· Editorial · Advances in Polar Science
doi: 10.12429/j.advps.2025.1111 December 2025 Vol. 36 No. 4: 265-267

New horizons in the exploration of polar biodiversity, ecosystems, and genetic resources

JI Mukan[1*], LIAO Li[2*], Maggie C.Y. LAU VETTER[3], SHAO Changwei[4], ZHANG Xiying[5] & Ben LUISI[6]

[1] Center for Pan-third Pole Environment, Lanzhou University, Lanzhou 730000, China;
[2] Key Laboratory for Polar Science, Ministry of Natural Resources, Polar Research Institute of China, Shanghai 200136, China;
[3] Department of Extraterrestrial Ocean Systems, Institute of Deep-sea Science and Engineering, Chinese Academy of Sciences, Sanya 572000, China;
[4] Yellow Sea Fisheries Research Institute, Chinese Academy of Fishery Sciences, Qingdao 266071, China;
[5] Sate Key Laboratory of Microbial Technology, Shandong University, Qingdao 266237, China;
[6] Department of Biochemistry, University of Cambridge, Cambridge CB2 1GA, UK

Received 27 December 2025; accepted 29 December 2025; published online 30 December 2025

Citation: Ji M K, Liao L, Lau Vetter M C Y, et al. New horizons in the exploration of polar biodiversity, ecosystems, and genetic resources. Adv Polar Sci, 2025, 36(4): 265-267, doi: 10.12429/j.advps.2025.1111

The polar regions host one of the harshest and most unique ecosystems on Earth. These habitats, encompassing the Arctic and the Antarctic and from deep-marine sediments to glacial ice/ice sheets, represent one of the final frontiers of terrestrial biological exploration. Traditionally viewed as desolate, ice-covered lands, polar regions are now recognized as vibrant, complex, and highly sensitive ecosystems. In these “cryospheric oases”, polar microorganisms do more than just survive; they thrive through extraordinary taxonomic and genomic novelty that allows them to dominate their icy niches (Shu and Huang, 2022). The application of molecular methods has revealed highly diverse microbial communities of the polar region. Previous research across the Antarctic Dry Valleys, Antarctic Peninsula, and Arctic fjords demonstrates that microbial distribution is increasingly governed by micro-environmental abiotic factors (Malard and Pearce, 2018; Varliero et al., 2024), leading to a highly heterogeneous spatial distribution. Additionally, polar microorganisms have evolved sophisticated structural and functional adaptations to overcome the life-endangering influence of extreme cold, intense UV radiation, and severe desiccation, offering excellent opportunities to understand the limits of life on Earth and its potential existence elsewhere in the universe, such as on icy moons (Holmberg and Jørgensen, 2023). These properties also offer unparalleled opportunities for bioprospecting, providing potential for the next generation of bioactive natural products for medicine, agriculture, and industrial bioremediation.

The “polar amplification” of global warming is driving air and sea temperatures changes at rates significantly faster than the global average (Xie et al., 2023), leading to massive deglaciation and the thinning of sea ice. These changes significantly disrupt the polar biota, causing shifts in ecosystem connectivity and community structure that could trigger irreversible shift in microbial composition and functions (Ernakovich et al., 2022). Furthermore, the increasing human footprint—from scientific research to tourism—introduces the dual threat of non-indigenous species invasions and the mobilization of ancient or “intrinsic” antibiotic resistance genes (Hwengwere et al., 2022). We are currently in a race against time to document this biodiversity; otherwise, we risk losing endemic species

---

[*] Corresponding authors. E-mail: jimk@lzu.edu.cn (JI Mukan). E-mail: liaoli@pric.org.cn (LIAO Li)

and unique genetic resources before they are even cataloged. Moreover, the melting of the polar sea ice and ice sheets releases trapped organic matter, iron, and legacy contaminants into the Southern and Arctic Oceans, stimulating primary production in coastal and even lower latitude regions (Vancoppenolle et al., 2013). This hydrographic connectivity suggests that microbial shifts at polar regions have a regional and/or even global impact on marine nutrient composition. Thus, understanding the distribution and physiological limits of polar microorganisms is no longer just a fundamental scientific pursuit but a critical necessity for predicting global responses to climate change.

