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Editorial: Recent and emerging innovations in deep-sea taxonomy to enhance biodiversity assessment and conservation

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Editorial on the Research Topic

Recent and emerging innovations in deep-sea taxonomy to enhance biodiversity assessment and conservation

Deep-sea areas that extend from the shelf break down into hadal trenches are vast and cover more than half of the Earth's surface. In the early days of deep-sea exploration, the deep sea was seen as an enormous, dark, and hostile environment barren of life (Tyler, 2003; Danovaro et al., 2014), but it has since become clear that the deep ocean is in fact an environment rich in biodiversity, which provides essential ecosystem services (Cochonat et al., 2007; Armstrong et al., 2012; Thurber et al., 2014). Deep-sea ecosystems are of immense importance for biogeochemical processes and cycles at a global scale (Armstrong et al., 2012), and the latter are inevitably linked to biodiversity (Danovaro et al., 2008). Increasing anthropogenic pressures on deep-sea ecosystems, stemming from resource exploitation, pollution and climate change (Clark and Dunn, 2012; Pham et al., 2014; Sweetman et al., 2017; Smith et al., 2020) will lead to a loss of biodiversity in deepsea ecosystems, thus affecting their structure and function (e.g., Danovaro et al., 2008; Niner et al., 2018). Therefore, protecting deep-sea biodiversity should be a global concern, and now is the time to grow our knowledge in this area.

Species are a basic unit of biodiversity. Taxonomy, the classification and naming of taxa, is the fundamental science for exploring biodiversity and its drivers, thus underpinning conservation management initiatives. However, with its high undescribed diversity, taxonomy in the deep sea is facing major challenges. Most of the species collected

from greater depths are new to science (Glover et al., 2002; Brandt et al., 2007; Poore et al., 2015). Furthermore, with more sampling and expeditions, also using advanced equipment such as Remotely Operated Vehicles (ROV), help to more (new) species being discovered (Bribiesca-Contreras et al., 2022). This large unknown biodiversity not only impairs adequate estimation of global deep-sea biodiversity, but also poses a great risk that species will be lost before they are even discovered, let alone named. A declining number of taxonomists (a rapidly growing issue known as the taxonomic impediment) further exacerbates the situation (Convention on Biological Diversity [CBD], 2010; Mora et al., 2011; Engel et al., 2021). Deep-sea taxonomy is thus caught between the need to robustly describe species and the implicit requirement to do so as quickly as possible to keep up with ongoing environmental changes.

Our aim for this Research Topic in Frontiers in Marine Science was to bring together studies that advance the taxonomic analysis of deep-sea metazoan species with focus on the application of new methods and approaches. In particular, we sought to highlight the role of taxonomy as a key discipline for understanding and ultimately conserving deep-sea biodiversity. This Research Topic comprises 14 scientific papers that shed light on deep-sea taxonomy from very different perspectives, involving different taxonomic groups and different organizational levels of biodiversity – from genes to ecosystems.

To discriminate species and identify them as known or new to science is the first step in taxonomy. However, even this can often prove very difficult. Traditionally, deep-sea species have been delineated and identified by their morphological appearance. The presence of morphologically identical or similar but genetically distinct species, polymorphisms, ontogenetic plasticity or severe sexual dimorphism have led to incorrect species assignments (e.g., Vrijenhoek, 2009; Brasier et al., 2016; Christodoulou et al., 2020). A number of studies in this Research Topic highlight these issues and provide novel approaches to solving them. Several studies advocate an integrative taxonomic approach as the most robust method for accurately delimiting species. For example, using species' biogeographical or bathymetric distributions, ecological requirements, or phylogenetic origins, can help distinguish between different species. Kürzel et al., for example, combined evidence from morphological and molecular (DNA barcoding and proteomics) analyses of a family of Icelandic isopods with species distribution models to elucidate species boundaries. In particular, they found proteomic fingerprinting to be a promising tool for rapid and inexpensive species differentiation. In addition, the authors recommend the use of interactive keys, so-called multiple-access keys, especially for the identification of deep-sea species, since they are very flexible and can be modified to include newly described species. Frutos et al. present a comprehensive overview of traditional and new methods for peracarid crustacean taxonomy, with a focus on morphological tools, but providing an overarching presentation

