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The unique microbial diversity of Antarctic ice-free areas: a comparative review

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Abstract Antarctic ice-free areas (<0.4% of the continent) represent Antarctic biodiversity oases, where microbial communities sustain terrestrial ecosystem functions. These habitats—encompassing mineral, ornithogenic soils, biological soil crusts, and hypolithic/endolithic niches—are shaped by environmental factors such as pH, organic C/N ratios, moisture, elevation, and trace element availability. The diversity of prokaryotes, eukaryotes, and viruses is lower than in other regions, yet the communities exhibit strong endemism, with site-specific uncultivated lineages. Microorganisms persist through cold and stress adaptations, performing organic carbon decomposition, phototrophy, and oxidation of trace gases to drive carbon and nitrogen cycling in various Antarctic soil habitats. Climate change and anthropogenic disturbances are shifting communities toward copiotrophic generalists, altering elementary cycling and feeding back to climate change. Culturation and genomic-based techniques reveal novel microbial taxa with broad biotechnological potentials on bioactive compounds and cryotolerant enzymes. In summary, this review offers a foundation for exploring Antarctic microbial biodiversity, ecosystem resilience, and the development of novel biotechnologies, while also highlighting the urgent need for effective monitoring and preservation strategies to mitigate the impacts of ongoing environmental changes on Antarctic soil ecosystems.

Keywords **Antarctic ice-free areas, stress adaptations, microbial diversity, climate change, conservation and biosecurity**

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1 Introduction

Antarctica, the Earth's fifth-largest continent, is located at the southernmost tip of the globe, covering an area of approximately 14 million km^2. It encircles the South Pole and is surrounded by the Southern Ocean. Around 98% of the continent is covered by a several-kilometer-thick ice sheet, making it the largest freshwater reservoir in the world and the continent with the highest average elevation. Compared with other continents, Antarctica remains virtually free of permanent human settlements, preserving a relatively pristine and undisturbed natural state. These unique and extreme conditions make Antarctica an ideal place for studying global climate change, life under extreme

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conditions, and the natural evolution of ecosystems.

The harsh environment of Antarctica imposes formidable challenges on life. Persistent low temperatures, aridity, intense solar radiation, polar day and night cycles, as well as sea ice and strong winds, greatly restrict the colonization and development of complex terrestrial life (Peck et al., 2006). The barren, saline, nutrient-poor soils intensify survival pressure, shaping sparse yet highly specialized and adapted communities (Magalhães et al., 2012). Despite the overall severity and limited habitats, less than 0.4% of Antarctica's surface (approximately 50,000–60,000 km^2) is exposed land, known as the ice-free areas (Vieira et al., 2010), which serve as the primary habitats and centers of terrestrial biodiversity (Patterson et al., 2025) (Figure 1).

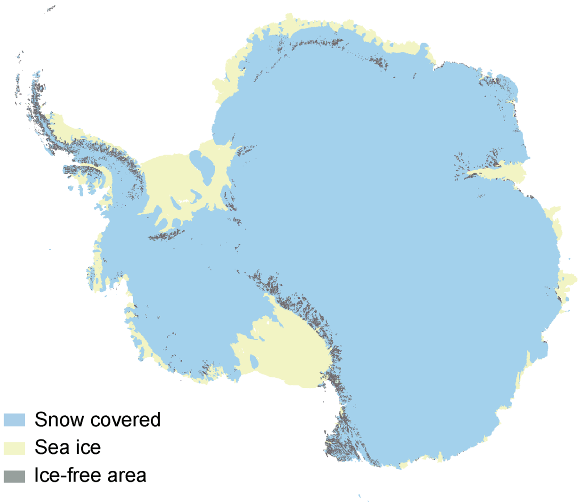

Figure 1 The location of ice free areas across the Antarctica, citation from Tóth et al. (2025).

Ice-free areas are mainly distributed along the Antarctic Peninsula and its coastal hills, the McMurdo Dry Valleys, exposed mountain peaks, and wind-eroded zones (Bockheim and McLeod, 2015; Ravindra et al., 2021; Schmid et al., 2021; Simas et al., 2015). Due to their exposed rock and soil substrates, seasonal liquid water, relatively stable temperatures, solar conditions, and limited nutrients, these regions provide relatively suitable habitats for life (Cowan et al., 2014). Thus, these regions are considered important refugia and biodiversity oases for Antarctic terrestrial organisms. The vast majority of the continent's terrestrial life is concentrated in these areas, with microorganisms dominating, alongside mosses, lichens, and a small number of highly adaptable invertebrates (Zhang M M et al., 2025), making ice-free areas crucial carriers of Antarctic biodiversity and key objects of ecological research.

The fragile Antarctic ecosystem is threatened by global climate change and increasing anthropogenic activities, which substantially impact microbial diversity and the ecological roles these organisms fulfill. Consequently, understanding how these pressures reshape soil microbial communities and the biogeochemical processes they regulate is both urgent and essential. The aim of this review is to synthesize current knowledge on Antarctic soil microorganisms—in terms of their diversity, survival strategies, metabolic functions, responses to climate change, and potential industrial implications—and to identify key knowledge gaps in Antarctic microbial research.

2 The physical and chemical landscape of Antarctic Ice-free areas

2.1 Geological and climatic features

The overall low temperature of Antarctica underlies all its climatic characteristics, with annual average temperatures in inland regions dropping as low as −50 ℃ or even lower. The persistent cold results in extremely low atmospheric moisture content, making snowfall and ice crystals the primary precipitation. The annual average precipitation is only about 165 mm (Oshima and Yamazaki, 2006), mostly concentrated in the peninsula and coastal areas; in inland regions, it typically falls below 50 mm (Bromwich, 1988). Under the erosion of katabatic winds, the evaporation and sublimation of surface moisture are accelerated, further intensifying the dryness (Devi and Maheskumar, 2022). The continuous low temperatures and limited precipitation restrict chemical weathering and organic matter accumulation, leading to the relatively poor soil conditions of the Antarctic oases. Together with freeze-thaw cycles and aeolian deposition, this process enhances physical weathering and leads to soils dominated by fractured bedrock and mineral particles.

However, the climatic conditions of the ice-free areas are significantly different from the ice sheet zones. Due to the low albedo of exposed soils, these regions absorb substantial solar radiation during the austral summer, causing surface temperatures to rise above freezing and enabling the formation of seasonal meltwater (Wilhelm and Bockheim, 2017). This meltwater gives rise to periglacial lakes, glacial streams, and moist zones that are essential for microbial metabolism and dispersal (Salvatore et al., 2023). Meanwhile, ice-free areas often lie within katabatic winds, where the surface soils are more prone to the accumulation of aeolian deposits and salt crystals, providing microorganisms with microhabitats of different scales, such as bare rock fissures, weathered material, salt crusts, and sand grains (Diaz et al., 2020).

The chemically weak and physically dominant weathering processes result in organic matter-poor soils in the ice-free areas. However, various trace elements, including iron (Fe), manganese (Mn), copper (Cu), zinc (Zn), and nickel (Ni), originating from weathering of parent rock and external deposition, are present (Diaz et al., 2020). Although these elements are not abundant, they are essential for microbial enzyme activity and metabolic processes, widely participating in the electron transport chain, regulation of enzyme activity, and the construction of antioxidant systems (Zilhão et al., 2025). This variation in the abundance and bioavailability of trace elements profoundly influences the microbial community distribution and adaptation strategies.

2.2 Soil environments

The Antarctic Peninsula, particularly Cierva Point and King George Island, contains smaller, isolated ice-free areas characterised by diverse terrestrial biodiversity and complex geomorphological features (Schmid et al., 2018). Other large areas of ice-free areas are identified in the McMurdo Dry Valleys, Schirmacher Oasis, and Larsemann Hills in East Antarctica (Ravindra et al., 2021). These regions support unique ecosystems, with the Antarctic Peninsula's ice-free areas being particularly rich in biodiversity, including diverse fungal communities and significant bird populations (Zhang et al., 2022).

