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Commentary

MEER: Extraordinary flourishing ecosystem in the deepest ocean

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https://doi.org/10.1016/j.cell.2024.12.037

Here, we introduce the Mariana Trench Environment and Ecology Research (MEER) project, which provides the first systematic view of the ecosystem in the hadal zone.

The hadal zone, the deepest ocean with water depths exceeding 6,000 m (or 6,500 m according to UNESCO), represents one of Earth's least explored frontiers. Exploration of the hadal zone has never stopped but has always been challenging. For example, before 2020, only nine people had visited the deepest point—the bottom of the Mariana Trench. The pioneering expeditions of the past six decades have laid crucial groundwork for our understanding of hadal zones, though often at great cost and sacrifice. Their unwavering commitment and innovative spirit, even in the face of setbacks, have established the foundation upon which modern hadal research stands. Recent technological advances, building upon these predecessors' valuable lessons and experiences, have opened new possibilities for exploring these deep and mysterious regions, attracting growing interest from the international research community.

The full-ocean-depth-rated manned submersible *Fendouzhe* (placed in active service in 2021) provided new opportunities for systematic hadal investigation based on its unique 220 kg loading capacity for the sampling basket and its 6 h benthic operating time. Compared with other traditional sampling equipment, such as gravity cores and box cores, sampling in the hadal zone via *Fendouzhe* is incredibly improved in both accuracy and frequency. During our TS21 expedition from August to November 2021, we carried out 33 *Fendouzhe* dives and 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 depths from 6,000 to 10,900 m. Sampling sites were mainly selected at the southern end of the Mariana Trench, including the western and eastern depressions in the Challenger Deep along the bottom axis and also from the southern to northern slopes, including both concave and convex normal faults. The dives were also made in the neighboring 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.

We integrated the canonical geophysical and geochemical investigation methodologies and developed a series of equipment, techniques, and pipelines to explore further. To conduct studies of microorganisms in hadal sediments, we developed a semiautomated process from DNA extraction to sequencing and constructed a metagenome framework that fulfilled the requirements of both the treatment of a large sample amount and sufficient sequencing depth (77.26 ± 32.41 G base pairs per sample). In that case, a total of ~92 T base pairs of metagenomic data and 16S rRNA amplicons were completed within a year, and we constructed a unique dataset for the Earth ocean microbiome. Extraordinarily high novelty, diversity, and heterogeneity were observed in the hadal microbiome, especially among prokaryotes and viruses, which are impacted by both the broader context of extreme environmental conditions as well as the delicate topography in the hadal zone. To reveal the active microbiome and metabolism in hadal seawater, a submersible-loaded *in situ* filtration equipment associated with a metagenome-metaproteome coextraction and coanalysis framework was developed. In addition to hadal microorganisms, two representative hadal macroorganisms (fish and amphipod) were also included, constituting a special food chain in the hadal zone. The hadal amphipod (*Hirondellea gigas*), with 622 individuals, illustrates the horizontal population exchange of invertebrates across different trenches. The hadal snailfish (*Pseudoliparis swirei*), in comparison with 10 other deep-sea fishes, illustrates the vertical invasion of vertebrates from the deep sea to the hadal zone.

MEER results provide a systematic picture of the amazing hadal ecosystems, especially the abnormal flourishing of microorganisms under ultra-high pressure (UHP) in the deepest ocean (Figure 1). We specifically answer the following questions: (1) Why does the hadal microbiome have extremely high novelty and diversity? (2) How do hadal microorganisms adapt to the hadal zone? (3) How do hadal macrofauna adapt to the extreme hadal conditions (invertebrates vs. vertebrates)? Notably, shared adaptive mechanisms were observed among hadal macrofauna (amphipods and snailfish) and microorganisms, such as the enhanced

