1 and F2 shared ~20% of methylation sites (~50k) with similar methylated depth (±10%), which are potential inheritable sites. By annotating these heritable sites and combining the transcriptomic data, DNA methylation-dominated inheritable genes responsive to OA were screened. Such methylation modification can help oysters quickly respond and adjust to environmental changes in epigenetic plasticity and genetic adaptation, highlighting the coordinated molecular and micro-evolutionary mechanisms of marine invertebrates to rapidly respond to future climate change.

P8-18: Deep-sea Ostracods Faunal Turnover in the Southern Ocean During the Eocene-Oligocene Transition

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The Eocene-Oligocene (E-O) transition was a key global climate change event in Earth's history, marked by a significant cooling of the globe, particularly at high latitudes. This process contributed to the transformation of Antarctica from a warm, ice-free continent to an ice-covered region, triggering a fundamental reorganization of the global climate and ecosystems. The E-O transition is also considered to be an important stage in the major turnover of the Cenozoic deep-sea benthic fauna. In this study, we investigated the turnover of deep-sea fossil ostracods during the E-O transition by analyzing 60 sediment samples from ODP Site 744A, the Kerguelen Plateau, Southern Ocean. A total of 27 genera and 42 species of ostracods were identified. The most abundant genera are *Anebocythereis* and *Krithe*, showing relatively stable abundance during the Late Eocene and early Oligocene. Other genera show significant temporal deviations, suggesting that the composition of the ostracod fauna underwent considerable structural adjustments during the E-O transition. Combined with isotope data from the same site, we suggest that the decrease in deepsea temperature, the decrease in calcium ion concentration, and the enhanced upwelling during the transition may have been the driving factors for this faunal turnover. This study contributes to a better understanding of the response of the deep sea ostracod fauna to the E-O transition and provides important clues for the long term evolutionary turnover of deep-sea ostracod fauna in the Southern Ocean.

P8-19: The impacts of Aluminum on Marine Diatoms: Structural Al in Biogenic Silica Quantified Using Advanced Nanomaterial Characterization Techniques

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Marine diatoms play a crucial role in global carbon fixation and the marine carbon-silicon cycle. Aluminum (Al), one of the major components of atmospheric dust, was suggested to enhance the growth of marine diatoms. The incorporation of Al in silica frustules may improve their structural stability and lower their solubility in the water column, thereby increase the export efficiency of biogenic silica, a vital carbon sequestration carrier, to the deep sea. Therefore, it was hypothesized that Al is important in the natural ocean fertilization process in High Nutrient Low Chlorophyll (HNLC) regions, just like iron (Fe). To test and validate the modified Fe-Al hypothesis, we assessed the effects of iron-aluminum coupling on the growth and photosynthesis of three common marine diatoms—*Phaeodactylum tricornutum*, *Thalassiosira weissflogii*, and *Nitzschia* sp.—under various concentrations of Fe and Al. To explore the characteristics of Al-bound biogenic silica from diatoms, we employed three techniques for nanomaterial characterization: Focused Ion Beam (FIB), Scanning Electron Microscopy (SEM), and Energy Dispersive Spectroscopy (EDS). We discover that Al enhances the growth of all three diatom species by increasing maximum cell density and growth rates. Under low Fe concentrations, low Al conditions can enhance the maximum photochemical quantum yield of photosystem II (PSII) (Fv/Fm) of all species. By employing the FIB to cut the *T. weissflogii* frustules, we successfully exposed their internal structures for clear images and elemental mapping via SEM-EDS, which support the incorporation rather than absorption of Al in diatom frustules.

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P8-20: Assessing the Response of Marine Fish Community to Climate Change and Fishing

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Globally, marine fish communities are being altered by climate change and human disturbances. In spite of numerous empirical studies from local to continental scales, a general pattern of fish communities' response to climate change has remained elusive. Heterogeneity of the marine environment at different scales presents a challenge, and publication bias toward significant results has over- emphasized local ecological effects. In this study, we take the latter into account and present a comprehensive evaluation of fish communities at a global scale. We examined global fish community data to assess changes in community-weighted mean (1) temperature affinity, (2) maximum length, and (3) trophic levels, as well as the influence of climate change and fishing on these characteristics. Fishing pressure increased fish communities' temperature affinity in regions experiencing climate warming. Furthermore, climate warming was associated with an increase in the size and trophic levels of fish communities. Lower long-term ambient water temperature appeared to mitigate the effect of climate warming on temperature affinity and trophic levels. We further found that the effect of climate warming on relative abundance of different trophic classes and size classes both exhibited a nonlinear pattern. Smallest and larger fish might gain benefits, while median and largest size group were at disadvantages. In conclusion, global marine fish community are expected to undergo reorganization in physiology, morphology and ecosystem functioning, manifested respectively as changes in community weighted-mean of temperature affinity, length, and trophic levels, under the synergistic effect of climate change and human disturbance. These findings provide new perspectives for sustainable management practices in a warming ocean.

P9-1: Developing Automated Multi-Modal Monitoring Strategies of Vulnerable Marine Ecosystems (Vmes)

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Anthropogenic impacts on the marine environment are increasing as growing resource demands must be met. Recently (2024), the Norwegian government voted to open an area of the Norwegian Continental Shelf for seabed mining, putting the deep-sea bed, which harbours a rich diversity of ecologically and economically valuable, yet vulnerable, ecosystems under serious threat. It is critical that extensive accurate maps of the seafloor are created to establish baselines and support monitoring of impacts and recovery. Given the region's vastness and isolation, such monitoring is logistically challenging and too slow to meet the requirements. It must therefore be conducted with photography and machine learning (ML) used to automatically identify and quantify seafloor organisms; avoiding labour-intensive manual analysis. This project aims to design and develop a multimodal DL model for automated identification of VMEs and VME indicator-species in Norwegian waters. This model will help to optimize mapping efforts, by promoting efficiency, consistency and quality of ecological data extraction. Crucially, this will better enable sustainable management of VMEs. Current monitoring efforts do not provide the scale and resolution of data required to protect and conserve these valuable seabed assets. Specifically, we are investigating how effective can off-the-shelf Vision Transformers (ViT) automate classification of VMEs from seabed imagery compared to current approaches (CNNs). We are also exploring whether the addition of environmental data (from other sensors such as local topography and water temperature), in a new multimodal architecture can increase accuracy of automated analysis and refine the level of biological details used to make predictions, which is currently not possible for ML with images alone. Importantly, we will consider explainability of model decisions, opening up the 'black-box', and seek to generalize the approach across target seabed communities and datasets.

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P9-2: Vehop: A Versatile, Easy-To-Use, and Homology-Based Phylogenomic Pipeline Accommodating Diverse Sequences

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Phylogenomics has become a prominent method in systematics, conservation biology, and biomedicine, as it can leverage hundreds to thousands of genes derived from genomic or transcriptomic data to infer evolutionary relationships. However, obtaining high-quality genomes and transcriptomes requires samples preserved with high-quality DNA and RNA and demands considerable sequencing costs and lofty bioinformatic efforts (e.g., genome/transcriptome assembly and annotation). Notably, only fragmented DNA reads are accessible in some rare species due to the difficulty in sample collection and preservation, such as those inhabiting the deep sea. To address this issue, we here introduce the VEHoP (Versatile, Easy-to-use Homology-based Phylogenomic) pipeline, designed to infer protein-coding regions from DNA assemblies and generate alignments of orthologous sequences, concatenated matrices, and phylogenetic trees. This pipeline aims to 1) expand taxonomic sampling by accommodating a wide range of input files, including draft genomes, transcriptomes, and well-annotated genomes, and 2) simplify the process of conducting phylogenomic analyses and thus make it more accessible to researchers from diverse backgrounds. We first evaluated the performance of VEHoP using datasets of Ostreida, yielding robust phylogenetic trees with strong bootstrap support. We then applied VEHoP to reconstruct the phylogenetic relationship in the enigmatic deep-sea gastropod order Neomphalida, obtaining a robust phylogenetic backbone for this group. The VEHoP is freely available on GitHub (https://github.com/ylify/VEHoP), whose dependencies can be easily installed using Bioconda.

