CellPress

Cell Host & Microbe

Forum

Seeking the invisible microbial oases in extreme environments

Weishu Zhao (赵维殳)[1,2,3] and Xiang Xiao (肖湘)[1,2,3,4,*]

[1]Institution of Deep Life and Resource Investigation (IDLRI), International Center for Deep Life Investigation (IC-DLI), State Key Laboratory of Microbial Metabolism, School of Life Sciences and Biotechnology, Shanghai Jiao Tong University, Shanghai 200240, China

[2]Hainan Research Institute, Shanghai Jiao Tong University, Sanya 572025, China

[3]Shanghai Changxing Ocean Laboratory, Shanghai Jiao Tong University, Shanghai 201913, China

[4]Shanghai Academy of Natural Sciences (SANS), Shanghai, China

*Correspondence: zjxiao2018@sjtu.edu.cn

https://doi.org/10.1016/j.chom.2026.07.005

Deep-sea exploration traditionally focuses on visible animal oases, but extreme pressure in hadal zones (>60 MPa) unlocks metabolic capacities and supports flourishing microbiomes. Beyond the deep sea, convergent adaptation strategies suggest that diverse environmental stressors may serve as activators, providing opportunities for discovering invisible microbial oases across Earth's extreme environments.

Introduction

The quest for life in Earth's extreme environments has historically been guided by the search for visible biological oases—places where macrofaunal communities thriving under extreme conditions stand as landmark discoveries. Even in deep-ocean exploration, a defining moment came in 1977, when hydrothermal vents were found at ~2,500 meters deep along the Galápagos Rift,[1] revealing chemosynthetic ecosystems as "deep-sea oases" sustained entirely without sunlight. Subsequent discoveries of additional hydrothermal vents and cold seeps worldwide ignited successive waves of research. Yet this success has understandably led to research efforts prioritizing visible oases, while the vast, seemingly barren regions of the deep ocean remain comparatively understudied. This has, in turn, raised a prevailing question: in the absence of visible oases, should microbial activity be so limited as to render the surrounding areas biological "deserts"?

Invisible microbial oases in the deepest ocean

The Mariana Trench, the deepest ocean region on Earth extending to nearly 11 km deep, provides a compelling example. Despite humans first reaching its bottom in the 1960s, the prevailing view over the following six decades held that the trench was a biological desert. Finding no classic animal oases in the Mariana Trench, researchers increasingly turned to the microbial communities of these extreme depths.

Understanding hadal microbiology is crucial for several reasons: it informs our knowledge of life under extreme pressure, deep-ocean biogeochemical cycling, microbial evolution in extreme environments, and the fundamental limits of life on Earth. However, this has proven far from straightforward, in large part because these organisms are so difficult to access. The earliest discoveries of deep-sea microorganisms came not from direct sampling but from microorganisms associated with deep-sea animals: in the pioneering work of A. Aristides Yayanos in 1979, the first piezophilic microorganism was isolated from amphipods at a depth of 5,700 meters.[2] Because hydrostatic pressure is the most defining feature of the deep-sea environment, understanding how microorganisms adapt to it soon became an enduring focus of the field. Researchers such as Douglas Bartlett employed strain isolation, genetic manipulation, mutant libraries, and comparative genomics approaches to search for conserved and specialized "piezophilic genes."[3] These efforts identified hundreds of candidate genes,[4] but rather than converging on a conserved set, these genes varied considerably across piezophilic strains, revealing greater complexity than early models predicted. Understanding the high-pressure adaptation strategy thus became a major challenge that has engaged our field for decades.

Advanced deep-sea exploration technology and large-scale microbiome approaches have begun to characterize microbial life at hadal depths. Recent large-scale multi-omics datasets from the Mariana Trench Environmental and Ecological Research (MEER) project revealed that despite the sampling footprint representing just 10^{-8} of the global ocean by area, the microbial diversity was comparable to that reported for the upper ocean, with 89.4% of identified taxa not represented in existing reference databases.[5] Beyond diversity, recent metagenomic-guided metaproteomic analyses revealed that specific active populations, rather than bulk abundance, drive hadal microbial metabolism. Rather than relying on conserved piezophilic genes, hadal microorganisms adopt two opposing adaptation strategies: (1) species-dependent streamlined genomes for specialized functions, which enable efficient resource utilization under nutrient-limited conditions, versus (2) versatile metabolism with larger genomes for generalist lifestyles, which exploit diverse substrates available in heterogeneous hadal environments.[5] Indeed, against the general trend of declining microbial activity with increasing water depth, hadal environments sustain higher respiration and carbon turnover than the shallower abyssal plain, standing out as deep-sea hotspots of microbial activity.[6]