The Antarctic dry desert mineral soils are low in carbon (<2%) and nitrogen (<0.1%) (Niederberger et al., 2008; Pan et al., 2013; Siciliano et al., 2014; Wood et al., 2008) (Figure 2a). Soil moisture levels range between 0.2% to 5.3%, with levels notably decreasing as the distance from the coastline or a lake increases (Aislabie et al., 2008; De Maayer et al., 2014; Delille, 2000; Lee et al., 2012). However, in contrast to inland Dry Valleys, the water content in islands and coastal soils can be much higher (up to >10.5%), and is attributed to melting glaciers and seasonal snow as water sources (Zdanowski and Węgleński, 2001).

In comparison to desert soils, ornithogenic soils are formed as a result of bird activities, especially penguin rookery (Aislabie et al., 2009; Speir and Cowling, 1984). Consequently, ornithogenic soils are acidic and high in carbon, nitrogen, and phosphorus, at least 10–1000 fold higher than that of the desert soils (Aislabie et al., 2008; 2009) (Figure 2b). As a result, ornithogenic soils contain distinctly different bacterial communities than those present in Antarctic desert soils, with an extremely high abundance of Bacillota (formerly Firmicutes) or Bacteroidota (formerly Bacteroidetes) reported (up to 83.5% Bacillota was identified from Cape Hallett) (Aislabie et al., 2008; Fernández et al., 2024; Teixeira et al., 2010). Furthermore, the total abundance of bacteria measured in small subunit ribosomal RNA (SSU RNA) copy number (10^{12} copies of SSU RNA gene per g) (Ma et al., 2013) is several magnitudes higher than Antarctic desert soils (ranged between 10^7–10^9 SSU RNA gene copies per g of dry soil) (Ji et al., 2016; Kudinova et al., 2015; Magalhães et al., 2014; Nichols et al., 1999).

On the surface of soils, biological soil crusts (BSCs) formed by mosses, lichens, and mineral soils provide highly active environments for microorganisms, yet differ markedly in their physical structure, microbial communities, and ecological functions (Figure 2c). Moss-associated habitats enhance capillary water retention capacity through their porous structure and retain water via specialized cells, such as hyaline cells by the moss, thereby creating locally moist microenvironments (Park et al., 2018). The internal porosity also traps air, buffering against temperature fluctuations and stabilising the microclimate (Xiao and Bowker, 2020). In addition, the thin-layered structure and dark surfaces of moss crusts absorb more solar radiation, resulting in surface temperatures about 9 ℃ higher than those of surrounding soils (Perera-Castro et al., 2020). These features collectively create favourable conditions for photoautotrophic microorganisms (e.g., *Nostoc*) and nitrogen-fixing bacteria (Zhang M M et al., 2025). In contrast, lichen-associated habitats retain moisture by trapping condensed water within internal micropores, and they reduce surface water loss through hard crusts formed by fungal hyphae and secondary metabolites such as lichen acids (Baptista et al., 2024). This compact structure, together with secondary metabolites like UV-screening pigments, helps maintain stable temperature and humidity within the microenvironment. Moreover, the lichen matrix is rich in recalcitrant polysaccharides (e.g., lichenin and cellulose), which selectively support drought-tolerant and oligotrophic microorganisms such as *Acidipila* (Acidobacteriota, formerly Acidobacteria) and *Blastocatella* (Actinomycetota, formerly Actinobacteria) (Armstrong, 2017).

In addition, well-developed microbial communities have been identified in various lithic environments, including rock fissures, the undersides of translucent rocks, and subsurface crevices within coarse crystalline rock types (Cary et al., 2010) (Figure 2d). For example, cryptoendolithic microbial consortia are found within fine-grained, translucent rocks like Beacon Sandstones, a few millimeters below the rock surface (Brinkmann et al., 2007). The internal pores provide space for microbial colonization; the translucent rock allows for the growth of autotrophic microbes while also filtering some light; and living within the rock helps protect them from wind erosion, sand abrasion, and surface temperature fluctuations (Cary et al., 2010). Hypolithic communities exist on the bottom and edges of surface translucent rocks (Cary et al., 2010). These translucent rocks (such as quartz and marble) do not provide a temperature buffer but significantly increase local humidity. At the same time, these rocks allow for the survival of photoautotrophs like mosses and Cyanobacteriota (formerly cyanobacteria) and the heterotrophic microbial communities that depend on them, providing local hotspots of productivity (Smith et al., 2000). Chasmolithic communities are common on the surface of Dry Valley regions, such as weathered granite flakes.

Climate change is expected to significantly alter the extent and configuration of ice-free areas. Under high-emission scenarios, these areas could expand by over 17,000 km^2 by the end of the century, particularly in the

Antarctic Peninsula (Lee et al., 2017). This expansion could lead to increased habitat connectivity, potentially affecting biodiversity through biotic homogenization and the spread of invasive species. Additionally, changes in temperature and precipitation patterns have already been observed, affecting lacustrine systems and permafrost stability in regions like the Antarctic Peninsula (Vieira et al., 2024). Understanding and monitoring the impact of climate change on soil microbial communities is crucial for preserving Antarctica's unique environments and biodiversity.

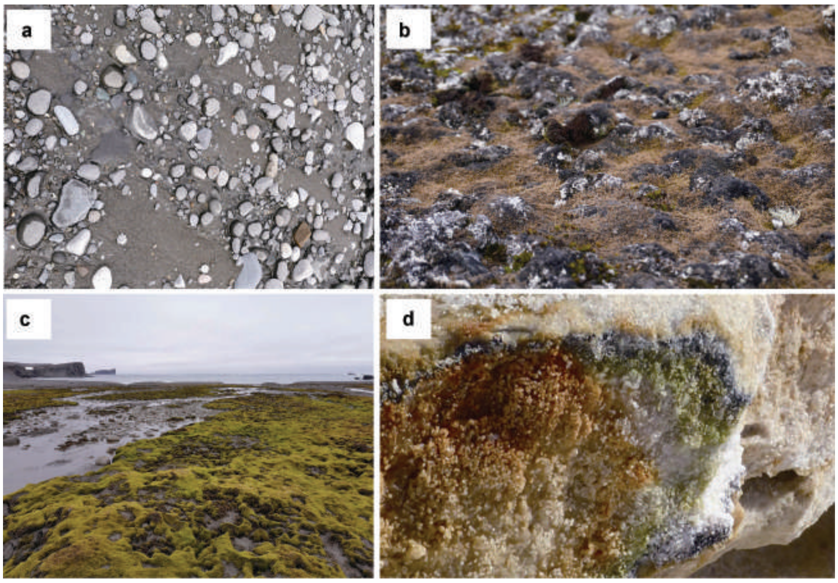

Figure 2 Main types of soil/rock habitats where bacteria colonize in the ice-free area of Antarctica. **a**, mineral soils; **b**, ornithogenic soils; **c**, microbial mat; **d**, sandstone-associated endolithic communities. Photos in panels **a**–**c** were taken by Li Liao during the 36th Chinese National Antarctic Research Expedition; panel **d** is reproduced from Biagioli et al. (2023).

Although previous studies provide comprehensive descriptions of the geological and physicochemical heterogeneity across Antarctic ice-free zones, much uncertainty remains regarding how micro-scale variability drives microbial habitat partitioning. Furthermore, previous studies largely depend on isolated observations, with limited integration of temporal data that captures seasonal changes in soil properties. Future studies should adopt long-term, spatially resolved monitoring to better constrain the interplay between physicochemical gradients and microbial functional distributions, especially under ongoing climate-induced landscape shifts.