P9-3: VARS + AI: Can We Train a Machine to Annotate Midwater Animals?

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Researchers at the Monterey Bay Aquarium Research Institute (MBARI) have assiduously archived and annotated over 28,000 hours of deep-sea expedition video using our custom-designed Video Annotation and Reference System (VARS). VARS enables users to create detailed descriptions of marine organisms, geological features, and habitats from video recorded by remotely operated vehicles (ROVs), autonomous underwater vehicles (AUVs), and other camera platforms. These observations are coupled with ancillary data—such as salinity, temperature, position, and depth—and are easily accessible within a searchable relational database. Recently, the exponential increase in visual data streams has necessitated the development of new tools for adding AI assistance to our annotation workflow. To that end, our team has made significant advancements towards integrating machine learning (ML) technology into VARS. We have, thus far, produced over 500,000 bounding box localizations for training our ML models and have used the subsequent models for detecting and tracking objects on 200 hours of ROV video and 800 hours of AUV video. These efforts have already proven successful for benthic deep-sea surveys. The focus now is on tackling the challenge of training models on transparent and amorphous pelagic animals. This involves strategically reviewing and adding to the existing subset of roughly 180,000 midwater localizations. Here we explore several key questions, including: how much training data do we need for midwater animals? Is it possible to create a one-size-fits all ML pipeline? And can we take the human out of the loop?

P9-4: High-Resolution 2D Elemental Mapping of *Desmophyllum Dianthus* Cold-Water Corals in Comau Fjord, Chile

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Desmophyllum dianthus are a species of long-lived cold-water coral found in deep-sea regions across the globe. Coral skeletons accrete over time, incorporating trace elements into their aragonitic structures through various physiological and environmental processes. Thus, the development of reliable microchemical proxies for physical variables such as pH and dissolved oxygen in the skeletons of *D. dianthus* may enable long-term and wide-ranging environmental datasets in the deep sea. The fjords of the Chilean Patagonia are one of a few sites globally where *D. dianthus* appear at depths as shallow as 7 meters. The Comau Fjord is particularly unique, subject to inputs from freshwater runoff, cold vents, and anthropogenic disturbance from local salmon aquaculture. Previous studies have used advanced analytical microchemistry techniques, such as LA-ICPMS (laser ablation – inductively coupled plasma mass spectrometry) to measure isotopic species in coral structures at high resolutions across interpreted growth axes. However, line transect analyses offer a limited dataset and further application of LA-ICPMS to develop 2D elemental maps offers the ability to observe the broader distribution of elements in the coral structure. While other 2D elemental mapping technologies exist such as scanning X-ray fluorescence microscopy, these methods lack the ability to observe certain key elements. In this study, we explore the development of high resolution 2D elemental mapping via LA-ICPMS of *D. dianthus* samples collected in Comua Fjord across various growth axes within the skeletal structure. To evaluate differences across growth axes we generated maps for both transversal and longitudinal sections of coral septa and theca at resolutions of up to 10 microns per pixel. The use of 2D elemental maps can provide critical information about the elemental distribution of species with complex structures and morphologies.

[This work would not be made possible if not for funding support provided by the Lerner-Gray Fund for Marine Research generously offered by the American Museum of Natural History.]

P9-5: Exploring the Growth of Deep-Sea Bivalves in Areas of Potential Seafloor Mining: Methods in Sclerochronology

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The Clarion Clipperton Zone (CCZ) is a region in the Pacific Ocean that is being targeting for deep-sea mining. Here on the abyssal seafloor 4,000-6,000m deep, are the highest concentration of polymetallic nodules, which contain valuable minerals such as copper, cobalt, and nickel. However, these nodules are one of the few hard substrates in the region, and they provide a diversity of habitats that support faunal abundances living on them and within their crevices (and in the surrounding sediment). Of these, bivalve molluscs are an abundant group. Bivalves grow by accretion, where new shell material is added onto the shell's growth margin, creating consecutive growth lines. The study of the growth of bivalve shells—sclerochronology—has been largely confined to shallow water taxa which are relatively large and show growth on a variety of tidal, daily, monthly, seasonal, and yearly schedules. This research aims to extend the techniques of sclerochronology to the tiny and fragile bivalves of the deep CCZ (some of which have only been recently discovered or still remain undescribed) to address questions of age, growth rate, and longevity. Common sclerochronological techniques, such as cross-sectioning and staining to reveal internal growth patterns, have been adapted for the very small shell sizes (~1-2mm length) & resulting fragility of these deep-sea bivalves. These methods may be applied to small specimens from other taxa (e.g., gastropods, sclerosponges) that grow by accretion and/or produce a hard skeleton, and will be applicable for preserving fragile specimens while still allowing various other methods of manipulation (e.g., sectioning and staining).

[The present work was supported by the Leeds-York-Hull Natural Environment Research Council (NERC) Panorama Doctoral Training Partnership (DTP) under grant no. NE/S007458/1.]

P9-6: DNA Barcoding: Comparing the Efficiency and Accuracy of Third Generation Sequencing Oxford Nanopore as A Tool for Species Identification of Deep-Sea Marine Invertebrates

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The increasing global demand for metals supporting the green transition has created unprecedented interest in deep-sea habitats with mineral resources, with the Clarion-Clipperton Zone (CCZ) in the eastern Pacific Ocean being the main abyssal region of interest. Abyssal ecosystems are the largest yet most poorly understood ecosystems on the planet, thus accurately documenting and identifying abyssal biodiversity will be highly relevant to the management of potential deep-sea mining activities. Biological inventories are essential for understanding biodiversity and community structures, however morphology-based taxonomy requires specialists, significant time and resources. Furthermore, it is known that diversity estimates based exclusively on morphological assessment can underestimate biodiversity (e.g. cryptic species), thus new approaches are needed. DNA barcoding provides rapid organism identification using a short and conserved gene region. The effectiveness of DNA barcoding with the developments in high-throughput sequencing has accelerated access to cost-effective methods that overcome performance issues and reduce the costs relative to classic Sanger sequencing for large numbers of samples. Oxford Nanopore Technologies (ONT) has the capacity to generate high-quality DNA barcodes yet has scarcely been evaluated in marine invertebrates. We assessed the accuracy of megafaunal and macrofaunal identification using the MinION sequencer from ONT. We will summarise the outcome from different sets of amplicons across different taxa generated with two robust DNA polymerase sequenced in a MinION R10.4 flow cell. Based on these results, we aim to propose a barcoding workflow for deep-sea marine invertebrates. The analysis of hundreds of marine invertebrate specimens collected from the deep sea will contribute to the limited reference library of barcode sequences, critical information for implementing new biodiversity assessment approaches in the CCZ, such as environmental DNA or metabarcoding to accelerate the availability of essential information for conservation and management in a hypothetical scenario of deep-sea mining in the region.

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P9-7: Defining the Target Population to Make Marine Image-Based Biological Data Fair

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Marine imaging studies have unique constraints on the data collected requiring a tool for defining the biological scope to facilitate data discovery, quality evaluation, sharing and reuse. Defining the 'target population' is way of scoping biological sampling or observations by setting the pool of organisms to be observed or sampled. It is used in survey design and planning, to determine statistical inference, and is critical for data interpretation and reuse (both images and derived data). We designed a set of attributes for defining and recording the target population in biological studies using marine photography, incorporating ecological and environmental delineation and marine imaging method constraints. We describe how this definition may be altered and recorded at different phases of a project. The set of attributes records the definition of the target population in a structured metadata format to enhance data FAIRness. It is designed as an extension to the image FAIR Digital Objects metadata standard, and we map terms to other biological data standards where possible. This set of attributes serves a need to update ecological metadata to align with new remotely-sensed data, and can be applied to other remotely- sensed ecological image data.

P9-8: A New Framework for Assessing Hydrodynamic Model Suitability for Biological and Ecological Studies

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Hydrodynamic models are computational tools that predict the physical, chemical and/or biological properties of water bodies. They have an extremely wide range of applications in oceanography, and increasingly in ecology, biology, meteorology and other disciplines. They are especially valuable in deep-sea research, where *in-situ* data can be scarce and collecting observational data is hampered by access and financial constraints.