What sustains such rich microbial life in these environments where the macrofaunal communities that typically signal productive ecosystems are rare? Growing evidence from hadal research indicates that these microorganisms exhibit metabolic preferences markedly distinct from shallower marine environments. Based

on these collective findings, we propose the "hadal high-pressure activation" hypothesis: extreme pressures (>60 MPa) may trigger substantial reactive oxygen species (ROS) generation, which serve not merely as cellular stressors but as oxidative agents enabling breakdown of typically refractory organic compounds. This dual function of ROS is similar to that previously described in sunlit ocean regions[7]; however, unlike the upper ocean, where ROS production is dominated by photochemical processes and declines with water depth, hadal ROS may instead be elevated through pressure-enhanced electron leakage from membrane-bound respiration and metal-catalyzed Fenton-like reactions fueled by heavy metals accumulated in the funnel-shaped hadal topography (Figure 1A). Such processes drive metabolic expansion by rendering otherwise inaccessible carbon sources (e.g., aromatic polymers, halogenated compounds, and D-amino acids) and electron donors/acceptors such as redox-active heavy metals (e.g., Cu^{+}/Cu^{2+} and As^{3+}/As^{5+}) that remain inaccessible to microorganisms in typical marine environments.

This pressure-driven metabolic expansion may contribute to the high taxonomic novelty and diversity of hadal microorganisms, sustaining microbial communities of unexpected richness in the deepest ocean (Figure 1A). Here, we highlight a striking paradox: these environments' extreme physical conditions appear to preclude life, yet they harbor unexpectedly high microbial biomass, diversity, metabolic activity, and functional novelty. We term this phenomenon "invisible microbial oases." Our recent study revealed that hadal microbial activity is further modulated by local topography, where concave features function as microbial hotspots sustaining elevated biomass and metabolic activity relative to surrounding convex terrain. This spatial heterogeneity echoes the very nature of an oasis—thriving life flourishing in discrete patches amid otherwise barren surroundings.

Convergent adaptation strategies across extreme environments and life forms

Beyond hadal high pressure, a natural question emerges: when microorganisms face different extreme environmental stressors, do they employ similar adaptive strategies? In seeking high-pressure adaptation genes, researchers found that hundreds of genes involved in high-pressure adaptation also participated in responses to other extreme conditions, such as extreme temperatures, salinity and pH conditions, as well as drought, oligotrophic conditions, heavy metals, and radiation stresses.[8,9] Evidence for such a shared, stress-driven adaptive strategy emerged from the comparative analysis between microbial communities from the Mariana Trench and Mount Everest. Despite distinct physical characteristics—extreme pressure versus low pressure or darkness versus intense UV radiation—90% of the microbial adaptation strategies shared commonalities.[8] These commonalities reveal a convergent adaptation strategy across microbiomes from diverse extreme environments: regardless of the specific type of environmental stress, the common consequence for microorganisms is the induction of ROS, making antioxidant systems critically important for adaptation to extreme environments through both enzymatic defenses (e.g., catalase Kat and superoxide dismutase Sod) and non-enzymatic antioxidants and compatible solutes (e.g., organic acids, polyols, and polysaccharides).[9] Collectively, enhanced antioxidant systems appear to serve as a widespread adaptation strategy among microorganisms responding to diverse extreme environmental parameters (Figure 1B). These similar stress response strategies that evolve across different organisms and habitats represent what we term "convergent adaptation."