of molecular genetic methods as part of an integrative practice. Fixation and imaging procedures are presented in great detail. Great importance has been attached to some microscopic techniques, some of which have only rarely been applied to deep-sea species, on the one hand to improve the morphological analysis and on the other hand as a bridge to other biological disciplines. Martínez-Sanjuán et al., used computed microtomography (Micro-CT) for taxonomic research on species in the molluscan class Solenogastres. While it was not possible to obtain a sufficient resolution of some body parts, micro-CT seems to be particularly valuable as a non-destructive technique for morphological analysis in this taxon, and other rare deep-sea animals. Micro-CT thus joins a number of other microscopy techniques, including Confocal Laser Scanning Microscopy (CLSM) or Environmental Scanning Electron Microscopy (ESEM, Frutos et al.), in which the individual specimen is not destroyed but remains available, for example as invaluable collection material for future analyses including, under certain conditions, also for molecular applications. As deep-sea organisms are often only collected in limited numbers, these methods enable high-quality imaging of this precious material, while keeping a voucher as a reference.

In a deep-sea context, one is often confronted with the inability to identify species unequivocally, whether due to damaged specimens, cryptic species or if the species is new to science. Open Nomenclature (ON) procedures are therefore used to make these identifications consistent and thus available for biodiversity data sets (e.g., Sigovini et al., 2016). Prerequisite for this is that a physical specimen is present. However, assessment of the biodiversity of deep-sea megafauna is often based on analysis of still or video images. In their study, Horton et al. provide guidelines for using ON for image-based identifications and its implementation into repositories for biodiversity data. The standardized use of ON is likely to significantly improve the quality and comparability of biodiversity datasets, thereby aiding monitoring of deep-sea biodiversity changes.

Estimates of how many species occur in the deep sea are greatly divergent (Grassle and Maciolek, 1992; May, 1992; Poore and Wilson, 1993) because our view of deep-sea biodiversity is strongly biased - both geographically and taxonomically. Some areas are better sampled than others, e.g. sampling effort in many areas of the North Atlantic is greater than knowledge of the Southern hemisphere (e.g., Howell et al., 2020 and citations therein). Furthermore, species with larger body sizes and wide-ranging distributions tend to be discovered and described earlier, while knowledge about small-bodied, less conspicuous groups and those with restricted ranges is much more limited (Mora et al., 2011; Higgs & Attrill, 2015). As different taxa have been shown to exhibit different biodiversity patterns in the deep sea (e.g., Brandt et al., 2007; Washburn et al., 2021), and small-bodied taxa in particular contribute significantly to overall biodiversity (Hessler and Sanders, 1967;

Rex et al., 2006), a fundamental improvement in our knowledge here is crucial. In this Research Topic, a number of papers focused on understudied geographic regions or taxonomic groups where much more research is required. Kniesz et al. studied scavenging amphipod communities associated with active and inactive hydrothermal vents in the Central and South East Indian Ocean. Since the first vent fields in the Indian Ocean were only discovered at the beginning of this century, they are among the least explored habitats in the deep sea. The authors discovered a rich assemblage of amphipods. Yet, although the region was poorly explored, several species were already known. A vent-endemic fauna could not be inferred with certainty; however, some species appear to be well adapted to the extreme conditions, particularly high temperatures and hypoxia, that prevail at vents. Jażdżewska et al. investigated the distribution of two widespread scavenging amphipod species by means of integrative taxonomy. The authors were able to provide evidence of cosmopolitanism in a species spanning the Atlantic, Pacific and Indian Oceans, while the other species likely represents a complex of six previously undescribed species.

Australia has a very extensive continental slope, but sampling at this depth in the region has been remarkably limited (McCallum et al., 2015; Poore et al., 2015; O'Hara et al., 2020). Very few samples have been taken especially within the Australian Exclusive Economic Zone (EEZ), which has been shown to have a highly diverse fauna (Poore et al., 2015; O'Hara et al., 2020). The focus of the study by Błażewicz et al. were tanaidacean crustaceans of the genus Pseudotanais collected from the southern Australian slope. Prior to this, only one species was known from Australian waters, with the authors' new descriptions increasing the number to six. Similar to Australia, national waters of many countries include deep-sea habitats. Yet, although the deep sea is here practically on the doorstep, it is often only little explored (cf. Woodall et al., 2021; Amon et al., 2022). The studies by Stępień et al. and Jóźwiak et al. examining the biodiversity of cumaceans and tanaidaceans along a bathymetric gradient along the Ghanaian slope (West Africa, central Atlantic) help to fill one of these major biogeographic gaps. A high level of diversity was found in both taxa, with most species previously undescribed. In fact, Stępień et al. label the region as a biodiversity hotspot for cumaceans. The region is exposed to hydrocarbon pollution from the oil industry, which poses significant risks to biodiversity.

