EXPLORING THE MARINE BIODIVERSITY WITH ENVIRONMENTAL DNA

ABSTRACT (in English)

Marine sedimentary archives are an important repository of the whole marine biodiversity comprising both benthic and pelagic organisms. Environmental DNA (*e*DNA), which accumulates and preserves in marine sediments, can be used to study the taxonomic composition of living communities as well as to reconstruct past biodiversity depending on whether it concerns modern or historical *e*DNA deposits. The analysis of sedimentary DNA (*sed*DNA) or sedimentary ancient DNA (*seda*DNA) opens up entirely new possibilities for the study of short- and long-term responses of marine ecosystems to environmental changes. Recent advances in high-throughput sequencing technologies allow to rapidly sequence DNA from marine environments and led to a consistently increasing number of metabarcoding studies, especially for microbial biomes. However, various challenges and biases that affect the generation and analysis of metabarcoding data are not fully resolved. To unlock the full potential of *e*DNA metabarcoding applied to both modern and paleoceanographic studies more research is needed to better understand the relation between *e*DNA taphonomy and environmental changes in marine settings.

In order to further enhance the use of *e*DNA in present and past marine biodiversity studies, this thesis addressed the following research tasks: i) investigating the biodiversity of eukaryotes in water column and surface sediments and the preservation of planktonic *e*DNA on the seafloor; ii) investigating the biodiversity of selected eukaryotic taxa (foraminifera) and their responses to environmental parameters; and iii) summarizing the current advances in marine *seda*DNA research and discussing potential methodological pitfalls and limitations.

The first part describes the marine eukaryotic communities (RA I), from water column to surface sediment, and their *e*DNA taphonomy. The main advantage of the *e*DNA approach is the possibility of obtaining a holistic record of marine biodiversity. However, very little is known about how accurately marine biodiversity is recorded in sedimentary DNA archives, especially in terms of planktonic taxa. To address this important question, we provided a vertical and horizontal survey of eukaryotic diversity in the Nordic Seas and compared eukaryotic diversity throughout the water column to surface sediment. Our study has led to the following conclusions: i) the taxonomic composition of water and sediment *e*DNA samples differs significantly; ii) a large amount of plankton DNA is transported to the surface sediments and

dominates sediment DNA data in terms of abundance but not diversity; iii) not all plankton taxa are equally archived on the sea floor, with some nano- and picoplankton taxa being underrepresented in sediment DNA samples. Overall, these results suggest that the composition and structure of the plankton community recorded in sedimentary *e*DNA differ from what is observed in the water column. This highlights potential taxonomic and abundance biases that should be taken into account when reconstructing past marine biodiversity changes.

The second part focuses on the diversity of benthic foraminifera and their role as ecological indicators. This part comprises two studies. In the first study (RA II), we used an *e*DNA metabarcoding of surface sediments to investigate the diversity of Arctic foraminifera in fjords and open sea areas of the Svalbard Archipelago. Our analysis of metabarcoding data revealed a very high phylogenetic diversity of foraminifera compared to traditional morphology-based studies. More than half of the Amplicon Sequence Variants (ASVs) could not be assigned to any group in the reference database, suggesting a high genetic novelty of Svalbard foraminifera. The taxonomic composition of the foraminiferal community varied between sampling localities (fjords and open sea areas), influenced by different water masses. Numerous potential molecular foraminiferal indicators of water mass characteristics were identified, particularly regarding the impact of Atlantic Water in the Svalbard region. This study provided the first comprehensive metabarcoding data on foraminiferal biodiversity in the Svalbard area and contributed to a better knowledge on how the foraminiferal community responds to Arctic environmental gradients.

In the second study (RA III), we analyzed the deep-sea foraminifera, focusing on a huge unknown diversity revealed by metabarcoding data. We tackled this problem by using the specific genetic signature to classify unassigned foraminiferal sequences, which usually dominate in *e*DNA metabarcoding datasets. We applied this approach to benthic foraminifera from Clarion-Clipperton Fracture Zone biodiversity in the Eastern Pacific Ocean, comparing their diversity to available foraminiferal datasets from other deep-sea and shallow-water regions. As a result, 61 new foraminiferal lineages placed in 27 phylogenetic clades were identified by unique signatures in the 37F hypervariable region of the 18S rRNA gene. Most of these novel lineages were also found in other deep-sea areas, but only a few of them appeared in coastal datasets. This suggests that deep-sea benthic foraminifera form a unique group highly adapted to the abyssal environment and that the migration between shallow and deep-sea habitats is relatively limited. The signature-based approach provides an alternative to investigating the distribution and ecology of deep-sea foraminifera, given the limited current

reference database. It could be especially useful in future applications of foraminiferal metabarcoding for environmental monitoring.

The last part of this thesis (RA IV) provides an overview of spectacular advances that have been made in reconstructing the history of marine ecosystems using the *seda*DNA approach. In this article, we conducted a systematic literature review of 55 original studies to examine the last two decades of marine *seda*DNA research. We focus on both planktonic and benthic microbial (prokaryotes and single-cell eukaryotes) and meiofaunal organisms, whose genetic traces are deposited in marine sediments. We describe an in-depth overview of taphonomic or preservation processes, key issues related to the use of *seda*DNA, and the current state of knowledge and applications in marine *seda*DNA research. We anticipate that *seda*DNA approaches will soon be routinely included in paleoceanographic studies and will provide a unique insight into the biodiversity changes at geological timescales, recent anthropogenic impacts, and the past and present evolution of marine ecosystems. The continued development of the *seda*DNA field might also help to establish and optimize strategies for the conservation and management of marine ecosystems.

Overall, my PhD thesis presents various applications of *e*DNA metabarcoding to study past and present ecosystems and highlights its potential and limitations. The results obtained in this thesis contribute to exploring the diversity of deep-sea and polar foraminifera and provide insights into the biases associated with the *e*DNA taphonomy of marine eukaryotes. As demonstrated in this thesis, the use of *e*DNA metabarcoding is crucial to further advance the surveys of marine biodiversity across time and space.