As with many types of tool, hydrodynamic models are not “one size fits all”, and differences between models arise in their fundamental assumptions about the behaviour of water and other chemicals; the manner in which the water interacts with land, atmospheric and other water at the boundaries, and the granularity and resolution of the data outputted. However, when it comes to selecting which hydrodynamic model to use, there is very little practical guidance available in published literature. This gap is a barrier for researchers looking to use hydrodynamic models and the corresponding suite of research approaches.

We have reviewed the way in which models feature in key publications, identified model characteristics that will impact their suitability for study and used this information to create a generalised framework for identifying key criteria that models may need to best fit a research study.

P9-9: Cultivation of Novel Marine Bacteria from Deep Ocean Sediment Using Spent Culture of *Ca. Bathyarchaeia* Enrichment

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Most microorganisms resist pure cultivation under conventional laboratory conditions. One of the primary issues for this un-culturability is the absence of biologically produced growth-promoting factors in traditionally defined growth media. However, whether cultivating microbes by providing spent culture supernatant of pivotal microbes in the growth medium can be an effective approach to overcome this limitation is still an under-explored area of research. Here, we used the spent culture medium (SCM) method to isolate previously uncultivated marine bacteria and compared the efficiency of this method with the traditional cultivation (TC) method. In the SCM method, *Ca*. Bathyarchaeia-enriched supernatant (10%) was used along with recalcitrant organic substrates such as lignin, humic acid, and organic carbon mixture. *Ca*. Bathyarchaeia, a ubiquitous class of archaea, have the capacity to produce metabolites, making their spent culture supernatant a key source to recover new bacterial stains. Both cultivation methods resulted in the recovery of bacterial species from the phyla *Pseudomonadota*, *Bacteroidota*, *Actinomycetota*, and *Bacillota*. However, our SCM approach also led to the recovery of species from rarely cultivated groups, such as *Planctomycetota, Deinococcota*, and *Balneolota.* In terms of the isolation of new taxa, the SCM method resulted in the cultivation of 80 potential new strains, including one at the family, 16 at the genus, and 63 at the species level, with a novelty ratio of ~35% (80/219). In contrast, the TC method allowed the isolation of ~10% (19/171) novel strains at species level only. These findings suggest that the SCM approach, which utilizes the enriched spent supernatant of *Ca*. Bathyarchaeia to provide essential growth-supporting factors and crucial metabolites while using the recalcitrant substrate for an optimal growth environment, effectively improves the cultivation of novel and diverse bacteria.

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P9-10: Past, Present and Future of *In-Situ* Deep-Sea Experiments Using Ocean Networks Canada's Cabled Observatories

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Ocean Networks Canada (ONC) operates large seafloor cabled observatory networks in the Pacific, Arctic and Atlantic. The 850+ km network of seafloor backbone cables connect over 100 instrumented sites (>1000 oceanographic instruments, >12,000 sensors), in habitats ranging from coastal fjords to deep-sea canyons, cold seeps, abyssal plains and hydrothermal vents, with some of its long-term observations surpassing 18 years. A range of in-situ experiments have been performed in coastal and deep-sea settings making use of real-time video and oceanographic sensor data. Here we present an overview of past, current and planned experiments covering a wide range of research topics, including human forensics, faunal behavioural studies and benthic community succession near organic falls, and marine carbon dioxide removal (mCDR). We discuss all the required steps between funding acquisition, planning and preparation of the observatory digital and physical infrastructure and the final deployment of experiments using ONC's ship and ROV time during its yearly maintenance operations. Also, we provide highlight results from each experiment carried out to date demonstrating the key advantages of the fiber optic real-time connectivity with all seafloor experimental instrumentation. Finally, we showcase a new benchmark artificially-implanted whale fall experiment that will take place ~1,000 m deep in Barkley Submarine Canyon. A remotely operated crawler and fixed camera platform will provide continuous multi-year high-resolution monitoring of carcass degradation and benthic community succession under the severely hypoxic settings of the NE Pacific oxygen minimum zone.

P9-11: Madeira Island: A Natural Deep-Sea Research Vessel in the Atlantic

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Can we work together to make deep-sea research more efficient? MARE-Madeira in Madeira Island, Portugal is working with partners at the Helmholtz Center for Ocean Research Kiel (GEOMAR) and the Norwegian University of Science and Technology (NTNU) to do just that. Funded by the European Commission Horizon Europe program and within the project TWILIGHTED (TWInning Laboratory for an Innovative, Global Hub To Explore the Deep), we are working to strengthen deep-sea research capabilities in Madeira and create a global hub for deep-sea researchers.

Why Madeira? Situated in the Northeast Atlantic, Madeira is a volcanic island with steep slopes diving straight into the deep sea. Within a few kilometers from shore, ocean depths already reach 500-1,000m. Another dozen kilometers and depths reach over 3,000m. Furthermore, and thanks to Madeira’s relatively calm seas and mild climate, these depths are accessible to researchers year-round by small boats.

To better host deep-sea research partners in future, MARE-Madeira is first improving its own deep-sea research capacity. Learning from the deep-sea expertise at GEOMAR and NTNU, we are improving our knowledge of the Mesophotic and Twilight Zone habitats and species around Madeira, as well as adapting our research technologies for deeper waters. Recognizing a need to democratize deep-sea research such that institutes from other small islands and less-developed economies can more easily participate in this research, TWILIGHTED is also dedicated to developing lower-cost methods to explore and monitor deep-sea environments.

We invite all members of the deep-sea research community to join our capacity-building journey – perhaps participating in our Impossible Things Workshops or International Twilighted Conference. We hope to engage more fully in this important and globally underfunded area of research in the coming years and together help build a future where deep-sea research is done more easily, more cheaply and even more collaboratively.

[The TWILIGHTED project is funded by the European Commission’s Horizon Europe Twinning program.]

P9-12: A Diffusion-Based Integrative Approach Toward the Cultivation of Previously Uncultured Bacteria in Marine Sediment

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Traditional cultivation methods with defined growth media can only isolate and cultivate a few microbes. However, much higher microbial diversity has been detected by cultivation-independent tools across various natural ecosystems, uncovering a vast reservoir of unexplored biological novelty. This highlights that the majority of these microbes have yet to be cultured and require dedicated efforts for successful cultivation. To address this, we developed a diffusion-based integrative cultivation approach (DICA) to efficiently isolate novel taxonomic candidates from marine sediment, a vast and underexplored microbial reservoir. DICA utilizes a specially designed diffusion-based apparatus, termed the “microbial aquarium”, paired with modified low-nutrient media to optimize microbial recovery. To determine the efficiency of DICA, we applied both DICA and the traditional cultivation approach (TCA) to deep-sea sediment samples. While both methods successfully isolated numerous representatives from phyla *Pseudomonadota*, *Actinomycetota*, *Bacteroidota*, and *Bacillota*, DICA uniquely recovered species from rarely cultivated phyla like *Verrucomicrobiota*, *Cyanobacteria*, and *Balneolota*. Moreover, DICA enabled the cultivation of 115 novel species candidates, including 39 at the genus level and 4 at the family level, resulting in a 58% novelty ratio. In contrast, the TCA achieved only 12%, with all isolates being novel at the species level only. The isolated microbial diversity showed that species recovered by the DICA belong to 12 diverse classes, two times higher than that of the TCA. Notably, the bacteria recovered demonstrated ecological significance. For example, strain LMO-MO1^T represents the first cultured member of *Synoicihabitans* and has the genomic potential to utilize complex organic substrates as sole carbon source. Additionally, strain LMO-JJ12^T exhibited unique combinations of sulfur metabolism genes. These outcomes demonstrate that DICA is a highly effective tool for isolating a diverse range of previously uncultured, ecologically important bacteria, substantially advancing our understanding of microbial diversity and potential in marine sediments.