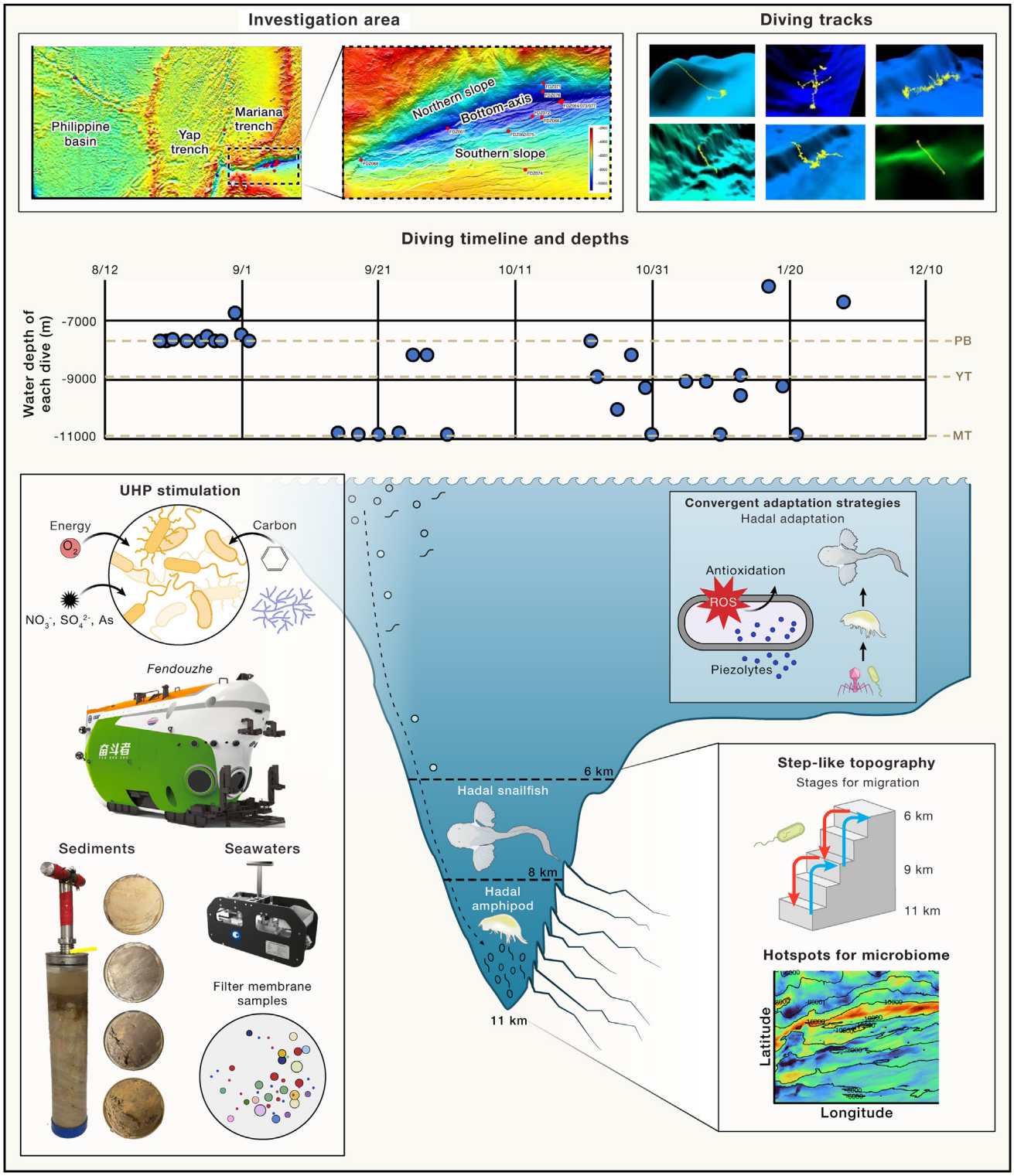

Figure 1. Information on dives and sampling from the MEER project and its main scientific findings

antioxidation capabilities and the intercellular accumulation of compatible solutes. These findings suggest the existence of convergent adaptation strategies to hadal environments that transcend species boundaries and biological domains.

In summary, hadal trenches are the endpoint of plate subduction, communicating between the surface ocean and

the deep Earth and playing irreplaceable roles in global processes with unique ecosystems and extreme life processes. MEER complements the view of global ocean ecosystems with upper-ocean data. Additionally, the extraordinarily high novelty and diversity of hadal microorganisms indicate resource potentials of novel genes, structures, and functions, which may be alternative choices to alleviate the current depletion of terrestrial biological resources taking place over the past decades.

The MEER project facilitates comprehensive access to hadal data for the scientific community. These datasets can be accessed via an online portal and scientific repositories. The online web portal divides the data into two categories: one focusing on MEER microorganisms (https://www.biosino.org/mash/meer) and the other on hadal amphipods (https://db.cngb.org/search/project/CNP0003471) and fishes (NCBI BioProject database with accession number PRJNA1138967).

ACKNOWLEDGMENTS

The authors would like to thank the pilots and crew members of the submersible *Fendouzhe* and *R/V Tan Suo Yi Hao* for collecting samples and providing effective support for the MEER project. We would also like to highlight the critical contributions to this study from the entire science team of the TS21 expedition. We are grateful to Professor Guoping Zhao, the chair of the research plan ''Mechanisms Underlining Elemental Cycling on the Earth by Microorganisms in the Hydrosphere'' from the National Natural Science Foundation of China (NSFC no. 92351000), for his valuable suggestions in preparing the MEER manuscripts. The TS21 cruise was supported by the Major Science and Technology Research Project of Sanya Yazhou Bay Science and Technology City (SKJC-2021-01-001) and the Strategic Priority Research Program of the Chinese Academy of Sciences (XDA22000000). We also thank Dr. Weishu Zhao from Shanghai Jiao Tong University for figure drawing and text editing of this manuscript, as well as her valuable intellectual input in conceptualizing and coordinating the MEER project.

DECLARATION OF INTERESTS

The authors declare no competing interests.