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Editorial: 16th deep-sea biology symposium

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Editorial on the Research Topic
16th deep-sea biology symposium

Introduction

The Research Topic on the 16th Deep Sea Biology Symposium compiles a range of articles presented during the conference that was held in Brest (France) in September 2021 and hosted by the Institut Français de Recherche pour l'Exploitation de la Mer (Ifremer). This triannual event is the central meeting for deep-sea research, where scientists from all over the world gather together to showcase and discuss the latest advances in their field. For the first time in 2021, this event was held in a hybrid mode with participants attending on site and online. Puccinelli et al. showed that, while meetings organized by the Deep-Sea Biology Society had typically less than 400 participants, the use of a hybrid format increased participation by 33% (581 attendees), 73% of whom joined online.

The 26 articles of this Research Topic span research conducted by 138 authors across all ocean basins, encompassing a range of topics that we classified in four sections: 1) zoology and systematics, 2) biodiversity, 3) ecology and 4) conservation and policy. These works investigated most trophic levels from phytoplankton to benthos, fish and whales, across diverse deep-sea environments such as mesopelagic to abyssal environments, vents, seeps and seamounts. This Research Topic provides novel insights on the largest biome of the planet, while advancing our understanding of the complex interactions between organisms and their physical environment, and how such equilibrium is affected by human-induced activities and climate change.

Zoology and systematics

Given the difficulty of accessing deep-sea habitats and their large extent, there are big knowledge gaps related to the biology, ecology and evolutionary history of deep-sea species (Howell et al., 2020). To fill these gaps, eight articles of this Research Topic focused on

taxonomy, species delimitation, phylogeography and biology of deep-sea species. Two articles described species collected in the Clarion-Clipperton Zone (CCZ), an abyssal region in the Northern Pacific Ocean harboring large deposits of polymetallic nodules. Using a combination of morphological and genetic analyses, Eichsteller et al. provided a revised identification key of the brittle star genus *Ophiotholia* and described a new species (*Ophiotholia saskia*) (Eichsteller et al., 2023). In addition, Gooday and Wawrzyniak-Wydrowska described macrofaunal assemblages of foraminifera in four areas of the CCZ, including a protected area (i.e. APEI). Among almost 2,000 collected specimens, the authors recognized 280 morphospecies. Interestingly, diversity assemblages were very different among the four areas, highlighting that APEIs may not serve as refugia for deep-sea species in case of anthropogenic disturbance in the CCZ. Improving biodiversity assessments in the CCZ is particularly important in the context of possible future deep-sea mining of polymetallic nodules in this region.

Precise taxonomy of deep-sea species can benefit from additional data types when morphological characters are not sufficient or reliable. Specifically, Montenegro et al. assessed if morphological characters typically used to differentiate the medusozoans *Botrynema brucei* and *B. ellinorae* have an evolutionary significance. Using four genetic markers, they found that the current species separation based on morphological characters was inaccurate. As a result, *B. ellinorae* was assigned as a subspecies of *B. brucei*. Similarly, Korfhage et al. used four genetic markers to delimit species of deep-sea corals. They compared genetic data with proteomic fingerprinting, a technique that measures the variability in composition of peptides and small proteins in each individual. They found that both techniques can successfully discriminate coral species, although proteome fingerprinting lacked power when sample sizes were small and when reference databases were lacking.

Genetic data bring important insights into deep-sea species phylogeography and evolutionary history. For instance, Jang et al. investigated the genetic structure of *Alviniconcha* snails in seven hydrothermal vents from the Indian Ocean. Using eight genetic markers, the authors found strong genetic differentiation between snails from northern and southern vents, suggesting the discovery of a cryptic *Alviniconcha* species. In contrast, Weston and Jamieson focused on the distribution of the hadal amphipod *Hirondellea dubia* across multiple oceans. Using morphological and genetic data, they found that *H. dubia* has a much wider bathymetric and geographic distribution than previously described. In fact, *H. dubia* is not restricted to hadal depths, but it can occur between 4,700 m and 10,800 m, and it is found in multiple broad oceanic regions including the Southern, Northwest and Central Pacific, as well as the Northern and Southern Atlantic. Importantly, genetic data allowed the authors to exclude the possibility of cryptic species among the investigated populations.