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P9-13: Using Deep Learning in The Deep Sea: Using AI To Elucidate Biogeochemical Impact of Unknown Genes

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More than half of all genes in microbial communities have no identified function, and this is especially true in the deep sea. These unidentified genes represent significant gaps in knowledge, including their potential role in global biogeochemical cycles, including carbon, nitrogen, phosphorus, and sulfur. We developed and applied a new gene annotation approach leveraging AI to predict the function of genes of unknown function. To develop the model, we tuned the protein language model ESM-2 with 2.6 million genes falling into 36 pathways related to methane, sulfur, nitrogen, and phosphorus cycling. We found the method to outperform currently used annotation approaches employing sequence alignment such as KEGG and COG searches, identifying a suite of new genes not previously associated with these critical cycles. Further, we apply the model to metagenome-assembled genomes from seep sediment and make predictions of the metabolic functions of seep taxa down to species-level resolution. We find that our AI annotation approach is an important new tool in building hypotheses as they relate to the biogeochemical function of microbial communities, informing future research questions and efforts in the deep sea.

P9-14: Mussel Adhesion and Fatty Acids – A New Approach to Look into Adaptation of Mussel to the Environment

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Mussels are widely distributed from coastal waters to deep sea. They are present in different ecosystem including the extreme environments like the hydrothermal vents and cold seeps. The adhesion of mussel to the substrates or other mussels is through the byssal thread. One of the major proteins in the byssal thread is mussel foot protein-1 (Mfp-1). Numerous research has found that Mfp-1 binds to the substrate surface via its DOPA (3,4-dihydroxy phenylalanine). Our research indicated that lipids are involved in the mussel adhesion process and can facilitate Mfp-1 adhesion. By using a dissipative quartz crystal microbalance (QCM-D), we found that lipids can greatly increase the binding capacity of Mfp-1 to both SiO2 and Au surfaces. The presence of common seawater cations like Ca2+, Mg2+, Na+, and K+ would lead to varying degrees of reduction in the adhesion performance of Mefp-1 on different substrates. The degree of this reduction, however, were much alleviated in the presence of palmitic acid which is involved in the mussel adhesion process. While helping us to better understand biofouling mechanisms and develop biomimetic adhesive materials, looking into the involvement and function of palmitic acid in the mussel adhesion might also help us to gain better idea on the development of mussels living in different environment.

P9-15: Fathomverse: Where Gaming Meets Community Science to Explore Our Ocean

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The deep sea is the largest habitable ecosystem on the planet and remains one of the least explored. Very little is known about deep sea inhabitants, their behavior, and the limits and drivers for their survival. Researchers estimate that anywhere between 30-60% of life in the ocean is unknown to science, and these gaps in knowledge need to be filled to inform exploitative activities like aquaculture, offshore wind, and deep-sea mining. In order to fully explore our ocean and effectively steward the life that lives there, we need to increase our capacity for biological observations; massive disparities in effort between visual data collection and annotation make it prohibitively challenging to process this information. State-of-the-art approaches in automation cannot solve this problem alone, and we must aggressively build an integrated community of educators, taxonomists, scientists, and enthusiasts to enable effective collaboration between humans and AI. FathomVerse, a mobile game designed to inspire a new wave of ocean explorers, teaches casual gamers about ocean life while improving machine learning models and expanding annotated datasets (FathomNet). Of the three billion gamers worldwide, up to 70% say they care about the environment; FathomVerse taps into this engaged community with innovative gameplay and rich graphics that draw players into the captivating world of underwater imagery and cutting-edge ocean science. Here we will share our process of designing FathomVerse, discuss early successes from the v1 launch on May 1, 2024, and highlight some areas of future focus. In less than two months after v1 launch, 9k players from 100 different countries generated >3.5M annotations that are currently being used to generate consensus labels. Through FathomVerse, we hope to activate audiences in high school and up, providing social engagement and workforce education, with the goal of increasing public awareness and inspiring empathy for ocean life. [This present work was supported by NSF Convergence Accelerator (grant no. (2230776), the Monterey Bay Aquarium Research Institute, and Schmidt Marine Technology Partners.]

P9-16: Seawater Nitrate Assessment Using a Correction Algorithm of Temperature and Pressure up to 10000 Meters

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Nitrate is a crucial nutrient that supports primary production in natural water bodies and marine ecosystems. Recent advancements in deep-sea research have shown that the ultraviolet absorbance of seawater is influenced by temperature, salinity, and pressure. In this research, we propose a novel nitrate measurement method suitable for seawater under pressures ranging from 0 to 100 MPa. This method integrates the orthogonal projection to latent structure (O-PLS) algorithm to correct spectral data for pressure and temperature variations. The method's effectiveness was validated using three spiked seawater matrices: Western Pacific seawater, Aoshan Bay seawater, and Yellow Sea seawater, each exhibiting different nitrate concentrations. The results indicate that within a temperature range of 0 to 30 degree and a pressure range of 0 to 100 MPa, the proposed approach achieves a prediction accuracy of 0.39 μmol/L and an R^2 value of 0.999. These outcomes demonstrate a significant enhancement in nitrate measurement precision. Importantly, this method is distinguished by its capability to operate effectively at a pressure rating of 100 MPa, equivalent to a depth of approximately 10,000 meters, making it particularly advantageous for nitrate measurements in deep-sea environments.

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P9-17: High-Precision Deep-Sea Pressure Sensor Based on Fast Wavelength Scanning of DFB Lasers

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High-precision pressure detection is essential for understanding seabed instability, detecting geological disasters like submarine landslides, and improving tsunami early warning systems. However, traditional electrical sensors face limitations, and while optical sensors, particularly Optical Fiber Bragg Gratings (FBGs) and EFPI-based diaphragm sensors, offer advantages like immunity to electromagnetic interference and strong environmental adaptability, challenges persist. This includes the fact that pressure measurements receive temperature influence due to the presence of temperature-pressure cross-sensitivities. In addition to this, the measurement range of the pressure sensor and the sampling frequency are in a contradictory relationship when the wavelength scanning technique of the DFB laser is used to realize the demodulation of the pressure signal. In response to the problem of temperature sensitivity present in the pressure transducer, a modified version of the Fabry-Pérot cavity was fabricated. It has two facets attached to different materials with different coefficients of thermal expansion. Adjusting the lengths of the two materials to realize the relative displacement of the two materials close to zero while the temperature changes. For the wavelength scanning technology, the original wavelength scanning signal with a single-frequency has been improved to realize the dynamic change of the scanning range following the shift of detection signal. These improvements have the potential to enhance the accuracy and efficiency of ocean pressure sensors by mitigating temperature sensitivity and increasing sampling frequency.

P9-18: The Development and Applications of a Controllable Lander for in situ, Long Term Observation of Deep-sea Chemosynthetic Communities

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Understanding the evolution of chemosynthetic communities and environmental changes near fluid seepages in the deep sea requires in situ long term observation data Demand is growing for platforms that can be used for in situ and long term observations A long term ocean observation platform (that uses a new controllable mode for launching and recovery with the aid of a research vessel and submarine vehicles, has been developed and used in the cold seep area of the South China Sea The effective observation times were 375 days and 414 days, respectively, during the 2016 and 2018 deployments, and LOOP is expected to become a universal underwater observation platform for in situ, long term, and continuous data acquisition.

P10-1: “Hoshizuna: The Floating Star-Sand” Art Installation

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3. *Bateau Alternatif d’Art, Paris, France*

From Saturday, March 25, through Saturday, April 30th, the Okinawa Institute of Science and Technology housed giant balloons in the shape of Hoshizuna: the Okinawa star sand.

The installation, entitled “Hoshizuna: the floating star-sand” is a science-art-education project that will feature large balloons in the shape of this symbol of Okinawa. Balloons were exhibited in the campus Tunnel Gallery.

“When the star sand enters the artistic dimension, they leave the sea, go beyond the limit of reality, floating freely in the air,” notes Harigaya in the project proposal.

Star sand are shells of Foraminifera, single-celled creatures that leave their star-shaped shells behind when they die. Okinawa has multiple beaches with sand made of these shells. The exhibition was seen by hundreds of visitors.