3 Microbial diversity in Antarctic ice-free areas

Microorganisms living in terrestrial Antarctica are subjected to very low temperatures, limited carbon, nitrogen, and water availability, strong UV radiation, and frequent freeze-thaw cycles. Despite this, active bacterial growth has been reported throughout the continent. Ever since the first bacteria were isolated from Antarctic soils (McLean, 1918), a combination of cultivation, amplicon sequencing, and metagenome sequencing approaches has been used to reveal the microbial diversity in the ice-free area of the Antarctic. Diverse prokaryotes (bacteria and archaea), microeukaryotes (fungi, algae, and protists), and viruses have been identified. These microorganisms play crucial roles in biogeochemical cycles and exhibit unique metabolic capabilities that are of significant ecological and biotechnological interest.

3.1 Prokaryotic communities

Microbial diversity in Antarctic soils is lower than that in temperate regions. In a meta-analysis that compared the soil prokaryotic diversity across the globe, the results showed that Shannon and phylogenetic diversity indices of the Antarctic are only 34% and 58% of those observed in non-polar soils, respectively (Ji et al., 2022). The low diversity is likely due to the extremely low temperatures and limited availability of carbon and nitrogen. The majority of Antarctica's terrestrial biodiversity is concentrated in the relatively small and fragmented ice-free areas (Shaw et al., 2014), including South Victoria Land (Ross Sea and McMurdo Dry Valley regions) and the South Shetland Islands regions. The broad taxonomy of the bacteria in Antarctic soils is similar to that identified in global soils, including Pseudomonadota (formerly Proteobacteria), Actinobacteriota, Bacteroidota, Cyanobacteriota/Oxyphotobacteria, Chloroflexota (formerly Chloroflexi), Acidobacteriota, Verrucomicrobiota (formerly Verrucomicrobia), Gemmatimonadota (formerly Gemmatimonadetes), Bacillota, and Planctomycetota (formerly Planctomycetes) (Fernández et al., 2024; Zhang et al., 2024). But at the finer taxonomic levels, a wide range of previously unidentified genera have been reported, highlighting the unique microbial diversity in these soils (Cui et al., 2023). Ammonia-oxidizing archaea have been identified in some Antarctic soils, but are present at a much lower abundance relative to bacteria. For instance, archaeal abundance was negligible in Livingston Island, with Woesearchaeales, Nitrosarchaeum, *Candidatus* Nitrosopumilus, and Marine Group II being most frequently identified (Doytchinov et al., 2024). Comparatively, Thaumarchaeota were relatively abundant in Larsemann Hills (Alekseev et al., 2020). Thus, Antarctic soils share broad bacterial phyla with global soils, while their overall lower diversity and the presence of many novel, site-specific genera highlight the distinctive and localized nature of terrestrial microbial communities across Antarctica.

Significant variations in microbial composition have been reported in both local and regional levels (Figure 3). Hypolithic (under translucent rocks) and endolithic (inside rocks) niches host cryptic communities of Cyanobacteriota and other taxa critical to oligotrophic mineral soils in hyper-arid Dry Valleys; these assemblages can differ sharply from adjacent surface soils (Cowan et al., 2011; Pushkareva et al., 2024). Metagenome analysis from 109 endolithic microbiomes revealed thousands of metagenome-assembled genomes, which captured many candidate bacterial species, suggesting considerable uncharacterized diversity in rock-hosted ecosystems (Coleine et al., 2024). Glacier forefields harbor pioneer microbial communities with low overlap between poles: only 8% of amplicon sequence variants were shared between Icelandic and Antarctic forefields, indicating habitat specialists and potential dispersal limits (Del Moral et al., 2021).

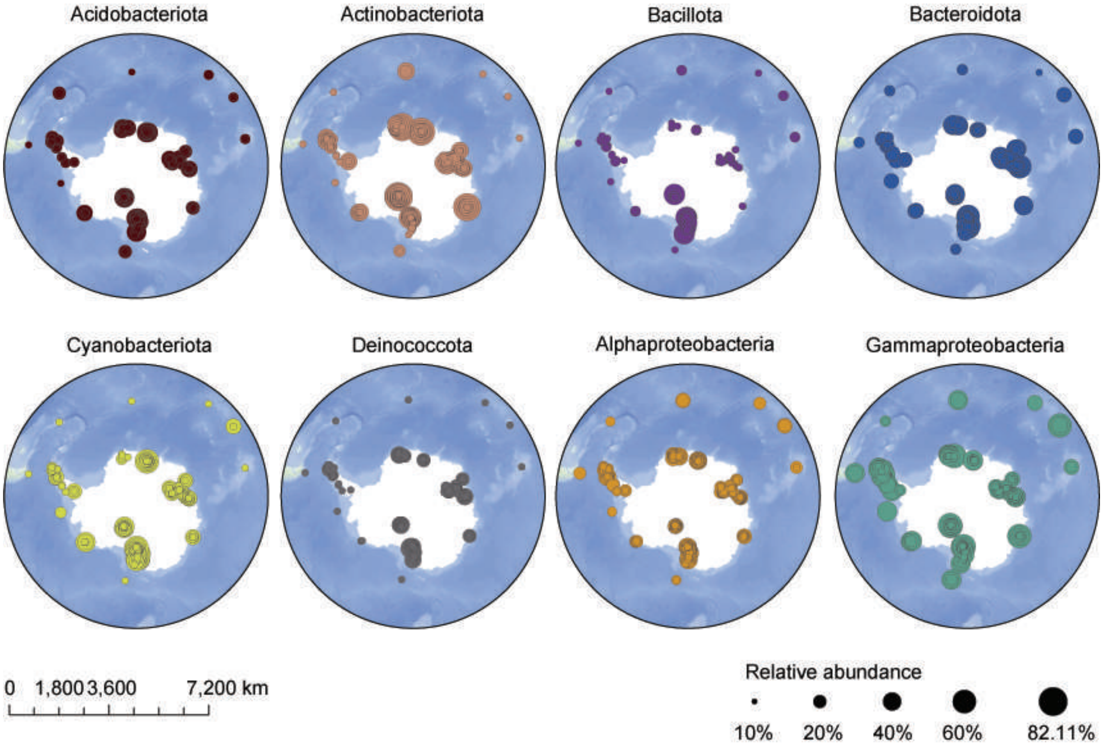

Figure 3 Relative abundances of dominant bacterial phyla and classes across Antarctica. Data are downloaded from Varliero et al. (2024).

Meta-analysis revealed the overall microbial biogeography across the Antarctic. A study of 35 locations reported that Antarctic soil bacterial communities tended to include a narrow range of species compared with those identified globally, with taxonomic distributions significantly correlated to soil parameters (Chong et al., 2012a). Furthermore, Varliero et al. (2024) compiled a large dataset of 1,164 samples, showing that 19% of bacterial community variability was explained by the Antarctic Conservation Biogeographic Regions, but considerable overlap in community structure exists within these regions. Thus, local environmental selection played a more important role than geographical dispersal in determining microbial communities (Alekseev et al., 2020; Doytchinov et al., 2024; Pushkareva et al., 2024; Zhang Y H et al., 2025).