To address these challenges, this Special Issue serves as a bridge, connecting the hidden life of the Poles to the visible changes in our global climate trajectory, by integrating multi-omics techniques and state-of-the-art modeling methodologies. The eleven papers in this collection form a cohesive narrative that scales from microscopic foundations to the management of regional ecosystems. Consequently, new knowledge has been gained regarding the surprising baseline of antibiotic resistance in “pristine” environments, the specific influence of topographical slope on soil carbon cycling, and the discovery of novel chemical scaffolds that challenge our understanding of microbial metabolism in the cryosphere.

To understand microbial structure in the Antarctic, Chen et al. reviewed current knowledge on the “biodiversity oases” of Antarctic ice-free zones, highlighting how extreme environmental filters shape unique, endemic microbial consortia that drive critical biogeochemical cycles. This is echoed in the work of Wang et al., which explored soil in the vulnerable tundra ecosystems on a hillside near the southern coastline of the Antarctic Great Wall Station, finding that *Actinobacteria* and *Sediminibacterium* as key players in nutrient cycling. Additionally, they demonstrated that slope-driven nutrient transport, amplified by vegetated areas is the primary driver of bacterial community, providing insights into the impact of landscape changes on microbial community structure in Antarctica. Moving from land to sea, Zhou et al. surveyed the phytoplankton community in the Cosmonaut Sea (East Antarctica), identifying 99 phytoplankton species dominated by diatoms and dinoflagellates. They also demonstrated that nutrient distribution was identified as the primary environmental driver shaping the phytoplankton community, with silicate levels having a significant negative impact on overall phytoplankton abundance and the dominant species. These results provide critical baseline data on microbial diversity and community composition, while establishing relationships essential for predicting the consequence of landscape and climate shifts.

On the topic of bioprospecting for genetic and biotechnological resources, Wu et al. provided a comprehensive review on more than a hundred structurally diverse secondary metabolites from polar microorganisms, detailing their origins in polar microbes and their significant potential in pharmaceutical and agricultural applications. This work emphasizes the role of advanced genomics and biosynthetic gene cluster (BGC) mining in unlocking the next generation of polar-derived natural products. This is exemplified by Zhang et al., who successfully activated “silent” gene clusters in an Antarctic sponge-derived fungus, leading to the discovery of novel polyketide–amino acid conjugates bipolamide C and variotin A. This was achieved by overexpressing the pathway-specific transcriptional factor TwnD, demonstrating a robust molecular strategy for unearthing cryptic metabolic richness that remains “hidden” under standard laboratory conditions.

To address the risks posed by climate warming and anthropogenic impacts in the modern era, Lyu et al. examined the vulnerability of polar sediments to polycyclic aromatic hydrocarbon (PAH) pollution. Their work revealed how PAHs addition significantly reduced microbial diversity in polar sediments while selectively promoting the dominance of Proteobacteria, specifically *Pseudomonas* and *Acinetobacter* genera. The findings provide critical baseline data for assessing the impacts of anthropogenic pollution and identify indigenous strains with high potential for bioremediation in cold environments. Parallel to this, Yan et al. used metagenomics to reveal a highly diverse but low-abundance “resistome” and “virulome” in intertidal zones. This work highlighted the “intrinsic” nature of these genes as survival mechanisms in extreme environments while warning that increasing human activity and climate change could mobilize these potential public health risks.

To advance our understanding of microbial survival in polar extremes and the habitability of other icy planets, Vetter et al. take a broader planetary perspective, comparing polar and ocean environments on Earth with conditions on icy moons like Europa and Enceladus. Their discussion outlines key questions to be answered in order to effectively guide future missions to icy moons. Meanwhile, given that small RNAs (sRNAs) in polar microbes have been rarely investigated, Jiang et al. summarized their regulatory roles by examining sRNA-mediated adaptation. This review provided foundational background for understanding sophisticated regulatory networks in multi-tolerant extremophiles in polar and other extreme environments. Collectively, these two reviews bridge the gap between molecular-scale adaptation and planetary-scale habitability, providing a multi-level perspective on life in extreme environments. After acceptance, the two reviews will be published in a forthcoming issue.