P10-2: Depicting the Deep: The Art of Illustrating Science Authors'

Tanya Young[1], Christopher Barrio Froján[2], Maria Baker[2]

1. *Tanya Young Studio, Del Mar, California, USA*
2. *Deep-Ocean Stewardship Initiative, University of Southampton, Southampton, UK*

Soon after its inception in 2013, the Deep-Ocean Stewardship Initiative (DOSI) commissioned a bespoke artwork to illustrate its subject and scope. The resulting image by artist Tanya Young has become DOSI′s calling card, used in all DOSI′s digital outlets, presentations, promotional materials and event backdrops. Its power to entice is not only in its intricate and wholesome beauty, but also in its detail and scientific accuracy of the fauna, activities and impacts it depicts. This poster explores the origin story of the artwork, the inspiration, techniques and processes that led the artist to its creation, as well as Tanya′s own story of her interest in the deep ocean as a subject matter for her art. DOSI has certainly benefited from the attention the artwork attracts, opening DOSI′s work on the provision of science-based knowledge to a wider audience of scientists and artists alike, and showing how the art-science collaboration is a potent tool to create understanding. DOSI receives core support from Arcadia (2017-2031)

P10-3: REV Ocean: Bridging Science and Solutions for Ocean Health

Eva Ramirez-Llodra and the REV Ocean team

REV Ocean, Lysaker, Norway

REV Ocean is a game-changing initiative that has an ambitious yet simple goal - to ensure 'One Healthy Ocean'. Working together with an extensive network of experts, we will champion a new generation of ocean solutions and inspire stakeholders to take action to combat harmful global impacts on the marine environment. We intend to create positive, measurable impact and provide a pathway for others to follow, motivating the next generation of ocean leaders. REV Ocean will strive to fill critical knowledge gaps, develop innovative solutions, and bridge science, business and policy sectors to achieve positive change in three key areas: marine plastic pollution, unsustainable fishing and climate change.

The REV Ocean vessel uniquely combines a fully equipped research vessel with a superyacht. The vessel will be operated in research mode two thirds of the time and chartered one third of the time. The charter revenue will contribute to cover research operations. Under research mode, the vessel and its equipment (including a Triton 7k3 submersible, deep-diving ROV, AUV, pelagic trawl, acoustic systems, coring equipment, eight labs, classrooms and a lecture hall, amongst others) will be offered at no cost to scientists around the world. Shiptime will be allocated through an annual peer-reviewed call for proposals. Projects with allocated shiptime will focus on solutions and demonstrate scientific excellence, will be co-developed with regional experts and early-career professionals, and will promote diversity, equity and inclusivity. Our programme will support the UN Ocean agenda, the UN Decade of Ocean Science (2021-2030) and contribute to the achievement of the UN Sustainable Development Goals (2015-2030), with operations starting in the second half of 2026.

P11-1: Offshore Industry and Research Community Collaboration to Enable Greater Access to the Deep Ocean for Scientific Research

Lucy Harris[1,2], Andrew Gates[1]

1. *Ocean BioGeosciences, National Oceanography Centre, Southampton, UK*
2. *Ocean & Earth Science, University of Southampton, Southampton, UK.*

BORA Blue Ocean Research Alliance® aims to advance scientific knowledge of the deep ocean through integrating science into routine offshore operations and data collection, done in parallel to commercial work and as automated as possible. This is achieved through integration of novel sensors into offshore infrastructure, capturing in situ ecological observations, deployment of scientific research equipment or through recognising where valuable data can be derived from other operational information. To achieve this requires deep understanding of the types of work carried out by each alliance party. BORA Blue Ocean Research Alliance® is science focussed, increasing global reach for ocean observation into areas in which Subsea7 are operating. Fundamental to the scientific value of each project is to ensure that derived data are openly accessible and aim to meet FAIR data standards (Findable, Accessible, Interoperable, Reusable), so that the findings can be re-analysed in future or contribute to wider assessments of ocean health.

Building on the SERPENT Project and the blend of Subsea7's global deep-water reach, BORA Blue Ocean Research Alliance® is delivering new marine research from shallow to deep water, expanding knowledge for scientific and societal benefit.

P11-2: Fluid and Heat Exchange Between Seamounts and the Phenomenal Ecological Effects

Heidi Gartner[1], Cherisse Du Preez[1,2], Rayne Boyko[3], and Rachel Lauer[4]

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4. *Department of Earth, Energy and Environment, University of Calgary, 2500 University Drive NW, Calgary, AB, Canada, T2N 1N4*

There are three known sites in the world where paired seamounts, made of porous basalt, protrude from sediments and a subsurface hydrothermal circulation forms, with one recharge seamount and one discharge. With so few examples, little is known about the hydrogeological processes and associated ecological effects. Now, we have discovered the world's fourth! This finding was made by our NorthEast Pacific Deep-sea Exploration Project (NEPDEP) team in the Tuzo Wilson Seamount Complex (TWSC) offshore of Haida Gwaii, Canada, during three expeditions using submersible vehicles. We measured and confirmed a thermal gradient at 500 m intervals between the two seamounts. We documented fluid flux of significantly warm water venting from the summit of the discharge seamount with associated shimmering water and bacterial mats. Despite having almost the same depth (~1.5 km) and being only 4 km apart, the recharge and discharge seamounts support dramatically different benthic communities. The recharge seamount is dominated by dense carnivorous sponges and almost nothing else, while the discharge seamount has abundant, diverse life—including an extensive Bamboo coral forest, Canada's first Precious coral bed, and a highly productive deep-sea nursery ground. For example, at least three species of deep-sea skates use the seamount as a nursery, with literally millions of egg cases covering the summit and cascading down its flanks (the largest known nursery of its kind). Our spatial analyses of the nursery ground, corals, and venting have revealed the TWSC qualifies as an Ecologically and Biologically Significant Area on multiple scales—scientific information our team recently provided to the co-managing Council of the Haida Nation and Canadian Government, who have proposed a potential TWSC Marine Protected Area. While documented cases of this phenomenon are globally rare, the process is likely not, and understanding the hydrogeology and associated ecological effects is vital to seamount management.

P11-3: The Deep Ocean Observing Strategy: Identifying Collective Solutions for Global Challenges

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6. *Department of Ocean and Resources Engineering, University of Hawaiʻi at Mānoa, HI, USA*
7. *Alfred Wegener Institute Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany*

The deep ocean below 200 m houses diverse ecosystems, immense biodiversity and genetic resources, and is critical for climate regulation, yet it is still poorly-observed. Deep-ocean observations and scientific knowledge are required to inform sustainable development and management of deep habitats, which are increasingly impacted by anthropogenic pressures and emergent industries. The Deep Ocean Observing Strategy (DOOS) aims to address deep-ocean challenges through a community-driven initiative, working under the umbrella of the Global Ocean Observing System (GOOS) and endorsed as a UN Ocean Decade Programme. DOOS connects representatives of U.S. and international networks engaged in sustained deep-ocean observing, mapping, exploration, modeling, research, and management. DOOS initiatives currently center around six working groups: (1) habitat and ecological mapping for place-based management, (2) accessible ocean technology, (3) building synergies between the observing and modeling communities, (4) connecting deep ocean science and policy, including engaging with the UN Ocean Decade, (5) advancing the applicability of essential ocean variables for deep ocean observation, and (6) FAIR (Findability, Accessibility, Interoperability, and Reusability) data training. The Deep Ocean Early Career Researchers (DOERs) program within DOOS cuts across all working groups and aims to provide professional development and engagement opportunities for the next generation of ocean leaders. In this talk, we provide highlights of efforts across these initiatives as they support the challenges and goals of the UN Ocean Decade. Through effective coordination, DOOS aims to improve collaboration across the physical, biogeochemical, and biological disciplines, and better integrate observing and modeling communities, to accelerate the generation and use of data from a fit-for-purpose deep ocean observing system.

