



Microbial Diversity in Cold Desert Ecosystem: A Review and Bibliometric Analysis

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Abstract: Cold deserts play a unique and crucial role in the environment. Glaciers in these regions store significant amounts of freshwater, essential for ecosystems, while permafrost sequesters large quantities of carbon, preventing the release of greenhouse gases. These areas host diverse species, contributing to global biodiversity and a variety of extremophile life forms. The microbial communities in cold deserts-comprising bacteria, cyanobacteria, archaeobacteria, fungi, and lichens-have adapted to harsh conditions. They maintain ecological balance by forming symbiotic interactions with plants, enhancing soil fertility, and boosting crop yields. Additionally, several microorganisms are involved in bioremediation processes. Microorganisms found in cold desert environments also serve as valuable biosignatures for detecting life, significantly advancing the field of astrobiology. This review explores the microbial diversity of cold deserts through bibliometric analysis using VOSviewer software. The software identified 47 countries engaged in cold desert research, with the United States leading in the number of publications. A total of 2009 keywords were analyzed, with “bacteria (microorganisms)” being the most common. This review encompasses studies on the microbial diversity of cold deserts and their applications, highlighting crucial directions for future research.

Key words: Bibliometric analysis, anthropogenic, limiting factor, ecological homeostasis, biosignatures, conservation

Cold deserts, characterized by their low temperatures and arid conditions are found in Antarctica (with valleys such as McMurdo Oasis, Taylor, Wright, Victoria, McKelvey, etc.; Pointing *et al.*, 2009), the Arctic, parts of the United States (Antunes *et al.*, 2023), and various regions around the Himalayas in India (Gupta *et al.*, 2015; Jain *et al.*, 2021, <https://whc.unesco.org/en/tentativelists/6055/>). Cold desert regions are excellent natural laboratories for researching microbial diversity and ecosystem dynamics because they are largely unaffected by excessive human disturbances. The harsh temperature and other seasonal variations along with a significant water scarcity create unique challenges for plants, animals as well as microorganisms, influencing their life cycles, behavior, and physiological adaptations (Dhakar and Pandey, 2020). The microflora of cold deserts represents a fascinating and intricate web of life, showcasing remarkable

adaptations to the harsh environmental conditions that characterize these ecosystems (Zakaria *et al.*, 2021). The microbial community plays a vital role in maintaining ecological balance, contributing to nutrient cycling, soil stability, and the overall health of the ecosystem (Choe *et al.*, 2021). A study reported by Williams *et al.* (2024) serves as an instance to the significant adaptation attained for cold temperature survival. The authors studied metagenome-assembled genomes (MAGs) and found the enzymes encoding for sugar catabolism. Additionally, the energy source includes hydrogenases for trace gas oxidation and metabolic water which in turn facilitate carbon fixation. The ability of microorganisms to thrive in cold desert conditions showcases the resilience and adaptability of life in some of the planet's most challenging environments (Antunes *et al.*, 2023). Understanding the intricacies of the microbial communities in cold deserts is crucial for comprehending the broader ecological dynamics in these fragile ecosystems.

Research on the microbial frontiers in cold desert habitats is expanding due to the increasing understanding of their ecological relevance and their uses. This review explores the scientific environment around this specialized area by bibliometric analysis using VOSviewer software. It offers a quantitative insight into the important trends, prominent research gaps, and developing novel subjects (Van Eck and Waltman, 2010; Zakaria *et al.*, 2021). They provide users with an access to a wealth of academic literature and a variety of methods for gauging the influence of research and following trends within a certain field of study (Stasi *et al.*, 2023). These databases are available for use by researchers to locate and examine publications from many domains; this is very helpful for interdisciplinary study (Khurshid Wani *et al.*, 2023). This review offers a thorough summary of recent findings and throws insight on how microbial research in cold desert habitats has developed over time. In this ever-evolving sector, such insights are essential for directing future research objectives and promoting multidisciplinary cooperation.

Transformations in cold desert environments

The delicate ecosystems of cold deserts, characterized by their unique microflora,

face numerous challenges. Human activities—such as industrial development, mining, and urbanization—have significant and multifaceted impacts on these regions, disrupting the fragile balance of these ecosystems (Davila *et al.*, 2021). Habitat destruction and fragmentation from these activities lead to soil disturbance and changes in hydrological patterns, which directly affect the composition and diversity of microbial communities (Dhakar and Pandey, 2020; Coleine *et al.*, 2024). Furthermore, the introduction of invasive plant species and alterations in land use practices can disrupt microbial dynamics, potentially favoring opportunistic species and undermining the stability of native microbial populations.