Multiple studies identified a set of environmental factors that shape Antarctic soil prokaryotic communities. Soil pH repeatedly emerges as a primary predictor of soil bacterial community, including Rothera Point and Keller Peninsula soils (Chong et al., 2012b; Roesch et al., 2012). Meanwhile, organic carbon and nitrogen are also key environmental drivers of bacterial community composition in Larsemann Hills (Alekseev et al., 2020). Similarly, organic carbon and pH were key factors differentiating terrestrial (pristine and ornithogenic soils) from marine habitats (intertidal and marine sediments) in the Fildes Region (maritime Antarctica) (Zhang Y H et al., 2025). Additionally, elevation, which is a proxy for colder temperatures and lower moisture, was the dominant factor explaining prokaryotic community structure across Shackleton Glacier forefield soils and Robinson Ridge soils. Specifically, soils with higher elevations exhibit lower diversity, slower potential growth, and weaker trace gas metabolism (Dragone et al., 2022), enriching environmentally resistant phyla like Actinobacteriota and Ascomycota (Di Menna, 1966).

3.2 Eukaryotic microbes

Eukaryotic communities, spanning green algae, diatoms, protists (e.g., Cercozoa and Ciliophora), and fungi, are a vital component of soil biodiversity and biogeochemical cycling. Their composition varies across microhabitats such as biological soil crusts, fellfields, hypolithic niches, and rhizospheres of mosses, lichens, and the few native vascular plants (Borchhardt et al., 2017; Khan et al., 2011; Pushkareva et al., 2024; Rodríguez et al., 2025).

Algae in Antarctic soils play a crucial role in the ecosystem, acting as primary producers synthesizing organic compounds from carbon dioxide and water, which supports other microbial communities (Hirose et al., 2020). In biological soil crusts, algae interact with lichens and other microorganisms, enhancing soil fertility (Borchhardt et al., 2017) and contributing to soil stabilization by forming aggregates that reduce wind erosion (Rybalka et al., 2023). Multiple morphological and molecular surveys show that Antarctic soils support diverse eukaryotic assemblages despite environmental stringency. In Ardley and King George Islands, 106 algal taxa were identified in BSCs, spanning Chlorophyta (41 taxa), Streptophyta (9 taxa), and Heterokontophyta (56 taxa), which is clear evidence that BSCs are hotspots of eukaryotic phototrophs (Borchhardt et al., 2017). The results of this study are consistent with an amplicon-sequencing-based study on surface soils of the Fildes Peninsula (King George Island). Specifically, 830 operational taxonomic units (OTUs) of algae across 58 genera were identified, highlighting Trebouxiophyceae as the predominant green algal class (Rybalka et al., 2023). Notably, 86.1% of algal OTUs in that study could not be identified to species, with Ulvophyceae and Xanthophyceae showing the greatest unknown diversity. Thus, Antarctic soils host a surprisingly rich diversity of algal species, which are adapted to survive and thrive in such environments, despite the harsh environmental conditions.

Algae in Antarctica have developed various adaptations to cope with extreme conditions, such as high UV radiation and desiccation. For instance, pioneer soil algae exhibit morphological changes in response to environmental changes (Wynn-Williams, 1996b). The presence of photosynthetic pigments in algae serves as a proxy for understanding their community structure and function, reflecting adaptations to local microclimatic conditions (Colacevich et al., 2009). Algal communities in mineral soils show higher diversity and adaptability compared to those in ornithogenic soils, suggesting a greater resilience to environmental changes (González Garraza et al., 2011). The distribution of soil algae in Antarctica is influenced by both biotic and abiotic factors, including soil pH, moisture, and nutrient availability (Colacevich et al., 2009), leading to distinct algal community compositions across the Antarctic (Hirose et al., 2020).

Fungi in Antarctic soils represent a diverse and complex community that is primarily saprophytic, contributing to the decomposition of organic matter and nutrient cycling in these nutrient-poor environments (Gonçalves et al., 2023, 2024). Nevertheless, some fungi exhibit pathogenic and symbiotic relationships, indicating a range of ecological interactions within the soil microbial community (Gonçalves et al., 2023). Ascomycota are the most dominant phylum, followed by Basidiomycota and Mortierellomycota (Durán et al., 2019; Gonçalves et al., 2023), while Chytridiomycota and Rozellomycota are typically considered rare phyla (Gonçalves et al., 2023; Rosa et al., 2020). Fungal communities vary significantly across different soil types, such as ornithogenically influenced soils, glacial soils, and ultraoligotrophic soils (Gonçalves et al., 2024). Such variations are influenced by soil chemical properties, including the carbon and nitrogen content (Dos Santos et al., 2020; Durán et al., 2019).

3.3 Viruses in the Antarctic soils

Antarctic soils exhibit a high diversity of viruses, including tailed bacteriophages (Siphoviridae, Myoviridae, and Podoviridae), algal-infecting phycodnaviruses, and virophages (Adriaenssens et al., 2017; Zablocki et al., 2014a). Novel viral sequences and unusual gene arrangements have been identified, indicating a significant potential for discovering new viral species (Zablocki et al., 2014a) and reflecting potential independent evolutionary trajectories (Rastrojo and Alcamí, 2018). These viruses play a crucial role in controlling microbial community dynamics by infecting and lysing host cells, thereby influencing nutrient cycling and energy flow in the ecosystem (Rastrojo and Alcamí, 2018; Robinson et al., 2024). The presence of auxiliary metabolic genes in viral genomes suggests that viruses may augment host metabolic processes, such as phosphorus acquisition and sulfur oxidation, thereby impacting biogeochemical cycles (Robinson et al., 2024).

Multiple virus surveys revealed abundant tailed bacteriophages in Antarctic soils, exhibited heterogeneity in community composition even at small spatial scales (Adriaenssens et al., 2017). Moreover, comparisons with global metaviromes showed that Antarctic viruses clustered by habitat type rather than geographical distance, supporting a niche-structured viral biogeography (Zablocki et al., 2014b). In soil samples from the Mackay Glacier forefields, tailed phages Siphoviridae and Myoviridae displayed inverse correlation in their relative incidences, suggesting competitive or host-partitioning dynamics (Adriaenssens et al., 2017). In comparison, Phycodnaviridae and Mimiviridae co-occurred rather than excluding one another. This co-occurrence implies complementary ecological roles or shared host ranges for these large eukaryotic viruses, rather than direct competitive exclusion. Compared with soil, hypolithic communities exhibited higher viral diversity, correlating with bacterial community diversity (Zablocki et al., 2014a). The viruses primarily infect Actinomycetota, dominated by Siphoviridae, Myoviridae, and Podoviridae (Zablocki et al., 2014a). Additionally, Cyanophages were relatively rare and phylogenetically distant from known cyanophages, despite the cyanobacterial dominance in hypoliths.

Bacteria are the dominant hosts of Antarctic soil viruses. In hyperarid deserts, *Mycobacterium* phages are the most prevalent, suggesting active interactions with mycobacterial communities (Zablocki et al., 2014a). However, host preferences inferred from McMurdo Dry Valleys support nonrandom host targeting among assembled viruses and underscore tight coupling between viral and bacterial community structures (Robinson et al., 2024). Together, these observations reinforce that Antarctic viruses are not only diverse but also closely patterned by the distribution and dynamics of bacterial hosts in each niche. Eukaryote-infecting dsDNA viruses, notably Phycodnaviridae and Mimiviridae, are also common, with the Sputnik clade being identified (Zablocki et al., 2014a). A virus survey across terrestrial niches reported viruses of algae and amoebae alongside tailed phages, aligning with the presence of microalgae and protists in these environments (Zablocki et al., 2014b).

The accumulated evidence highlights the remarkable microbial endemism and adaptation across Antarctic soils. However, a clear functional link between community structure and biogeochemical performance remains elusive. Many studies rely on 16S rRNA or ITS amplicon approaches, while metagenomic data remain limited, which constrains our ability to infer the metabolic functions or evolutionary processes underlying community differentiation. In the future, integrating more comprehensive metagenomics with cultivation techniques and isotopic probing could provide a mechanistic understanding of how Antarctic microbial biogeography translates into ecological function and ecosystem resilience.