This convergent adaptation also extends to macroorganisms, including multicellular plants and animals. Plants demonstrate this convergence through sophisticated antioxidant networks with multiple environmental stresses—drought, salinity, temperature extremes, and high-light stress—consistently inducing ROS detoxification as a universal baseline for cross-stress adaptation, where ROS signaling acts as a central integrator linking stress perception with multilayered regulatory responses.[10] Animals employ similar strategies. The tardigrade, a microscopic animal capable of surviving desiccation, intense radiation exposure up to 1,000× human lethal doses, the vacuum of space, and temperature extremes, relies on a sophisticated combination of robust ROS antioxidant systems coupled with highly efficient DNA repair mechanisms.[11] Notably, even mammalian cancer cells, which face hypoxic and nutrient-limited microenvironments, demonstrate convergent antioxidant strategies that parallel those found in environmental extremophiles. Cancer cells develop enhanced ROS antioxidation systems that can serve dual roles: limiting oxidative stress and enabling metabolic adaptation required for survival under adverse microenvironmental conditions.[12] These collective findings demonstrate that both plants and animals at the cellular level employ ROS-centered adaptation strategies remarkably similar to those observed in microorganisms, revealing that distinct extreme environmental stressors ultimately manifest as ROS-mediated oxidative stress across diverse life forms, making antioxidant systems the fundamental basis for convergent adaptation strategies (Figure 1B).

Beyond adaptation: Environmental stressors as microbial activators

Building on the recognition that diverse extreme environmental stressors consistently trigger substantial ROS production across a broad range of life forms,[10–12] a critical question arises: do microorganisms and macroorganisms respond identically to ROS-induced oxidative stress? Although multicellular eukaryotes generally prioritize the defensive elimination of excessive ROS, microorganisms may possess unique advantages. Environmental stressor-induced ROS present two interconnected opportunities for microorganisms: ROS may enhance metabolic activity and promote evolutionary dynamics rather than merely causing cellular damage, which may explain the extraordinary microbial diversity observed in extreme environments largely uninhabitable to macroorganisms. We therefore term this process "activation" (Figure 1B).

First, the strong oxidative conditions created by environmental stressors render typically recalcitrant organic compounds accessible for microbial metabolism, effectively expanding the range of available carbon and energy sources. Specifically, ROS-mediated oxidation facilitates the breakdown of complex polymeric substrates through bond cleavage and ring-opening reactions, converting recalcitrant macromolecules into accessible monomeric units that