Climate change, driven by human activities, poses an additional and profound threat to cold desert ecosystems and their microbial residents. Rising temperatures, altered precipitation patterns, and changing snowmelt dynamics create challenging conditions for microflora adapted to specific temperature ranges and moisture levels (Yan *et al.*, 2022; Barrón-Sandoval *et al.*, 2023; Coleine *et al.*, 2024). These shifts can disrupt symbiotic relationships between microbes and higher plants, affecting nutrient cycling, soil stability, and overall ecosystem functionality. The increasing frequency and intensity of extreme weather events, such as heat waves and droughts, further exacerbate the vulnerability of microbial communities, potentially leading to shifts in species composition and reduced biodiversity.

Factors affecting microbial communities in cold desert region

Undoubtedly, microbes are the most productive component and the primary driver of biogeochemical cycling in cold desert ecosystems. The dynamics and variety of microbial communities are greatly influenced by the climatic regime, and niche features (consisting of deterministic and stochastic mechanisms) can also have a significant impact on phylogenetic diversity and the methods that organisms use to survive, particularly in polar areas (Bahl *et al.*, 2011; Dhakar and Pandey, 2020; Choe *et al.*, 2021; Yan *et al.*, 2022; Barrón-Sandoval *et al.*, 2023). Geographic distance, precipitation, aridity, temperature, soil pH, organic matter availability and salinity have all been described as the primary drivers of

community assembly (Zhang *et al.*, 2021; Yan *et al.*, 2022; Shao *et al.*, 2023; Larsen *et al.*, 2024). The release of scytonemin and carotenoids has been reported by Vitek and Wierzbos (2020) to combat UV-induced damages due to absorption and production of free radicals. It can be impacted by the variety of edaphic and lithic niches, even if the niches share the same climatic pattern and are close to one another (Bahl *et al.*, 2011; Choe *et al.*, 2021). The intensity of light has been a potential limiting factor for microbial growth. Cyanobacteria were found dominant in light accessible zone while light inaccessible areas were suitable for Proteobacteria and Bacteroidetes (Lai *et al.*, 2024). Also the light accessibility governs the microbial metabolic pathways. Zakavi *et al.* (2022) observed a significant increase in microbial diversity with respect to altitude and enhanced resistance to abiotic stress factors; accompanied by a reduction in biomass. Barrón-Sandoval *et al.* (2023) determined the impact of topographical factors on carbon and nitrogen dynamics in a desert ecosystem. Cold desert microbiome follows a seasonal developmental process. The microbial community shifts as evidenced by Zhang *et al.* (2021a) with respect to climate conditions. It was found that the cyanobacteria predominating at the cold temperature has been replaced by Proteobacteria and Firmicutes at higher temperature. Yang *et al.* (2024) demonstrated the effect of cultivation duration on the selection of microbial colonization in a desert ecosystem. The relative abundance of bacteria was inversely proportional to cultivation years. Also, there was a significant modification in the type of carbon fixation mechanism adopted by the microorganisms. Attaining dominancy has been considered as the most prominent survival strategy opted by most microorganisms in response to cold. It is further characterized into two categories such as energy reserve and continual-energy-harvesting (Leung *et al.*, 2020).

Many researchers have attempted to determine the correlation and regression analyses among environmental factors, alpha and beta microbial diversities. For instance, Liu *et al.* (2022) observed a significant correlation between the microbial diversity and environmental conditions in deserts. Stability of microbial communities vary with different regions. Barrón-Sandoval *et al.* (2023) evaluated

the effect of climate change on the microbial communities by performing reciprocal transplant of biological soil crusts (BSC). In combination with high throughput sequencing methods, functional gene identification and metabolic dynamics, the cited study stated that the influence of climate change results in microbial community specialization. Larsen *et al.* (2024) used metagenomics approach to examine the microbial community inhabiting different rocks across Antarctica. The authors also reported that there is a remarkable difference in the richness of microbial diversity with respect to geographical distance. However, with a modification in elevation, shift in the demographic composition of the community was prevalent.