4 Microbial survival mechanisms and metabolic processes in Antarctica

4.1 Metabolic adaptations

Microorganisms in Antarctica have developed a range of survival mechanisms to thrive in the environments characterised by low temperatures, high radiation, and nutrient scarcity (Figure 4). These adaptations include metabolic versatility, structural modifications, and symbiotic relationships, which enable them to persist in such inhospitable conditions. Across Antarctic metagenomes from soils, common cold-responsive stress genes that have been identified include those encoding fatty acid desaturases and cryo/osmoprotectant synthesis (Bendia et al., 2021; Giovannini et al., 2024; Williams et al., 2024). The former support membrane fluidity; for example *Chryseobacterium frigidisoli* can adjust its cell membrane fatty acid composition in response to temperature and pH changes, enhancing its ability to withstand environmental stress (Bajerski et al., 2017). Cryo/osmoprotectant includes trehalose, glutamate, glycine, choline, and betaine that function as compatible solutes, accumulating without perturbing intracellular metabolism to preserve enzyme activity and membrane integrity. Psychrophilic organisms, such as *Glaciozyma antarctica*, produce antifreeze proteins that prevent ice formation and maintain cellular integrity in persistently cold habitats (Firdaus-Raih et al., 2018). Furthermore, exopolysaccharide biosynthesis genes are prevalent in several soil metagenomes that can help cells cope with freeze–thaw cycles and water stress by stabilizing extracellular matrices and retaining moisture (Koo et al., 2018). Several molecular adaptation strategies have been identified in Antarctic bacteria against UV stress. Functional gene profiling identified genes involved in carotenoid biosynthesis (Zhang M M et al., 2025). These pigments can quench reactive oxygen species generated by UV exposure, thereby reducing oxidative stress. Furthermore, genes associated with DNA damage repair (e.g., *lexA* and *uvrB*) are detected in higher abundance in some pristine and ornithogenic soils, reflecting adaptation to UV exposure (Zhang Y H et al., 2025).

A wide range of Antarctic microorganisms can produce cold-active extracellular enzymes that function at low temperatures, facilitating nutrient acquisition from complex substrates (Lamilla et al., 2017). Additionally, they have evolved a trace-gas chemoautotrophic lifestyle to adapt to the primitive and poorly developed Antarctic soils (Ji et al., 2017, 2021). Actinomycetota, Chloroflexota, *Candidatus* Dormibacterota, and *Candidatus* Eremiobacterota utilize atmospheric hydrogen (H_2) and carbon monoxide (CO) as energy sources. They oxidize these gases to fix atmospheric CO_2 via the Calvin-Benson-Bassham cycle, allowing them to survive in nutrient-poor soils (Montgomery et al., 2021). Such a carbon fixation pathway, which is later termed “atmospheric chemosynthesis”, provides energy and metabolic water necessary for survival in the hyperarid McMurdo Dry Valleys (Bendia et al., 2021). While trace-gas chemoautotrophy appears to be a dominant survival strategy for many prokaryotes in the oligotrophic soils (Yung et al., 2014), the carbon source of eukaryotes in these settings likely relies on phototrophy (for algae) and efficient use of recalcitrant substrates (for fungi) (Borchhardt et al., 2017; Khan et al., 2011). Such diverse

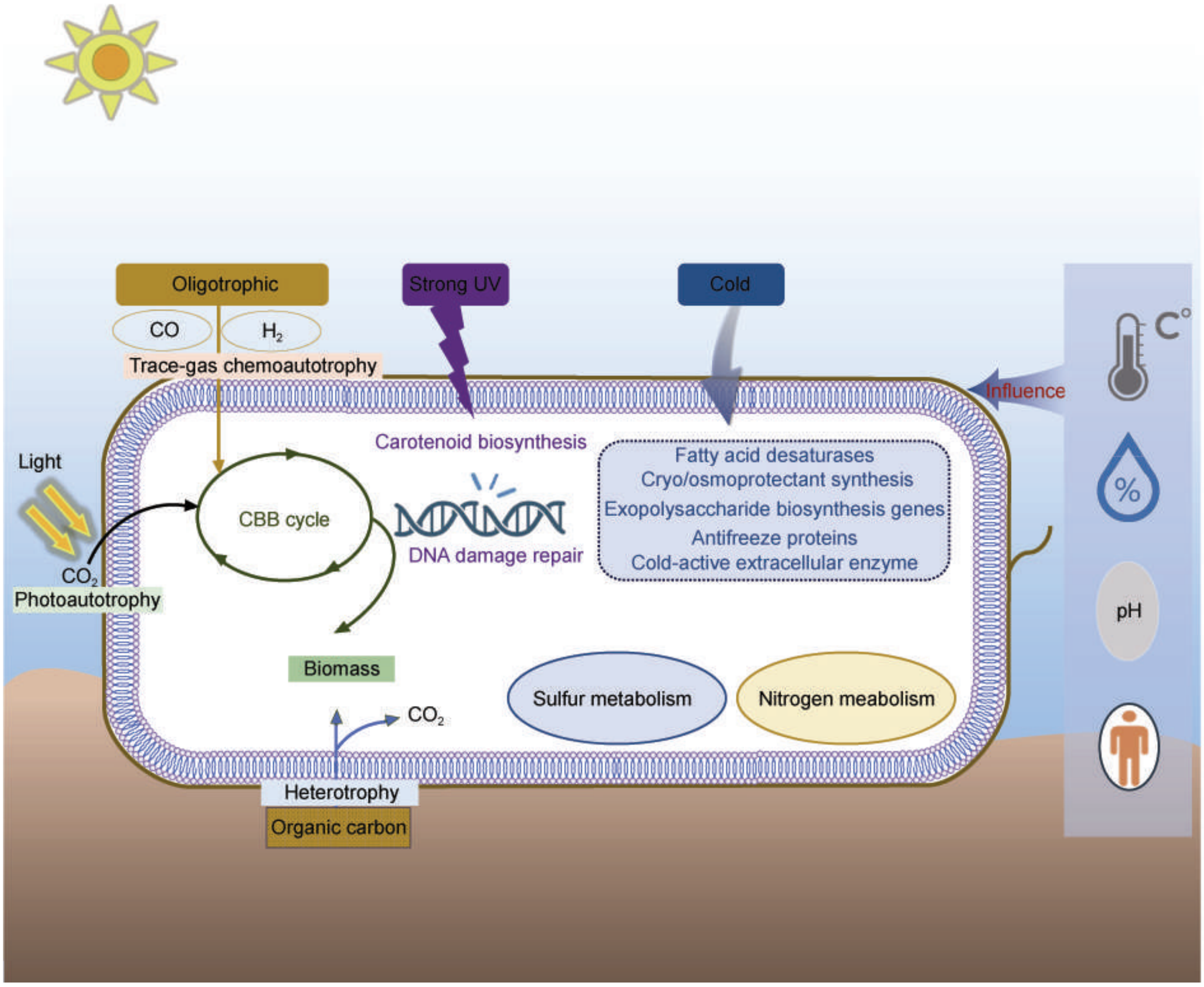

Figure 4 Schemetic representation of environmental adaptation strategies in Antarctic bacteria and their responses to environmental changes. CBB cycle, Calvin-Benson-Bassham cycle.

metabolic adaptations that sustain life in one of Earth's most extreme environments potentially shape our understanding of carbon flux in oligotrophic systems, and give hints to life finding in extraterrestrial environments.