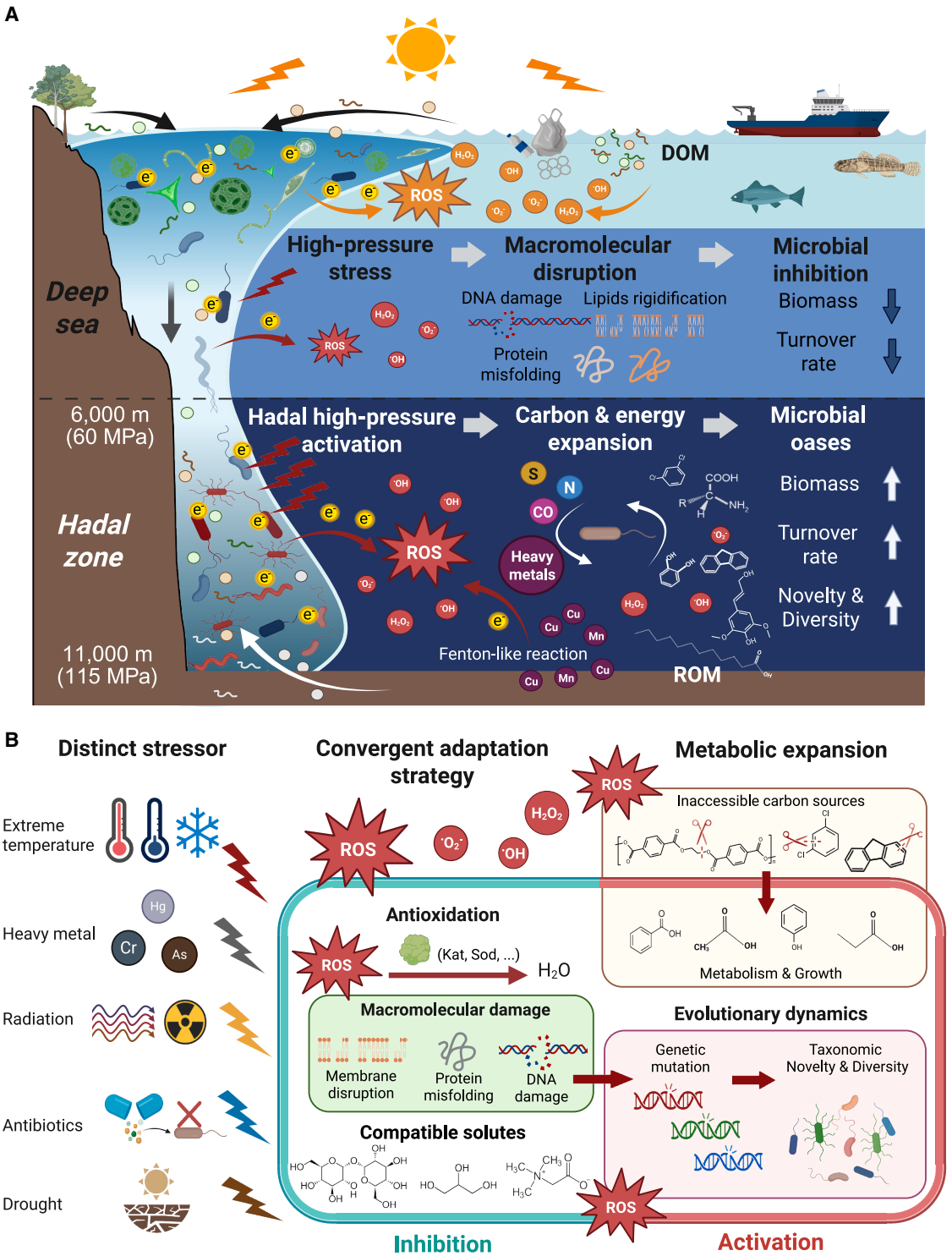

Figure 1. Invisible microbial oases in extreme environments

(A) Hadal high-pressure activation model showing how extreme pressure (>60 MPa) triggers ROS generation, enabling metabolic expansion and sustaining microbial oases in the deepest ocean. Abbreviations: ROS, reactive oxygen species; DOM, dissolved organic matter; ROM, refractory organic matter.

(B) Convergent adaptation strategies across diverse extreme environments, illustrating universal antioxidant responses and potential activation mechanisms through ROS-mediated processes.

Created in BioRender. Zhao, W. (2026) https://BioRender.com/0gmi65r

microorganisms can readily metabolize. Beyond this chemical breakdown, ROS exposure directly enhances the catalytic efficiency of oxidative enzymes themselves, with hydrogen peroxide demonstrably increasing the activity of lytic polysaccharide monooxygenases and other polymer-degrading enzymes, thereby accelerating the utilization of typically persistent organic matter.[13] We further propose that microbial utilization of these newly accessible substrates may in turn consume extracellular ROS, forming a positive feedback framework: extracellular ROS drives substrate expansion, while substrate utilization simultaneously yields energy for microbial growth and scavenges ROS.

Second, although ROS-induced DNA damage poses cellular challenges, it may simultaneously accelerate evolutionary innovation under the strong selective pressure of extreme environments. With their greater genomic flexibility and faster evolutionary rates, microorganisms are more tolerant of DNA damage compared to macroorganisms and can transform this oxidative damage into an evolutionary force. This DNA damage could be treated as a source of enhanced genetic variation; combined with intense environmental selection, this may drive the rapid emergence of novel metabolic capabilities and contribute to the taxonomic novelty observed in extreme environment microbiomes—such as the remarkably high proportion of undescribed taxa found in hadal environments.[5]

Thus, unlike the defensive responses typical of macroorganisms, ROS-inducing environmental stressors create unique activation opportunities for microorganisms through both metabolic expansion and evolutionary dynamics. Evidence from hadal zone research demonstrates this activation process, revealing that controlled ROS production serves not merely as a damaging agent but as a key driver stimulating new metabolic capacities and potentially promoting the emergence of new microorganism species. Some evidence suggests that this activation may extend beyond high pressure to other extreme stressors. For example, microorganisms from Mount Everest or under heavy metals and antibiotic stresses may also exemplify this activation process, triggering oxidative stress responses while simultaneously creating conditions that favor metabolic expansion and ROS-mediated mutagenesis.[8,14,15]

A global perspective on seeking invisible microbial oases

This fundamental difference in stress response strategies, from defensive survival mechanisms in macroorganisms to opportunistic exploitation of stress-derived resources in microorganisms, explains how invisible microbial oases can flourish precisely where visible life struggles to survive. Moreover, the limited presence of macroorganisms in these extreme environments concentrates available resources and energy within microbial communities themselves, potentially fostering the emergence of invisible microbial oases. This capacity to exploit extreme stressors may substantially expand microorganisms' ecological range and biogeochemical influence.