P11-4: Application of UN Decade Endorsed Deep-Sea Typical Habitats Programme on Deep-Sea Governance

Yinxia Fang

Second Institute of Oceanography, Ministry of Natural Resources, China

In order to prevent, mitigate, and reverse the declining trend of ocean health and function in the future, the United Nations has launched the "United Nations Decade of Ocean Science for Sustainable Development" (referred to as the "Ocean Decade") to integrate resources and strengths in global ocean related fields, scientifically protect the ocean, and achieve sustainable development and utilization of ocean resources. The deep sea has attracted international attention due to its abundant resources, unique biodiversity, and susceptibility to human activities and global changes. Based on the advantages of over 40 years of deep-sea resource exploration, environmental investigation and research, and high-tech research and development in China, China Deep Ocean Affairs Administration has organized and initiated the first "Ocean Decade" programme in the deep-sea field, "Digital Deep-sea Typical Habitats" which involves interdisciplinary and multi-disciplinary experts and stakeholders worldwide. This article provides an overview of the initiation, objectives, and recent progress of the "Digital Deep Sea Typical Habitat" programme, and further proposes suggestions to promote China's deep participation in the exploration of the "Ocean Decade" deep sea field, strengthen China's deep sea scientific and technological innovation, and international cooperation.

P11-5: New Discoveries in Deep-Sea Seamount Habitats

Xuewei Xu[1], Jian-Wen Qiu[2]

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2. *Hong Kong Baptist University*

The 2024 Western Pacific International Cruise aboard the Shen Hai Yi Hao research vessel, featuring the Jiaolong Human Occupied Vehicle (HOV), yielded significant findings on the biodiversity and environmental characteristics of the Magellan Seamount chain in the Northwest Pacific. Over the course of 45 days, this cruise focused on three work areas at depths ranging from 800 to 5,000 meters. Utilizing state-of-the-art sampling equipment, the team collected a diverse array of specimens, primarily sponges, cold-water corals and echinoderms, along with water and sediment samples. Notably, many benthic megafaunas were found associated with cold-water corals and sponges. Some of these are indicators of vulnerable marine ecosystems, characterized by their slow growth rates, long lifespans, and limited recovery capabilities. The study revealed that biomass along the Magellan Seamount chain is high in the northern regions and low in the south. Additionally, factors such as water depth, bottom current, and microtopography significantly influence the distribution of benthic organisms. These findings provide new insights into how seamount topography affects biodiversity distribution. With the Jiaolong completing 18 dives, the expedition successfully mapped biogeographic patterns that are crucial for understanding deep-sea ecosystems. Conducted in collaboration with scientists from 9 countries and regions, this first international mission under the "Digital Deep-Sea Typical Habitats" initiative marks a significant advancement in the conservation and sustainable management of deep-sea biodiversity in the face of climate change and human activities.

P11-6: Digital Representative of Deep-Sea Habitats Towards an Increased Oceanic Resilience

Yuntao Wang

Second Institute of Oceanography, Ministry of Natural Resources, China

The digital representation of deep-sea habitats stands as a pivotal innovation in bolstering oceanic resilience amidst escalating environmental challenges. The UN Ocean Decade endorsed actions, including Digital DEPTH, MoNITOR, DITTO, are targeting on creating digital representative of marine system, that are crucial for monitoring marine ecosystem health and enhancing resilience against natural disasters. This study delves into the development and utilization of digital technologies to construct comprehensive representations of these intricate ecosystems, shedding light on their complexities and vulnerabilities. Future goals involve refining predictive accuracy, expanding model applications across oceanic regions of the Western Pacific, Indian Ocean, and Mediterranean Sea, and improving disaster mitigation capabilities. The joint efforts from UN Ocean Decade actions aims to strengthen community resilience, protect biodiversity, and support sustainable ocean management by making ocean health data more accessible and predictive for diverse end-users. By fostering a deeper understanding of deep-sea habitats through digital means, this research aims to cultivate strategies that enhance the resilience of our oceans, paving the way for sustainable conservation efforts and informed decision-making in the face of global environmental shifts.

P11-7: Systematics of Deep-Sea Starfish Order Brisingida (Echinodermata: Asteroidea), with A Revised Classification and Assessments of Morphological Characters

Ruiyan Zhang

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Brisingida Fisher 1928 is one of the seven currently recognised starfish orders, and one of the least known taxa as being exclusive deep-sea inhabitants. Modern deep-sea expeditions revealed their common occurrences in various deep-sea settings including seamounts, basins and hydrothermal vent peripheral, underlining the necessity of clarifying their global diversity and phylogeny. In this study, we present a comprehensive molecular phylogeny of Brisingida which encompasses the highest taxonomic diversity to date. DNA sequences (*COI*, *16S*, *12S* and *28S*) were obtained from 225 specimens collected in the global ocean, identified as 58 species spanning 15 of the 17 extant genera. Phylogenetic relationship was inferred using both maximum likelihood and Bayesian inference methods, revealing polyphyletic families and genera and indicating nonnegligible bias in prior morphology-based systematics. Based on the new phylogeny, a novel classification of the order, consisting of 5 families and 17 genera, is proposed. Families Odinellidae, Brisingasteridae and Novodiniidae were resurrected to encompass the genera *Odinella*, *Brisingaster* and *Novodinia*. Brisingidae and Freyellidae were revised to include 11 and 3 genera, respectively. A new genus and species, two new subgenera and seven new combinations are described and a key to each genus and family is provided. Transformations of morphological traits were evaluated under the present phylogenetic hypothesis. A series of paedomorphic characters were found in many genera and species, which led to a high degree of homoplasy across phylogenetically distant groups. Our results provide new insights in the phylogeny and ontogeny of the order, and highlight the necessity to evaluate character convergence under sound phylogenetic hypothesis.

P11-8: Crust-Mantle Structure Characteristics of Ultraslow Mid-Ocean Ridge

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The crustal accretion pattern of the ultra-slow mid-ocean ridge is obviously different from that of the fast and slow mid-ocean ridge, and the coordinated control of the detachment fault and the transformation fault is more obvious. At the same time, the structure of the ultra-slow mid-ocean ridge lithosphere has been controversial. Based on the crustal structure and the brittle lithosphere bottom bound by microearthquakes obtained in only a few seismic investigation experiments, a systematic comparative analysis of the ultra-slow crustal accretion model is carried out, combined with other data (geochemical, gravity and magnetic data, etc.), in order to summarize the deep dynamic process of the new ultra-slow mid-ocean ridge, and provide new clues to the accretion mechanism of the mid-ocean ridge system.

P11-9: Capacity Building for Ocean Literacy Training on Marine Biodiversity in the Deep Sea

Qiuci Sun

Second Institute of Oceanography, Ministry of Natural Resources, China

The ocean, rich in biodiversity, is essential to Earth’s ecological balance, yet deep-sea regions remain among its least explored and understood habitats. As human activities—such as deep-sea mining, climate change, and pollution—pose increasing threats to these fragile ecosystems, raising awareness and understanding of deep-sea biodiversity becomes critical. To address this, ocean literacy training should target knowledge gaps, particularly for educators, researchers, and conservation practitioners. Training content should encompass the ecological roles of deep-sea organisms, the significance of biodiversity for ecosystem resilience, and the multifaceted conservation challenges specific to deep-sea habitats. By fostering a deeper comprehension of biodiversity's role in ecosystem stability and resilience, participants can better appreciate the interconnectedness of marine life and environmental health. Through hands-on workshops and scientific insights, we can equip participants with the tools needed for informed decision-making. This approach encourages sustainable practices and reinforces stewardship principles, ultimately supporting responsible management and preservation of deep-sea biodiversity in the face of mounting environmental pressures.