In addition to cellular adaptation to adverse environmental conditions, microhabitat partitioning is also a strategy to support microbial survival. Soil crusts and hypolithic niches can effectively buffer temperature fluctuations and reduce desiccation exposure (Borchhardt et al., 2017; Khan et al., 2011). Hypolithic habitats underneath translucent quartz provide shelter from environmental extremes, including UV radiation and desiccation, and support Cyanobacteriota-rich communities in hyper-arid Dry Valleys (Cowan et al., 2011; Hidalgo-Arias et al., 2023). A draft genome of a hypolith *Sphingomonas* isolate from Dry Valleys indicated genetic capacity to adapt to cold and arid conditions, with metabolic versatility and multidrug resistance offering a competitive advantage among hypolith colonists (Gunnigle et al., 2015). Subsurface horizons protected by gravel pavement offer microenvironments that foster soil and microbiome development, with distinct phyla detected below the surface (Alekseev et al., 2020). At Robinson Ridge, early biocrust formation, indicated by Cyanobacteriota and microalgae on surfaces, highlights the role of biogenic structures in stabilising soils and modulating microclimate (Di Menna, 1966).

4.2 Response to environmental changes

The Antarctic Peninsula is warming rapidly, despite the average temperature across Antarctica remaining stable. Antarctic microbial communities are highly sensitive to environmental change, responding to shifts in temperature, moisture, and other environmental factors. Warming caused macroscopic blighting of microbial mats on Livingston Island, which is possibly linked to high fungal abundance resulting in nitrogen depletion (Velázquez et al., 2016). These changes suggest that fungal dynamics under warming can destabilize microbial mat structure and nutrient cycling. Microbial mats are the hotspot of metabolic cycling and source of organic carbon and nitrogen in the maritime

Antarctic, highlighting the impact of warming on Antarctic ecosystems. Similarly, a 90-d warming experiment showed accelerated decomposition of humic substances with an increase in the relative abundance of Pseudomonadota. Depletion of organic carbon in nutrient-poor environments can have detrimental effects on the stability and integrity of ecosystems (Kim et al., 2022). Warming experiments in the rhizospheres of the Antarctic vascular plants on King George Island revealed that eukaryotic communities were more sensitive to warming than bacterial communities. Notably, Ciliophora showed significant changes in relative abundance by warming, indicating that protistan communities may respond markedly to modest temperature increases within plant-influenced soils (Parada-Pozo et al., 2022).

Warming-induced glacier melting increases soil moisture, which significantly impacts microbial community and functions. In the McMurdo Dry Valleys, microbial communities exhibit rapid changes in response to increased moisture, transitioning from arid to high-productivity states. This suggests that these communities are highly sensitive to climate-induced wetting events, which can alter biogeochemical cycling (Niederberger et al., 2019). The increased soil moisture and organic matter can work in synergy, causing greater impact on soil bacterial communities, causing a decline in taxonomic diversity, with bacteria increasing and eukaryotes decreasing. This suggests a shift towards generalists and copiotrophic taxa, as climate change increases water and nutrient availability (Buelow et al., 2016). Warming and increased soil moisture expand the distribution area of plants. In a study covering habitats from bare soils to moss and grass, the results indicated that projected climate warming and the expansion of vegetation communities will shift soil microbial communities (Ball et al., 2022). Together, these findings imply that warming and greening will reshape soil eukaryotic communities, particularly protists and fungi associated with plant cover and moist microhabitats, though the strength and direction of change may depend on initial vegetation and edaphic context (Parada-Pozo et al., 2022; Velázquez et al., 2016).

Human activity also has a strong impact on Antarctic soil microbiomes, often leading to a decrease in alpha diversity (Malard et al., 2019). Scientific expeditions and tourist activity have significantly increased in recent years. Larsemann Hills surveys detected bacterial taxa likely introduced via human activity, highlighting the need for biosecurity and careful interpretation of microbiome data in proximity to stations (Alekseev et al., 2020). Similarly, a conclusion has also been obtained on King George Island (Losapio et al., 2025). Another study identified viable faecal microorganisms in 30–40-year-old human faeces (Hughes and Nobbs, 2004). These findings suggest that the Antarctic ecosystem is particularly vulnerable to human activities, and the consequences can be long-lasting and difficult to rehabilitate. Hydrocarbon spills have been frequently reported near research stations (de Melo Carlos et al., 2024; van Dorst et al., 2014), which led to changes in the chemical composition of Antarctic soils. This contamination introduces selective pressures that enrich for hydrocarbon degraders and alter nitrogen cycling during remediation (van Dorst et al., 2021). For instance, diesel contamination negatively affects the enzymatic activity and alters the microbial community structure, increasing the abundance of the Pseudomonadota and fungi.

4.3 Microbial functions

Microbial communities play a crucial role in biogeochemical cycling and nutrient turnover in Antarctic ecosystems, acting as primary drivers of these processes in the extreme conditions of the region. These microorganisms are involved in the cycling of key elements such as carbon, nitrogen, and sulfur, demonstrating metabolic versatility, which is crucial for maintaining biogeochemical cycles under the extreme conditions of Antarctica (Wynn-Williams, 1996a). The microbial activities are influenced by the local environmental conditions, such as temperature, pH, and moisture. These factors govern the rate of organic matter degradation and nutrient cycling, highlighting the importance of microbial community composition and enzyme activity in these processes (Rousk and Bengtson, 2014; Yergeau et al., 2007). Retrospectively, microbial processes modify the chemical composition of their environment through nutrient cycling (Barrett et al., 2007), highlighting the complex interactions between microorganisms and soil environments.

Antarctic soil bacteria possess genes for labile carbon decomposition and nitrogen cycling, which are even more abundant compared to temperate soils (Zhang et al., 2024). Furthermore, Antarctic soil prokaryotes have evolved carbon cycling plasticity to adapt to favorable and adverse conditions. Pseudomonadota, Actinomycetota, and Bacillota can perform classical organic matter decomposition by expressing hydrolytic enzymes to degrade proteins, carbohydrates, and phosphoric compounds (Liu et al., 2021; Zhang et al., 2024). Many of these enzymes are psychrophilic, which are active at low temperature (4 ℃)—demonstrating capacity for cold-active decomposition (Lamilla et al., 2017). Additionally, these microorganisms may enter viable but non-culturable states to navigate fluctuating conditions (Papale et al., 2018). For autotrophs, Cyanobacteriota and eukaryotic algae use photosynthesis for carbon acquisition (Lee et al., 2024). Additionally, trace gas (H_2, CO, and CH_4) oxidation is also reported in endolithic communities and those in extreme oligotrophic soils, allowing them to persist at the limits of habitability (Coleine et al., 2024; Dragone et al., 2022). In comparison, fungi in Antarctic soils are mostly saprotrophs, which play important roles in soil organic matter turnover. Culture-based surveys in the Dry Valleys show that filamentous fungi tend to occur in moister, higher-pH niches, while yeasts occupy broader habitat ranges, consistent with flexible decomposition strategies across spatially heterogeneous soils (Connell et al., 2006).

Microorganisms are the dominant organic nitrogen source in Antarctic soils. Hypolithic communities possess nitrogen fixation capacity, confirmed by the presence of *nifH* genes and acetylene reduction activity (Cowan et al., 2011). These nitrogen fixers contribute significantly to nutrient turnover in these oligotrophic soils (Cowan et al., 2014). Although the Antarctic is nitrogen-limited, classical nitrification and complete ammonia oxidation have been reported in the Fildes Region (Bendia et al., 2023; Doytchinov et al., 2024; Zhang Y H et al., 2025) and coastal Antarctica (Han et al., 2024). In comparison, denitrification capacity has been widely identified in Antarctic soils, and biological emission of N_2O, most likely as a result of denitrification, has been reported in situ (Gregorich et al., 2006). Genes that are indicative of the presence of denitrification (*nirS*, *nirK*, *norB* and *nosZ*) have been detected in Antarctic soils but are less abundant in high altitude or low latitude regions, such as Fossil Bluff and Coal Nunatak (Chan et al., 2013; Jung et al. 2011; Yergeau et al., 2007). Furthermore, nitrogen cycling is heavily impacted by human activities. In a simulated hydrocarbon addition experiment, the abundance of *amoA* genes was significantly reduced, while that of *nosZ* significantly increased (van Dorst et al., 2014). During the hydrocarbon bioremediation at Casey Station, ammonia-oxidizers decoupled from nitrite-oxidizers, causing an accumulation of nitrite, demonstrating how human activity can disrupt nitrogen cycling (van Dorst et al., 2021).