Bibliometric Analysis

A bibliometric study was conducted to examine publications pertaining to the diverse life forms found in cold deserts and their applications. The investigation comprised of the articles published between from 2000 to 2024 in journals that were indexed in the Scopus databases (www.scopus.com; assessed on 29th April 2024). The search query used a combination of field qualifiers and Boolean operators. The search phrases are to be located in the title, abstract, and keywords of documents, according to the specification "TITLE-ABS-KEY". Bibliometric data collection for this study involved the search keywords as "Cold" AND "Arid". All pertinent papers were found using the Scopus indexing systems, and their bibliographic information was retrieved using the export feature of the databases (Zakaria *et al.*, 2021; Khurshid Wani *et al.*, 2023). In this study, the retrieved data was analysed through VOSviewer, free software for representing bibliographic information based on co-authorship (publishing countries), and co-occurrence (all keywords) data in form of three different visualizations viz., network, overlay and density (Van Eck and Waltman, 2010). The minimum number of occurrences for highest publishing countries (Total = 47) and all keywords (Total = 2009) data was selected as 1 and 5 respectively. The map followed full counting method.

Results and Discussion

Among 47 countries, United States had the highest link strength (Fig. 1) followed by

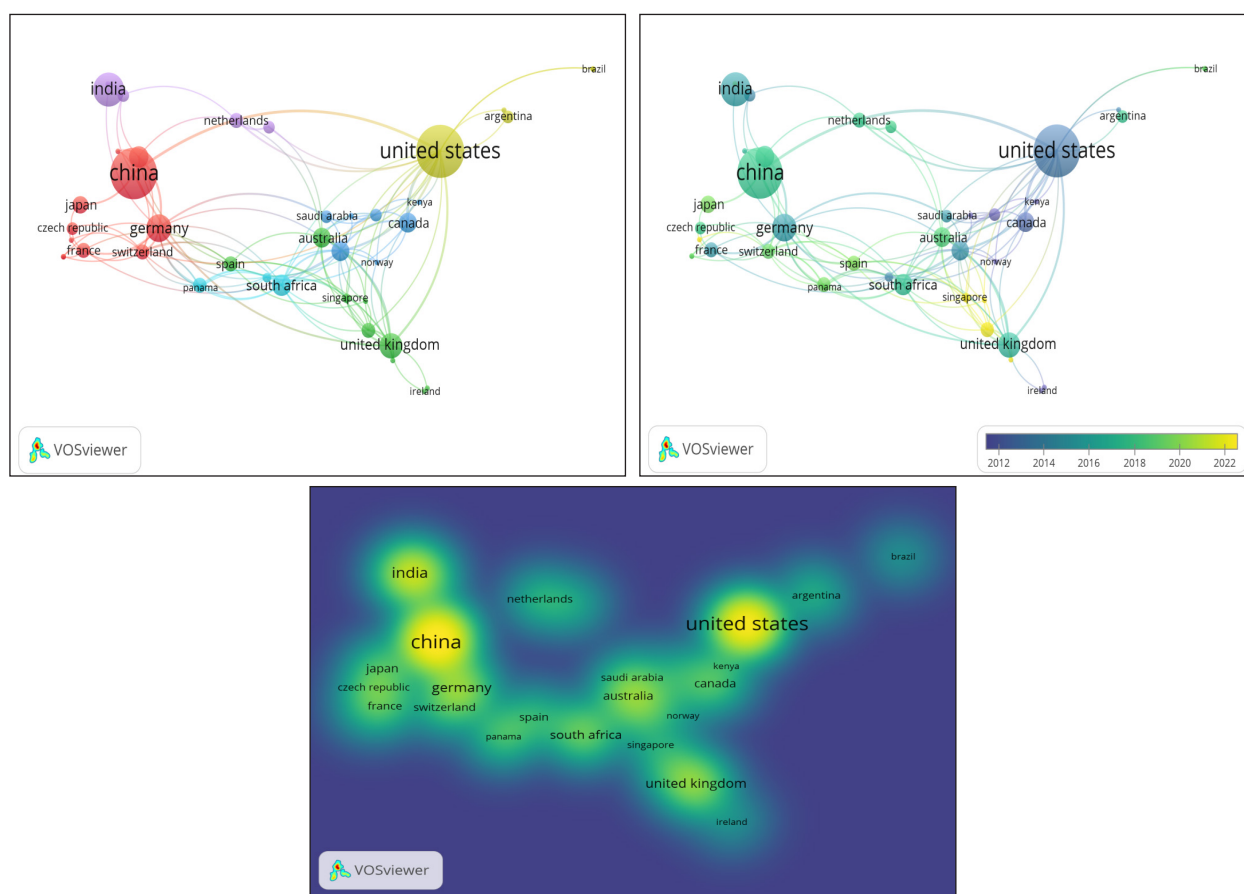


Fig. 1. Cluster map based on the publishing countries data, (a) network visualization, (b) Yearly distribution and (c) density determination.