P11-10: Accounting and System Construction for Resource Assets of Uninhabited Islands

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The development of an accounting system for uninhabited island resource assets is essential for advancing reforms in the property rights of natural resources, given these islands' defense, ecological, and economic significance. This research proposes an accounting framework based on the System of Environmental-Economic Accounting (SEEA-2012), following a structured approach of "physical statistics–price assessment–value accounting." This framework enables baseline data collection for resource assets at the beginning and end of each accounting period, supporting comprehensive resource management. Focusing on total ownership and development-utilization perspectives, the study examines both physical and monetary accounting methods to accurately reflect ownership and use rights of uninhabited island resources. An equity and operational price assessment model is constructed using the income capitalization approach, with extensive data from island use cases to ensure precision. The account system records physical and monetary changes, allowing uninhabited island resources to be integrated into national accounts. This approach enhances transparency and accountability, underscoring the strategic, economic, and ecological roles of these assets while supporting sustainable development and environmental protection efforts.

P11-11: Megabenthic Diversity Patterns on a Seamount in the Philippine Sea: Implications for Conservation Planning on the Kyushu-Palau Ridge

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The oligotrophic tropical western Pacific region is characterized by a high density of seamounts, with the Kyushu-Palau Ridge (KPR) being the longest seamount chain here. Effective spatial management plans for seamount ecosystems necessitate an understanding of distribution patterns and key environmental factors influencing benthic communities. However, knowledge regarding deep-sea biodiversity patterns over intricate topography remains limited. In this study, we investigated a seamount with a water depth of 522 m at the summit located in the southern section of KPR. Survey transects were conducted from 522 m to 4059 m. By analyzing video-recorded data obtained by a human occupied vehicle (HOV) during dives and environmental variables derived from bathymetry, distinct assemblages were identified through noise clustering. α- and β-diversity patterns within the seamount megabenthic community were analyzed across the depth gradient, along with investigation of their environmental drivers. A total of 10,596 megafauna individuals were documented, categorized into 88 morphospecies and statistically separated into six distinct community clusters using noise clustering analysis. Species abundance and richness were highest within the 700-800 m water depth range, declining notably beyond 2100 m, indicating a critical threshold for habitat classification in this region. The β-diversity of megabenthic communities was high (0.836). Although β-diversity patterns along the depth gradient were mostly dominated by differences in species richness, the contribution of species replacement increased with depth, becoming dominant at depths greater than 3000 m. Depth emerged as the primary driver of spatial variation in community structure, while near-bottom current velocity, topographic parameters (bathymetric position index, slope), and substrate type also influenced the formation of microhabitats. The study highlights the depth gradients, thresholds and other intricate environmental factors shaping the spatial heterogeneity of these communities. It provides valuable insights for the future development of effective survey and conservation strategies for benthic biodiversity on the KPR.

P12-1: Navigating Gender at Sea: Recommendations for Making Seagoing Fieldwork Safer for Transgender and Gender Diverse Scientists

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8. *CA, USA*
9. *University of San Diego, San Diego, CA, USA*
10. *Woods Hole Oceanographic Institution, Woods Hole, MA, USA*
11. *University of Chicago, Chicago, IL, USA*
12. *Loyola University Chicago, Chicago, IL, USA*

Fieldwork at sea is a key component of many marine scientists' careers, particularly for those in deep-sea biology. Recent work has highlighted the persistent harassment and discrimination that women and LGBTQ+ people face while participating in oceangoing research. However, less attention has been paid to the unique challenges facing transgender and gender diverse (TGD) scientists while on research vessels. An estimated 1-2% of the world population is transgender or/or intersex, so accounting and providing for TGD participants is necessary during any research cruise. We relate our personal experiences as TGD scientists at sea, including sexual harassment, misconduct, privacy concerns, and legal and medical struggles. We then provide suggestions for ways to promote inclusivity and safety on research cruises, directed at institutions, chief scientists, and all cruise participants. Key recommendations include not assuming gender from passports or other legal documents, asking for berthing preferences, and adopting and enforcing codes of conduct.

P12-2: Brazilian Women in Deep-Sea Biology: Representativeness, Challenges, and Prospects

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Since the 1980s, the marginalization of women in science have been discussed. Despite ongoing efforts, this issue persists, with women currently representing only 31% of the global research community. In Brazil, women are the majority in graduate programs – an increase noted until the 2000s – however their numbers in leadership roles remain limited, with only 33% holding such positions. Disparities are even more pronounced in specific fields, such as STEM and deep-sea biological science. Although we recognize women as an underrepresented group in science, during the last decades, some have been holding the leadership of programs, contributing with discoveries, and making substantial efforts in Brazilian deep-sea biological science. Not only are these contributions worth mentioning but the names and histories of these women. Noteworthy, these figures include the biologist Carmen Lúcia Del Bianco Rossi-Wongtschowski, who served as the coordinator of the regional sub-committee Sul for the REVIZEE Program, one of the largest surveys of marine biodiversity in Brazil; the marine biologist Helena Passeri Lavrado, who contributes to deep-sea benthonic community studies and holds leadership positions such as international committees COMARGE, COML, and IFREMER; and the fisheries engineer Flavia Lucena Frédou, who contributes to various studies of deep-sea organisms and holds leadership roles, including the Brazilian Ministry of Fisheries and Aquaculture. Although the representativeness of women in deep-sea biological science in Brazil has advanced in recent decades, challenges persist. These challenges permeate non-inclusive work environments, difficulties in accessing resources and funding, and the need for safer fieldwork conditions and

P12-3: Deep-Sea Ecosystems of the Indian Ocean > 1,000 M

Elin A. Thomas, Todd Bond, Jess L. Kolbusz, Yakufu Niyazi, Denise J. B. Swanborn, Alan J. Jamieson

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The Indian Ocean is the third largest of the world's oceans, accounting for ~20% for the global marine realm. It is geomorphologically complex, hosting a wide variety of ecosystems across basins, trenches, seamounts, ridges, and fracture zones. While modern exploration has contributed significantly to our knowledge of its coastal ecosystems, deeper waters (> 1,000 m) remain relatively unknown despite accounting for over 90% of its total area. We present the first comprehensive review of the Indian Ocean's diverse deep sea, providing ecosystem knowledge summaries for each major seafloor feature, contextualized with the broader historical, socioeconomic, geological, and oceanographic conditions. Unsurprisingly, some ecosystems are better characterized than others, from the relatively well-surveyed Java (Sunda) Trench and hydrothermal vents of the Carlsberg, Central and Southwest Indian Ridges, to the unexplored hadal features of the western Indian Ocean and the Southeast Indian Ridge. Similarly, there are large depth discrepancies in available records with clear biases towards shallower sampling. We identify four outstanding problems to be addressed for the advancement of deep-sea research in the Indian Ocean: 1) inconsistencies in research extent and effort over spatial scales, 2) severe lack of data over temporal scales, 3) unexplored deep pelagic environments, and 4) a need to place the Indian Ocean's deep-sea ecosystems in a global context. By synthesizing and championing existing research, identifying knowledge gaps, and presenting the outstanding problems to be addressed, we provide a platform to ensure this forgotten ocean is prioritized for deep-sea research during the UN Ocean Decade and beyond.

P12-4: Biodiversity and Nitrogen Metabolism in the Plastisphere impacted by Urban Nitrogen Loading from a Coastal Mega-City

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The plastisphere, recognized for its vast biomass and critical role in nitrogen cycling, is fast becoming an important component of marine ecosystems. The intricate relationship between the plastisphere and heightened nitrogen inputs from urban wastewater prevalent in coastal zones remains an area of limited understanding. Through the lens of metagenomics, metatranscriptomics and metabolomics, this research sought to elucidate the plastisphere's reaction to elevated nitrogen loading and pinpoint key microbial resources that could be harnessed. While the archaeal community composition within the plastisphere remains largely unaffected by high nitrogen concentrations, bacterial diversity experiences a substantial boost, inversely affecting fungal diversity. Furthermore, such conditions were found to curtail intricate microbial interactions. Moreover, the plastisphere subjected to nitrogen loading fosters an enrichment of genera and genes implicated in nitrogen fixation, nitrous oxide reduction, or L-glutamate synthesis. The metabolomics analysis highlighted the plastisphere's accumulation of L-glutathione, glycerophospholipids, and fatty acyl compounds responding to nitrogen loading. The research further highlights a quartet of microbial phyla - Actinomycetota, Bacteroidota, Cyanobacteriota, and Pseudomonadota – that not only manage to thrive but also constitute pivotal microbial resources within the plastisphere when confronted with strong nitrogen loading. In essence, this investigation illuminates the plastisphere's biodiversity dynamics and nitrogen metabolic adjustments in the face of augmented nitrogen loading, offering fresh perspectives on tapping into the plastisphere's untapped microbial potential.