Research on microbial adaptation has deepened our understanding of cold-environment survivability, but current evidence is fragmented across taxa and scales. Most findings emphasise individual stress-response genes rather than community-level interactions that govern survival under multiple concurrent stressors. Future research should focus on network-level metabolic interactions and model systems to quantify how community cooperation or competition enhances resilience. Linking metabolic plasticity to ecosystem-level feedbacks would also improve our ability to predict Antarctic microbial responses to environmental perturbations.

5 Biotechnological potential and conservation

5.1 Novel microbial taxa

Multiple Antarctic habitats exhibit striking microbial novelty and endemism, often with strong habitat specificity. Significant differences in microbial composition have also been observed in Antarctic soils, highlighting how the unique environments of Antarctica foster distinct microbial communities and contribute to the expansion of global biodiversity (Figure 5). For instance, a study on soils of Robinson Ridge, Eastern Antarctic, identified the dominance of candidate division bacteria WPS-2 and AD3 (Ji et al., 2016), which were later renamed as *Candidatus* Eremiobacterota and *Candidatus* Dormibacterota, respectively. The unique taxonomy of Antarctic microorganisms is rooted in the environmental conditions, such as high UV radiation, low pH, cold temperature, and low carbon and nitrogen nutrients, which foster

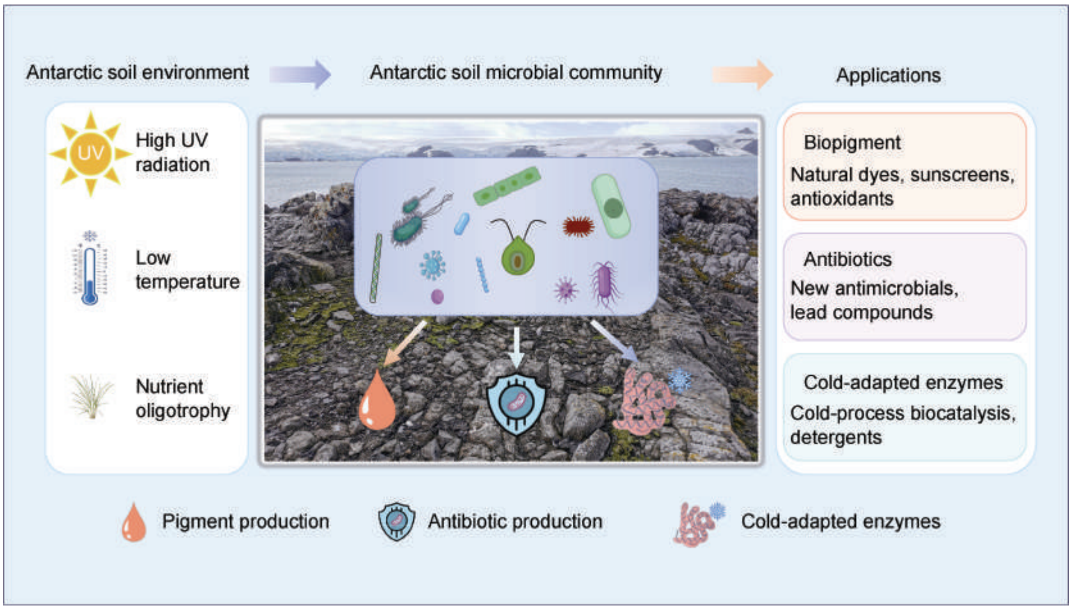

Figure 5 Potential biotechnological and industrial implications of Antarctic microorganisms. The extreme environmental conditions of Antarctica have shaped unique microbial communities in the soil. In order to adapt to these harsh environmental pressures, microorganisms have evolved various survival mechanisms, which hold significant potential for resource development.

evolutionary divergence. Furthermore, geographical isolation also warrants novel taxa discovery (Del Moral et al., 2021), such as the microbial taxonomy in the permanently ice-covered Lake Enigma, which exhibited significant differences compared with other habitats (Smedile et al., 2024).

Cultivation-based study identified 100 novel bacterial species, which were published in *International Journal of Systematic and Evolutionary Microbiology*, the official journal of the International Committee on Systematics of Prokaryotes. These taxa span Pseudomonadota (*n*=34), Bacillota (*n*=21), Actinomycetota (*n*=25), Bacteroidota (*n*=17), and Deinococcota (*n*=3). In the Darwin-Hatherton Glacier region, clone libraries from beneath desert pavement were dominated by Deinococcota (formerly Deinococcus-Thermus), Actinomycetota, and Bacteroidota, and culturable representatives included Arthrobacter, Adhaeribacter, and Pontibacter, providing model organisms for probing genomic and phenotypic attributes underpinning survival in Antarctic soils (Aislabie et al., 2013). Additionally, genome-enabled studies are also exposing novelty at finer scales. A *Pseudarthrobacter* strain (So.54) isolated from *Colobanthus quitensis* rhizosphere appears to represent a novel species based on nucleotide and amino acid identity; its genome harbors 64 genomic islands with stress defense traits (e.g., heavy metal resistance) and 6 biosynthetic gene clusters (BGCs) with low or no similarity to known clusters (González et al., 2025). Similarly, a draft genome of a *Salinibacterium* sp. from permafrost offers insight into the genetic bases of cold adaptation (Shin et al., 2012).

Many abundant Antarctic taxa remain difficult to culture: a direct comparison of culture-independent and culture-dependent datasets from 200 archived soils showed that many of the most abundant sequence-defined taxa were not readily cultivated, highlighting targets for future isolation efforts (Dragone et al., 2025). Thus, amplicon sequencing and metageome sequencing-based methods provide a broader view on the taxonomic novelty of Antarctic soils. Endolithic desert ecosystems—among Earth's coldest and driest—harbor particularly novel biota; metagenome-assembled genomes from 109 endolithic microbiomes revealed that 49.3% represented novel candidate bacterial species. Metabolic reconstructions suggest trace gas oxidation and atmospheric chemosynthesis underpin microbial persistence at these limits of habitability (Coleine et al., 2024). At and around research bases, amplicon surveys reveal mixtures of cosmopolitan groups with distinctive Antarctic elements. Around the Bulgarian Antarctic Base on Livingston Island, Oxyphotobacteria, Bacteroidia, Gammaproteobacteria, and Alphaproteobacteria predominated. Notably, most cyanobacterial reads were assigned to a single uncultured Leptolyngbyaceae taxon; fungal reads were often unresolvable to species, though *Betamyces* and *Tetracladium* were observed; archaea were rare, with Woesearchaeales, *Nitrosarchaeum*, *Candidatus* Nitrosopumilus, and Marine Group II dominating the archaeal signal.