The recognition of environmental stressors as potential activators opens new avenues for understanding microorganisms living in extreme environments. For example, this understanding helps us rethink the antibiotic resistance generation problem. Sublethal exposure to antibiotics as a strong environmental stressor has been shown to trigger ROS-mediated mutagenesis that facilitates the emergence of multidrug resistance across antibiotics with distinct cellular targets.[15] Thus, the balance between inhibition and activation, and the conditions for disrupting and restoring this balance, is crucial for microbial communities and equally important for assessment of Earth's microbiome activity.

Earth harbors vast expanses of extreme environments where visible animals appear absent, yet the microbial communities within these seemingly barren landscapes may be considerably more diverse and active than current estimates suggest. Our preliminary attempts to extract nucleic acids and proteins from samples traditionally considered "biological deserts," such as deep Antarctic ice cores and desert sands, have suggested microbial biomass substantially higher than anticipated, though further validation is needed. This emerging perspective of stress-induced microbial activation reframes extreme environments not as biological deserts but as reservoirs of microbial diversity and metabolic capacity yet to be fully characterized. This framework enables us to seek these hidden microbial worlds across Earth's most challenging environments—from deep seafloors to ice sheet depths, arid deserts, atmospheric extremes, and beyond.

Realizing this potential requires overcoming significant technical challenges. A critical and challenging step in extreme microbiology research remains obtaining high-quality data from low-biomass, heterogeneous, and precious samples. Our recently developed DNA-protein co-extraction and co-analysis methodology for hadal samples enables simultaneous multi-omics data acquisition and analysis from a single sample, which may also be suitable for other extreme environments. Integration of large-scale data approaches with artificial intelligence holds particular promise for analyzing datasets annotated by environmental context, potentially circumventing the long-standing challenges inherent in high-pressure adaptation research.

When diverse extreme environment microbial datasets are analyzed together across habitats, the biological principles underlying convergent adaptation strategies may reveal important insights into life's origins and evolutionary history. Understanding whether common thresholds govern the transition from stress inhibition to activation and how oxidative stress shaped major evolutionary transitions—including the prokaryote-to-eukaryote transition and the emergence of cellular complexity—could illuminate Earth's biological history and inform our understanding of the conditions permissive for life in extreme environments.

ACKNOWLEDGMENTS

The authors would like to thank the pilots and crew members of submersible *Fendouzhe* and *R/V Tan Suo Yi Hao* for collecting samples and providing effective support for the MEER project. We also thank the entire science team of the TS21 expedition for their contributions. 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. 92351001), for his valuable suggestion in preparing MEER manuscripts. This work was financially supported by the NSFC (grant nos. 42330206, 32530002, 32570058, and 92451301), Hainan Provincial Natural Science Foundation (grant no. 426ZD1006). We also thank the PhD student Rui Huang, Shanshan Huang, Ziheng Wu, Guanqi Xiao, and Dr. Luhan Yang from Shanghai Jiao Tong University for the help with figure drawing and text editing of this manuscript. X.X. is a SANS Exploration Scholar.

DECLARATION OF INTERESTS

The authors declare no competing interests.

DECLARATION OF GENERATIVE AI AND AI-ASSISTED TECHNOLOGIES IN THE WRITING PROCESS

During the preparation of this work, the authors used Claude (Anthropic) in order to assist with language polishing and manuscript editing. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the publication.

REFERENCES

1. Corliss, J.B., Dymond, J., Gordon, L.I., Edmond, J.M., von Herzen, R.P., Ballard, R.D., Green, K., Williams, D., Bainbridge, A., Crane, K., and van Andel, T.H. (1979). Submarine thermal springs on the Galápagos Rift. Science *203*, 1073–1083. https://doi.org/10.1126/science.203.4385.1073.