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P12-5: Corrosion Inhibition of Marine *Streptomyces* on Sulfate-Reducing Bacteria

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The development of environmentally friendly and sustainable corrosion protection technologies is a longstanding yet difficult problem, especially for the marine Microbiological Influenced Corrosion (MIC) caused by sulfate-reducing bacteria (SRB). It is an effective strategy to control MIC with beneficial microorganisms. In this study, X65 steel was selected as the research object, and a marine Streptomyces stain with inhibition effect on SRB was selected to explore the effect of Streptomyces on corrosion of X65 steel, evaluated the inhibition effect on SRB corrosion, and discussed the inhibition mechanism. The growth of Streptomyces and SRB alone and mixed was evaluated by growth curve. The average corrosion rate of X65 steel was measured by weight loss method. The surface films and pitting corrosion of the samples were analyzed by scanning electron microscope (SEM), Raman spectroscopy and confocal laser scanning microscope (CLSM). The electrochemical process of the steel surface was studied by electrochemical impedance spectroscopy (EIS). The results showed that Streptomyces formed uniform "honeycomb" tissue on the surface of X65 steel at the initial stage, which was conducive to the diffusion and adsorption of cell tissue and various metabolites to the surface of the material. With the extension of time, the film became denser and had a certain protective effect on the matrix, but in the early stage of bacterial growth, the consumption and metabolism of organic matter lead to the decrease of solution pH, which accelerated the corrosion of X65 steel. Compared with sterile system, Streptomyces inhibited pitting to a certain extent. The addition of Streptomyces inhibited the growth of SRB. Compared with SRB system, the film layer on the sample surface was denser and more continuous, which played a good protective role. The coexistence of the two bacteria may play a synergistic role in mineralization, thus reducing the corrosion rate of X65 steel. At the same time, the local corrosion caused by SRB was also significantly inhibited.

P12-6: Novel Natural Product Discovery from Red Sea Bacteria

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Natural products from bacteria have traditionally been candidates for pharmaceutical and biological agents. The Red Sea has been gaining attention as a source for novel natural products due to its high temperature and salinity environment. Although there has been a growing number of studies on secondary metabolites in bacterial communities in the Red Sea, many focused on bacteria associated with sponge and coral environments. There is still great potential to discover secondary metabolites in bacteria across diverse habitats. This study selects a diverse set of bacteria strains from a collection of 1704 unique bacteria samples, covering 11 sites in the Red Sea to identify novel natural compounds. Selected strains were sequenced for draft genome with 2nd generation Illumina sequencing and subsequently screened for biosynthetic gene clusters. These BGCs will be further analyzed based on factors such as predicted products and bacteria habitat, then selected for targeted compound discovery.

P12-7: Coevolution and Adaptation of TNPs and PRMs in Natural Ascrotal Mammals Support the Black Queen Hypothesis

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Protamines (PRMs) and transition nuclear proteins (TNPs) are two key classes of sperm nuclear basic proteins that regulate chromatin reorganization and condensation in the spermatozoon head, playing crucial roles in mammalian spermatogenesis. In scrotal mammals, such as humans, cryptorchidism, the failure of the testes to descend into the scrotal sac, is generally associated with higher rates of defective spermatozoon quality and function. However, ascrotal mammals, such as cetaceans, with naturally undescended testes, produce normal spermatozoa similar to their scrotal counterparts. This study investigates the evolutionary pattern and functional changes in PRMs and TNPs to explore the potential molecular mechanisms underlying spermatogenesis in naturally ascrotal mammals. Although we found a conserved genomic arrangement for PRM and TNP genes across mammals, the coevolutionary loss of intact *PRM2* and *TNP2* was observed in several species, correlating significantly with diverse testicular positions. Notably, in cetaceans, which lack intact *PRM2* and *TNP2,* we detected enhanced thermostability and DNA binding in PRM1, along with superior DNA repair capability in TNP1. These findings suggest that gene loss of *PRM2* and *TNP2*, combined with functional enhancements in PRM1 and TNP1 proteins, evolved in response to physiological challenges posed by natural cryptorchidism in most ascrotal lineages. This evolutionary strategy enhances chromatin condensation efficiency and promotes DNA repair during spermatogenesis in natural cryptorchid mammals, supporting the Black Queen Hypothesis.

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P12-8: Exploration of Proteomic Diversity and Cardiovascular Toxicity Mechanism of Stonefish (*Synanceia verrucosa*) Venom

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The *Synanceia verrucosa*, commonly known as the stonefish, is an important coral reef-dwelling fish species that employs venom and camouflage as its primary defensive strategies. The stings produced by its spines can induce intense pain, respiratory arrest, cardiovascular damage, convulsions, and skeletal muscle paralysis, sometimes leading to death. However, research on the proteomic diversity of the stonefish venom and the molecular mechanisms of its toxic components is currently limited.

The stonefish venom has known cardiovascular toxicity, with clinical reports of victims experiencing ventricular tachycardia. In this study, we tested the cardiovascular effects of the crude venom in C57BL/6 mice and found that a 30 mg/kg dose significantly reduced carotid artery blood flow. To further clarify the key toxic substances, we purified the stonefish venom and employed proteomic approaches to identify its diversity and ultimately grasp the key venom protein, Neoverrucotoxin (neoVTX).

The NaV1.5 channel is primarily expressed in cardiomyocytes and is an important target for studying cardiac arrhythmias and cardiovascular diseases. We hypothesized that neoVTX exerts its cardiovascular toxicity by acting on the NaV1.5 channel. Through the activity assay, we found that neoVTX is indeed functional and inhibits the opening of the NaV1.5 channel in a concentration-dependent manner. Further experiments revealed that neoVTX blocks the channel pore region to exert its effects.

In summary, our research has revealed the compositional and functional diversity of the stonefish venom. We have identified a key venom protein, neoVTX and explored its molecular mechanism of action. These findings lay a critical foundation for the creation of a marine fish toxin bioactivity library and the elucidation of the molecular mechanisms and ecological significance of these toxins.

P12-9: Global Distribution of Bioactive Compounds from Deep-sea Organisms: Exploring the Influence of Phylogeny and Environment

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The natural world has played a critical role in the discovery and development of pharmaceutical products, with ~42 000 marine natural products (MNPs) being reported in the last 50 years. However, less than 7 % of MNPs are derived from the deep sea (below 200 m) despite it accounting for 90 % of global oceans. The physiological and biochemical characteristics that enable environmental tolerance in extreme deep-sea environments can be linked to gene regulation and primary and secondary metabolic pathway modifications, thus offering the potential of discovering structurally diverse compounds versus the ocean's shallow water counterpart. Based on marine chemical databases MarinLit and CMNPD, this study generates a comprehensive review of deep-sea chemical novelty and bioactivity. Building on previous reviews and databases, the addition of taxonomic, phylogenetic, environmental and trait information, allows for an initial exploration of phylogeographic relationships to deep-sea bioactivity. With currently only ~3 000 records of chemical novelty and bioactivity in the global deep-sea, this study shows the potential value of a comprehensive database to support interdisciplinary metanalyses with the aim of guiding targeted biodiscovery in the future. Chemical diversity in the deep-sea is demonstrated with a highly isolated scaffold cluster analysis, which should encourage biodiscovery efforts in the deep-sea, that balances diverse investigation to understand novel compound evolution and a more targeted approach that can utilise phylogenetics and environmental conditions to efficiently screen compounds for pharmaceuticals. Finally, this study has highlighted the issue of sampling bias and major data gaps over geography, depth, taxonomy, phylogenetics and data quality. It should be a priority moving forward to collect and store comprehensive data according to FAIR principles. As the BBNJ agreement comes into force, its Clearing-House Mechanism may go some way in supporting deep-sea MGR data in the high seas.