5.2 Bioprospecting for novel compounds

Secondary metabolites are organic compounds produced by microorganisms that are not directly involved in the normal growth, development, or reproduction but mediate ecological interactions, which may produce a selective advantage by increasing their survivability (Figure 5). Antarctic bacteria are a promising source of secondary metabolites due to their adaptation to extreme environments, which often leads to the production of unique bioactive compounds. These metabolites have potential applications in pharmaceuticals, agriculture, and biotechnology, particularly in the development of new antibiotics and other therapeutic agents. Long-read metagenomic sequencing has revealed over 1,400 mostly full-length BGCs in uncultivated Antarctic soil bacteria, indicating a vast untapped genetic reservoir for novel compound discovery (Waschulin et al., 2022). The biosynthesis of secondary metabolites in Antarctic bacteria is influenced by their unique genetic and environmental adaptations, which enable them to produce novel compounds not found in more temperate regions. Two types of secondary metabolites have attracted significant attention in bioprospecting, including antimicrobial secondary metabolites and pigments.

Antarctica's extreme environments foster intense microbial competition for limiting resources, creating conditions that favor the evolution of antimicrobial secondary metabolites (Núñez-Montero and Barrientos, 2018). Antarctic bacteria from Pseudomonadota, Actinomycetota, Cyanobacteriota, Bacillota, and Bacteroidota produce diverse antimicrobial compounds. Actinomycetota, a prominent group in Antarctic environments, are known for their prolific production of bioactive metabolites. Studies have shown that Antarctic Actinomycetota possess significant antibacterial activity, including activity against methicillin-resistant *Staphylococcus aureus* (Hui et al., 2021). *Streptomyces* strains from Livingston Island soils carried core biosynthetic genes associated with multiple antibiotic classes (type II polyketide synthases, nonribosomal peptide synthetases, polyene and glycopeptide pathways) and inhibited several phytopathogenic bacteria in vitro, with 4 strains exhibiting broad-spectrum activity, demonstrating agricultural biocontrol potential (Encheva-Malinova et al., 2014). Fungi also contributed to antimicrobial compound production (Durán et al., 2019). *Cryptococcus gilvescens* and a *Penicillium* sp. inhibited *Escherichia coli*, *Klebsiella pneumoniae*, *Enterococcus faecalis*, and *Staphylococcus aureus* (Ordóñez-Enireb et al., 2022). Some fungi, such as *Pseudogymnoascus destructans* and *Mortierella* species, have shown antiparasitic and herbicidal activities, indicating potential for pharmaceutical and agricultural applications (Gomes et al., 2018).

Antarctic bacteria have developed unique adaptations to survive in cold, nutrient-poor, and high-radiation environments, which include the production of various pigments. These pigments, such as melanins and carotenoids, play crucial roles in protecting the bacteria from environmental stressors and have potential biotechnological applications. Melanins are black or brown pigments synthesised by many Antarctic bacteria, which protect bacteria from UV radiation, oxidative stress, and toxic heavy metals. They are produced through pathways related to tyrosine metabolism and are regulated at both metabolic and transcriptional levels (Pavan et al., 2020). Carotenoid pigment synthesis is a key cold adaptation strategy employed in many psychrophiles and psychrotolerants. Antarctic *Xanthophyllomyces dendrorhous* yeast isolates from King George Island soils produced the high-value aquaculture pigment astaxanthin. One isolate (ANCH01) produced approximately 6-fold more astaxanthin than typical wild-type strains, while others had beta-carotene as the dominant carotenoid (Contreras et al., 2015). Therefore, the discovery of novel secondary metabolites from Antarctic bacteria holds significant promise for the development of new antibiotics and other therapeutic agents, addressing the growing issue of antibiotic resistance (Núñez-Montero and Barrientos, 2018).

5.3 Bioprospecting for cold-adapted enzymes

Cold-adapted enzymes, also known as psychrozymes, typically exhibit high catalytic activity at low temperatures, high specific activity, and low activation energy (Kumar et al., 2021), making them attractive for industrial processes where low-temperature operation saves energy, protects heat-labile substrates, or improves selectivity (Figure 5). The screening of Antarctic microorganisms has yielded a diverse array of cold-active enzymes. For example, 30 culturable Actinomycetota isolated from the South Shetland Islands produce proteases, gelatinases, and cellulases that remain active at 4 ℃ (Lamilla et al., 2017). These enzymes have established or emerging roles in food processing, detergents, molecular biology, and bioremediation.

The presence of carbohydrate-active enzymes in Antarctic soil metagenomes, particularly those from Actinomycetota (*Streptomyces* and *Amycolatopsis*), suggests a robust potential for lignocellulose degradation. These enzymes can enhance the biological treatment of lignocellulose biomass, which is crucial for biofuel industries (Oh et al., 2019). Psychrophilic enzymes are used in laundry detergents to enhance cleaning efficiency at low temperatures, reducing energy consumption and preserving fabric quality. Their high activity at low temperatures allows for effective stain removal without the need for hot water, which is both cost-effective and environmentally friendly (Cavicchioli et al., 2011; Margesin and Feller, 2010). Psychrophilic enzymes also have applications in the food industry, which can be used for processes such as brewing, baking, and dairy production. Their ability to function at low temperatures helps preserve the nutritional and sensory qualities of food products while preventing spoilage and extending shelf life (Margesin and Feller, 2010).

Cold-active enzymes are also valuable in bioremediation processes in cold climates, where they can degrade pollutants efficiently at low temperatures. Indigenous hydrocarbon degraders are capable of aromatic hydrocarbon metabolism (Aislabie et al., 2000; Fernández et al., 2024). Psychrotolerant *Sphingomonas* and *Pseudomonas* strains isolated from oil-contaminated Antarctic soils degraded aromatic hydrocarbons and grew on JP8 jet fuel, reflecting the presence of indigenous hydrocarbon degraders similar to those worldwide. Over 5 years of managed bioremediation of hydrocarbon-contaminated soil, community shifts correlated with hydrocarbon degradation and increased *alkB* gene abundances, with genera such as *Alkanindiges*, *Arthrobacter*, *Dietzia*, and *Rhodococcus* being enriched (van Dorst et al., 2021).

Despite the rapid progress in uncovering new taxa and bioactive potential from Antarctic microorganisms, bioprospecting remains constrained by limited cultivation success and regulatory challenges concerning biopiracy and conservation ethics. A balanced framework is needed that encourages exploration of microbial genetic resources while ensuring compliance with Antarctic Treaty principles. At the same time, systematic cultivation efforts and genome-guided screening are essential to translate genetic potential into applied innovations, bridging ecological insight with sustainable biotechnology.

6 Conclusion and future directions

In conclusion, we provide a brief review of the current research on Antarctic soil microorganisms. These studies highlight Antarctic ice-free soils as biodiversity oases, where microbial consortia—bacteria, archaea, fungi, algae, protists, and viruses—sustain the ecological functions of the ecosystems. Geographical isolation and unique environmental conditions shape the unique microbial taxonomy and functions. These microorganisms exhibit extreme taxonomic novelty, with remarkable adaptations to cold, aridity, UV stress, and oligotrophic environments. Furthermore, the environments of Antarctica serve as a model for understanding how life might exist in the harsh environments of other celestial bodies. By examining the survival mechanisms of Antarctic microorganisms, scientists can better predict the types of life forms that might exist elsewhere in the universe and the conditions under which they could thrive.

Rapid warming and increased human activities are causing a decline in native microbial diversity and facilitating the invasion of non-native species, leading to homogenization of the Antarctic microbiome, reshaping biogeochemical cycling, and impairing the integrity of Antarctic ecosystems. However, existing studies primarily focus on microbial composition and function, leaving their responses to and feedback to climate change poorly understood. The rapid warming of the Antarctic Peninsula is driving changes in temperature, ice cover, and species distribution, which in turn affect biodiversity and ecological dynamics across the continent. These changes are simultaneously altering both the physical environment and the biological interactions and ecosystem services that many species depend upon for survival. Consequently, there is an urgent need to preserve Antarctic native species as both isolates and genetic resources for future applications and prospecting. Additionally, a comprehensive understanding of how Antarctic ecosystems respond to climate change is essential to mitigate its impacts.

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