China, India and Germany (Fig. 2). On the generated cluster maps, every term (countries and keywords) appears as a separate circle or node that is connected by one or more lines, referred to as links.

Following the similar methodologies, cluster map for all keywords were generated. The

keyword “bacteria (microorganisms)” has the highest link strength (Fig. 3).

Thus, the study was based on limiting growth factors, diversity and major applications of microbial communities in cold arid environments.

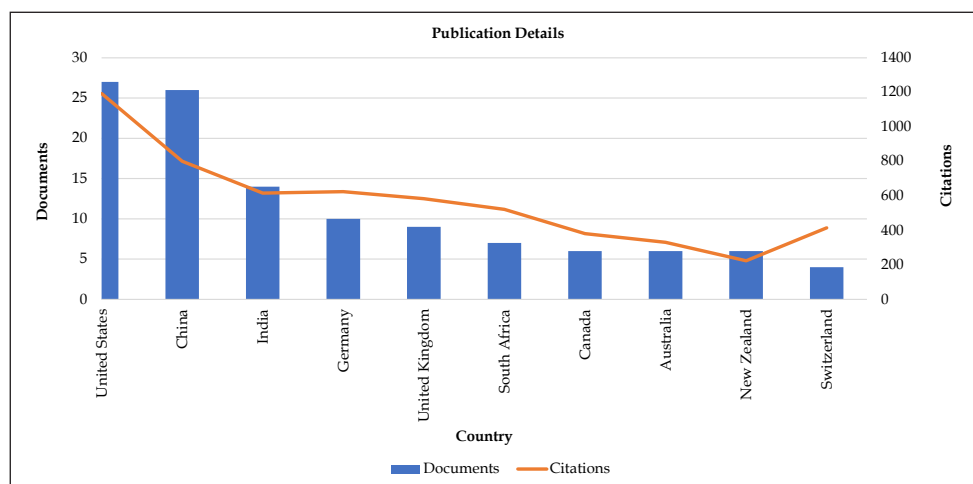


Fig. 2. Representation of the published documents along with their citation index for the top 10 publishing countries.