Finally, two articles focused on improving knowledge of deep-sea species biology. Azofeifa-Solano et al. described the reproductive biology of the yeti crab *Kiwa puravida* occurring in methane seeps of the Costa Rican Pacific margin. By examining several morphological characters, they tested for the presence of sexual dimorphism. They found differences in male and female claw size, suggesting that claw weaponry is under sexual selection in this species. In this last study, Piquet et al. examined the fate of chemosynthetic bacterial symbionts of the deep-sea mussel *Bathymodiolus azoricus* following starvation. Using fluorescence and electron microscopy, they followed the loss of symbionts in mussels maintained in the laboratory. They found that after 61 days all symbionts were lost, and that the epidermis that usually contains the symbionts had the same structure as the one of non-symbiotic mussels.

Biodiversity

Deep-sea biodiversity research is sparse, especially in the tropics (Costa et al., 2020). Jamieson et al. filled some of these knowledge gaps by conducting one of the few biological and high-resolution bathymetric surveys in Java Trench located in the Eastern Indian Ocean. During submersible transect surveys, they reported diverse hadal communities comprising 10 phyla, 21 classes, 34 orders and 55 families, with many new depth and biogeographic extensions, including a rare encounter of a hadal ascidian. In addition, they report putative evidence of chemosynthesis based on visual evidence of bacterial mats. With their observational work the authors lay the foundations for more hypothesis-driven research in hadal environments. Given that collecting new deep-sea biodiversity information can be expensive, there is value in synthesizing existing information that is often fragmented and sitting across different research institutions. Alvarado et al. provided a first synthesis of existing deep-sea echinoderm information from Costa Rica. By reviewing existing biodiversity information from public databases and biological specimens deposited in museum collections, they found a total of 124 taxa between 200-3600 m. Notably, they reported 22 new records for the Eastern Tropical Pacific, 46 for Central American waters, and 58 for Costa Rica, highlighting the value of conducting such synthesis efforts.

Global warming causes profound environmental shifts in the poles, altering the composition and structure of their communities. Pantiukhin et al. focused on collecting video observations of gelatinous zooplankton (jellyfish) in Fram Strait, the main gateway to the Arctic Ocean. By combining biological and environmental data that were collected simultaneously, the authors found that depth and temperature were key in explaining jellyfish distribution and abundance. Incorporating those observations into spatial distribution modelling approaches they were able to project that with further temperature increases, jellyfish communities in the Fram Strait would become less diverse but more abundant in the future. On the opposite end of the globe, Grimes et al. used photographic surveys to explore epifaunal communities along 6000 km of Western Antarctica, from the tip of the Antarctic Peninsula to the Ross Sea. Benthic communities were dominated by ophiuroids, pycnogonids, holothuroids, and demosponges, with a decrease in abundance at higher latitude sites. Both studies provide critical baseline information of key groups of Arctic and Antarctic biological communities that will allow to track future climate-driven changes.

Finally, there were significant new knowledge contributions to the biodiversity and ecology of chemosynthesis-based ecosystems. Astorch-

Cardona et al. conducted a unique spatial and temporal study of phylogenetic and chemical data of iron-rich microbial mats from the Lucky Strike Hydrothermal Field in the Mid-Atlantic Ridge. Their metabarcoding analyses revealed distinct microbial communities at each site, linked to the chemical composition of the diffuse fluids nourishing the mats. Notably, these variations remain constant over time except for years when a geological event took place. Furthermore, Velez et al. focused on sediment fungal diversity and community structure from low- and high-temperature vent systems (Pescadero Basin, Pescadero Transform Fault, and Alarcón Rise) and an Oxygen Minimum Zone (Alfonso Basin) in the southern Gulf of California. Using high-throughput sequencing, the authors reported 102 fungal amplicon sequences, mainly Ascomycota and Basidiomycota, the majority of which were from the high-temperature vent systems, corroborating these as diversity hotspots. This information, along with characteristic assemblages per studied ecosystem, will pave the way for further exploration work that includes an extensive sampling design, accounting for intra-sample variability. Lastly, Avila et al. investigated the role of whale falls as chemosynthetic refugia, by studying nematodes colonizing whalebones between 1500-4204 m in the Southwest Atlantic Ocean, off Brazil. Their findings showed the affinity of whalebone nematode assemblages to hydrothermal vents and cold seeps suggesting that organic falls may indeed act as intermediate refugia for meiofauna from chemosynthetic environments.