The discipline of biogeography relies on formally described species (Glover et al., 2018). Grzelak et al. presents a description of a new kinorhynch species collected from hadal depth of the Atacama Trench (SE Pacific), thus contributing to expanding the understanding of biogeographical patterns of isolation and connectivity of the trench fauna. Similarly, the study by Passos et al. focuses on a group that has only been little examined in the deep sea by describing a new species of caudofoveate mollusc from the Brazilian slope. Using species distribution models, their distribution was evaluated in comparison to other congenerics,

with strong differences in the ecological requirements and thus in the distribution of the species in this group being identified. Finally, the study by Stępień et al. examined the tandaidacean genus *Agathotanais* from across the Pacific. The authors provided a synopsis of the genus and a description of five new species, bringing the total to 17 species known worldwide, although it is likely that many more exist.

All studies of this Research Topic contributed to the goal of expanding knowledge of deep-sea biodiversity through taxonomy and thus offering tools and/or solutions for deep-sea conservation. To be highlighted here are the studies by Stefanni et al. and Thomas et al. Assessing the impact of human activities on the deep-sea floor requires accurate data on the distribution of biodiversity and its components - populations, species and communities. Due to the spatial and temporal dynamics of deep-sea ecosystems, the collection of long-term data is of crucial importance. Cabled observatories play a key role here, as they can record biodiversity data and relevant environmental parameters continuously and over the long term. Stefanni et al. present an overview of environmental DNA (eDNA) metabarcoding in conjunction with cabled observatories to support deep-sea biodiversity assessment. Due to the high biodiversity in the deep sea, coupled with low specimen numbers and the taxonomic issues of species identification and delineation mentioned above, eDNA metabarcoding is emerging as a very valuable tool for the study and monitoring of deep-sea biodiversity. In particular, the integration of optoacoustic technologies and eDNA seems to very much complement each other to more fully capture deep-sea biodiversity and its changes.

The risk of extinction of deep-sea species due to human activities is very real (Barbier et al., 2014). In addition to mapping and describing deep-sea biodiversity, conservation strategies need to be evaluated. The International Union for Conservation of Nature (IUCN) Red List of Threatened Species is one such tool to increase the visibility of threatened biodiversity and provide objective guidelines for conservation actions by listing species that are endangered or at the brink of becoming extinct. However, Red List criteria have rarely been applied to deep-sea species, although it has proven to be an ideal tool for identifying threats to species and protecting them (Sigwart et al., 2019). Thomas et al. evaluated the Red List status of more than 180 species of hydrothermal molluscs, particularly in light of forthcoming mining activities to exploit deep-sea minerals from these habitats and the associated risks to fauna. Given that only one deep-sea species has previously been Red listed (Sigwart et al., 2019), the study by Thomas et al. is unparalleled by classifying more than 62% of the assessed species as threatened. At the same time, the authors call for genuine conservation measures to protect deep-sea fauna, such as the designation of marine protected areas (MPAs), and, in the absence of sufficient knowledge of the deep-sea biota, advocate a precautionary approach to managing resource exploitation of deep-sea ecosystems and thus safeguarding their high biodiversity.

The destruction of habitats and the depletion of their resources will have unpredictable consequences on the largely undescribed deep-sea biodiversity, with further potential cascading effects on ecosystem functions and services. The articles summarized in this Research Topic each contributed a piece of the puzzle by using taxonomic information to advance our understanding of deep-sea biodiversity. Obviously, many gaps remain, but we think it has been convincingly demonstrated that taxonomic research will continue to play an important role in deep-sea exploration and conservation. Future directions in this discipline include encouraging the development of tools and techniques to describe biodiversity as quickly and accurately as possible, but also identifying ways to ensure stable taxonomy and taxonomic expertise over the long term. The latter concerns enabling the training of future taxonomists, but above all increased funding initiatives as well as employment opportunities for taxonomists. Taxonomy cannot be viewed in isolation, but is a highly integrative field and must remain open to interlinking with other biological disciplines. Similarly, the description of a species is greater than the sum of its parts; "Every species is a masterpiece, exquisitely adapted to the particular environment in which it has survived. Who are we to destroy or even diminish biodiversity?" (E.O. Wilson). Taxonomists are passionate about their research and it is also up to them to spread the spark and convey the value and appreciation of the variety of life in the deep sea.

Author contributions

All authors listed have made a substantial, direct and intellectual contribution to the work, and approved it for publication.

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Conflict of interest

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