2. Yayanos, A.A., Dietz, A.S., and Van Boxtel, R. (1979). Isolation of a deep-sea barophilic bacterium and some of its growth characteristics. Science *205*, 808–810. https://doi.org/10.1126/science.205.4408.808.

3. Bartlett, D., Wright, M., Yayanos, A.A., and Silverman, M. (1989). Isolation of a gene regulated by hydrostatic pressure in a deep-sea bacterium. Nature *342*, 572–574. https://doi.org/10.1038/342572a0.

4. Vezzi, A., Campanaro, S., D'Angelo, M., Simonato, F., Vitulo, N., Lauro, F.M., Cestaro, A., Malacrida, G., Simionati, B., Cannata, N., et al. (2005). Life at depth: *Photobacterium profundum* genome sequence and expression analysis. Science *307*, 1459–1461. https://doi.org/10.1126/science.1103341.

5. Xiao, X., Zhao, W., Song, Z., Qi, Q., Wang, B., Zhu, J., Lin, J., Wang, J., Hu, A., Huang, S., et al. (2025). Microbial ecosystems and ecological driving forces in the deepest ocean sediments. Cell *188*, 1363–1377.e9. https://doi.org/10.1016/j.cell.2024.12.036.

6. Glud, R.N., Wenzhöfer, F., Middelboe, M., Oguri, K., Turnewitsch, R., Canfield, D.E., and Kitazato, H. (2013). High rates of microbial carbon turnover in sediments in the deepest oceanic trench on Earth. Nat. Geosci. *6*, 284–288. https://doi.org/10.1038/ngeo1773.

7. Morris, J.J., Rose, A.L., and Lu, Z. (2022). Reactive oxygen species in the world ocean and their impacts on marine ecosystems. Redox Biol. *52*, 102285. https://doi.org/10.1016/j.redox.2022.102285.

8. Liu, Y., Zhang, Z., Ji, M., Hu, A., Wang, J., Jing, H., Liu, K., Xiao, X., and Zhao, W. (2022). Comparison of prokaryotes between Mount Everest and the Mariana Trench. Microbiome *10*, 215. https://doi.org/10.1186/s40168-022-01403-y.

9. Daly, M.J. (2009). A new perspective on radiation resistance based on *Deinococcus radiodurans*. Nat. Rev. Microbiol. *7*, 237–245. https://doi.org/10.1038/nrmicro2073.

10. Mittler, R., Zandalinas, S.I., Fichman, Y., and Van Breusegem, F. (2022). Reactive oxygen species signalling in plant stress responses. Nat. Rev. Mol. Cell Biol. *23*, 663–679. https://doi.org/10.1038/s41580-022-00499-2.

11. Li, L., Ge, Z., Liu, S., Zheng, K., Li, Y., Chen, K., Fu, Y., Lei, X., Cui, Z., Wang, Y., et al. (2024). Multi-omics landscape and molecular basis of radiation tolerance in a tardigrade. Science *386*, eadl0799. https://doi.org/10.1126/science.adl0799.

12. Schafer, Z.T., Grassian, A.R., Song, L., Jiang, Z., Gerhart-Hines, Z., Irie, H.Y., Gao, S., Puigserver, P., and Brugge, J.S. (2009). Antioxidant and oncogene rescue of metabolic defects caused by loss of matrix attachment. Nature *461*, 109–113. https://doi.org/10.1038/nature08268.

13. Bissaro, B., Røhr, Å.K., Müller, G., Chylenski, P., Skaugen, M., Forsberg, Z., Horn, S.J., Vaaje-Kolstad, G., and Eijsink, V.G.H. (2017). Oxidative cleavage of polysaccharides by monocopper enzymes depends on H_2O_2. Nat. Chem. Biol. *13*, 1123–1128. https://doi.org/10.1038/nchembio.2470.

14. Lemire, J.A., Harrison, J.J., and Turner, R.J. (2013). Antimicrobial activity of metals: mechanisms, molecular targets and applications. Nat. Rev. Microbiol. *11*, 371–384. https://doi.org/10.1038/nrmicro3028.

15. Kohanski, M.A., DePristo, M.A., and Collins, J.J. (2010). Sublethal antibiotic treatment leads to multidrug resistance via radical-induced mutagenesis. Mol. Cell *37*, 311–320. https://doi.org/10.1016/j.molcel.2010.01.003.