In addition to microbial life, animals play important roles in polar ecosystems and hold secrets to unlocking broader principles of evolution and survival on a changing planet, which underscores the urgent need for new methodologies to study these macro-organisms. On this topic Li et al. systematically evaluated multiple machine learning algorithms for predicting Antarctic krill (*Euphausia superba*) distribution at varying spatial resolutions, revealing fundamental trade-offs between predictive accuracy and ecological interpretability. Meanwhile, Wei et al. analyzed olith elemental signatures across life history stages of *Pagothenia borchgrevinki*. This study revealed that *P. borchgrevinki* populations exhibit consistent spawning patterns across the Southern Ocean while displaying complex connectivity patterns driven by ontogenetic vertical migration and ocean current transport. These 2 studies represent the advanced methodology scope, providing the predictive tools necessary for resource management.

Given the complexity of the Antarctic climate system and its pivotal role in regulating global climate, several critical questions remain that will define the next decade of polar microbial studies. First, we must move beyond taxonomic snapshots to resolve the temporal dynamics of microbial resilience; specifically, how do microbial communities in permafrost, glacier/ice sheets, and polar oceans respond to the unprecedented rate of "polar amplification"? Understanding the threshold at which a community shifts is essential for predicting global carbon and nitrogen feedback loops. Second, we need to bridge the gap between metagenomic potential and phenotypic reality by novel techniques that active "silent genes", thereby unlocking the full biotechnological potential of cold-adapted enzymes and secondary metabolites. Furthermore, a new research frontier lies in microbial biogeography and connectivity. As glacier/ice sheet melting and human activity intensifies, we must track the microbial dispersal between previously isolated polar niches and lower latitudes. This includes investigating the role of migratory fauna and ocean currents as vectors for both beneficial symbionts and potentially pathogenic "ancient" genes. Ultimately, advanced machine learning and artificial intelligent algorithms must be applied at microbial level to create predictive "digital twins" of polar soil and marine ecosystems. Such tools will be indispensable for proactive conservation and for managing the delicate balance between bioprospecting opportunities and the preservation of Earth's final biological frontier.

References

Ernakovich J G, Barbato R A, Rich V I, et al. 2022. Microbiome assembly in thawing permafrost and its feedbacks to climate. Glob Change Biol, 28(17): 5007-5026, doi:10.1111/gcb.16231.

Holmberg S M, Jørgensen N O G. 2023. Insights into abundance, adaptation and activity of prokaryotes in Arctic and Antarctic environments. Polar Biol, 46(5): 381-396, doi:10.1007/s00300-023-03137-5.

Hwengwere K, Paramel Nair H, Hughes K A, et al. 2022. Antimicrobial resistance in Antarctica: is it still a pristine environment? Microbiome, 10(1): 71, doi:10.1186/s40168-022-01250-x.

Malard L A, Pearce D A. 2018. Microbial diversity and biogeography in Arctic soils. Environ Microbiol Rep, 10(6): 611-625, doi:10.1111/1758-2229.12680.

Shu W S, Huang L N. 2022. Microbial diversity in extreme environments. Nat Rev Microbiol, 20(4): 219-235, doi:10.1038/s41579-021-00648-y.

Vancoppenolle M, Meiners K M, Michel C, et al. 2013. Role of sea ice in global biogeochemical cycles: emerging views and challenges. Quat Sci Rev, 79: 207-230, doi:10.1016/j.quascirev.2013.04.011.

Varliero G, Lebre P H, Adams B, et al. 2024. Biogeographic survey of soil bacterial communities across Antarctica. Microbiome, 12(1): 9, doi:10.1186/s40168-023-01719-3.

Xie A H, Zhu J P, Wang S M, et al. 2023. Polar amplification in the Earth's three poles based on MODIS land surface temperatures. Remote Sens, 15(23): 5566, doi:10.3390/rs15235566.