Ecology

A strong focus of the articles published is on deep-sea ecology. These works provided information on functional and trophic ecology of diverse deep-sea habitats including the mesopelagic, seeps and seamounts, focusing on a range of trophic levels from primary producers to benthos and fish. A few studies have investigated the relevance of alternative food sources to deep-sea benthos, with Cautain et al. highlighting the role of sympagic (i.e. ice-associated) production in supplying a high fraction of carbon to macrobenthos in the Barents Sea, although a large variation was observed between summer and winter. Åström et al. indicated that some benthic taxa in the seeps of the Svalbard-Barents Sea region acquire up to 50% of their carbon from chemosynthesis and have wider trophic niches in comparison to taxa inhabiting non-seeps. Finally, Stauffer et al. provided first observations of food falls (e.g., whale, penguin) in the Wadden Sea, and highlighted their relevance for the food web of deep-sea benthos.

Herrera et al. provided a clear understanding of benthic community early stages ecological succession using as a novel study system a deep seamount formed from the activity of the Vailulu'u volcano in American Samoa. Volcano eruptions represent disturbance events able to reset the ecological succession clock to zero, similarly to what is observed after anthropogenic disturbances (e.g., bottom trawling). The authors highlight how such knowledge could be applied to identify signs and states of recovery from human activities in deep seamounts.

Moving up in the water column, two studies are focused on the functional diversity of fish from the mesopelagic (200-1000 m). Aparecido et al. determined the functional diversity of mesopelagic

fish from over 7,000 specimens, using 17 functional traits related to feeding, survival, and locomotion functions. They identified high fish diversity, however with variation between day and night and a higher diversity in the deepest ocean layers. On the other hand, McGonagle et al. highlighted that diet and morphological diversity do not drive hyperspeciation in melanostomiine dragonfishes from the Gulf of Mexico, the most speciose group of mesopelagic fishes. Other factors, including sexual conspecific recognition and/or sexual selection, may be the main drivers of hyperspeciation in this sub-family. Finally, a focus was placed by Callery and Grehan on the potential application of a supervised machine learning methodology to provide a habitat classification system and preliminary habitat inventories, needed for marine management decision making, until seabed mapping is fully developed.

Conservation & policy

There is an urgent need for adequate environmental governance in the deep sea due to multiple lines of evidence of several anthropogenic impacts and threats to this system such as deep-sea mining (Vonnahme et al., 2020) or climate-induced thermal stress (Szuwalski et al., 2023). The study of Boteler et al. investigated the problem of connectivity, essential to design effective and resilient networks of Marine Protected Areas in view of conservation measures to protect and restore deep-sea biodiversity. Authors proposed a synthesis of existing data about the connectivity of the Salas y Gómez and Nazca ridges, two seamount chains in the Southeast Pacific recognized as some of the most important global areas to protect, mostly situated in areas beyond national jurisdiction. High rates of endemism and migratory corridors provide evidence of large-scale conservation measures necessary for developing management strategies for the region.

Among deep-sea habitat-forming species, cold-water corals (CWCs) are known to form Vulnerable Marine Ecosystems (VMEs). Angiolillo et al. reported the first attempt to describe the impact of longline fishing on a CWC *Dendrophyllia ramea* population on the Apollo bank (Ionian Sea). This study showed that deep-water fishing activities negatively affect this species stressing the importance of urgent conservation measures on this specific VME. Finally, another approach to balance sustainable development and biodiversity protection is the Ecosystem-based management (EBM). Following the declaration of the International Seabed Authority (ISA) about the need of incorporating EBM in its tools, Guilhon et al. analyzed understanding and implications of EBM of ISA stakeholders for deep-sea mining. This paper reveals different EMB views from ISA stakeholders highlighting the need for clarification on what EBM involves for seabed mining.

Conclusion

We received a large number of novel and cutting-edge submissions covering a broad range of topics, emphasizing the strong and increasing interest of the research community for deep-sea biology. We believe that the next deep-sea biology symposium

(17DSBS) taking place in Hong-Kong in 2025 will highlight further exciting research on the largest biome of the planet.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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