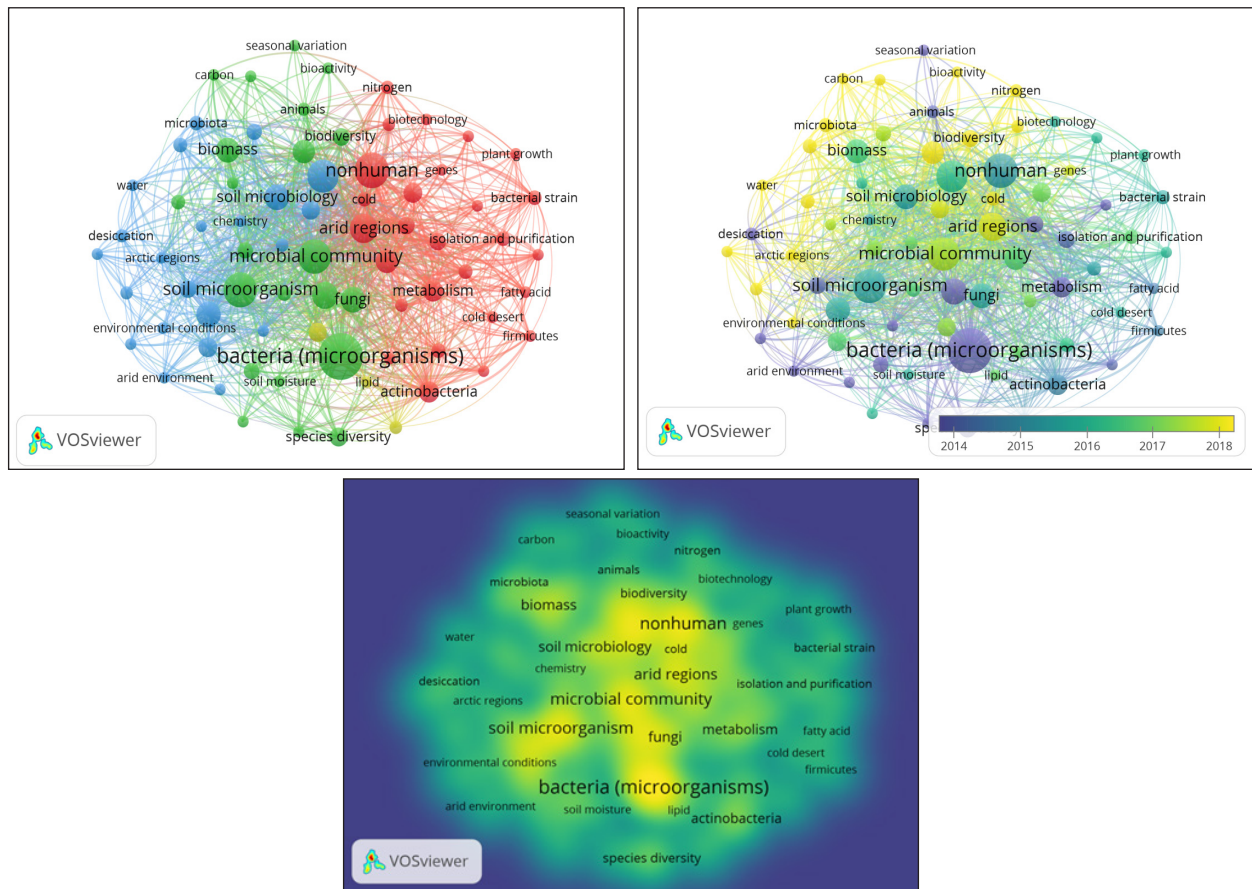


Fig. 3. Cluster map based on the keywords data- (a) network visualization, (b) yearly distribution and (c) density determination.

Microbial diversity inhabiting cold desert ecosystem

Dominating bacteria: The microbial community in cold deserts is a dynamic and diverse assembly of organisms that have evolved unique strategies to thrive in the face of adversity (Fig 4). Microorganisms living in cold deserts have adapted by producing

cryoprotectants to inhibit ice crystals formation, controlling osmotic balance to resist freezing stress, modifying membrane fluidity to allow for proper function at low temperatures, and releasing cold-adapted enzymes (Dhakar and Pandey, 2020). Certain microbes undergo dormancy or generate spores in order to endure extremely low temperatures (Alsharif *et al.*, 2020). These microorganisms, includes bacteria, fungi,

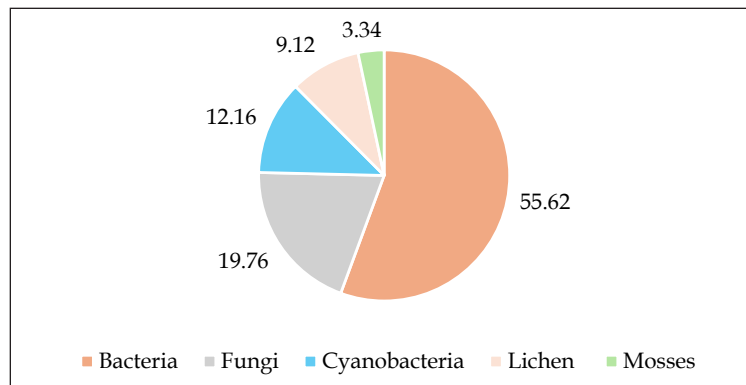


Fig. 4. The percentage of different organisms inhabiting cold deserts as reported in the publications (accessed from Scopus database).

and archaea contribute to nutrient cycling, soil fertility, and the overall health of the ecosystem (Jain *et al.*, 2021). Expedition of microbial communities from extreme desert regions around the world have uncovered an extensive number of fungal phyla like Ascomycota, Basidiomycota as well as bacterial communities similar to Proteobacteria, Actinobacteria, and Bacteroidetes (Bachran *et al.*, 2019; Vásquez-Dean *et al.*, 2020; Shao *et al.*, 2023; Mawar *et al.*, 2023; Yang *et al.*, 2024). Bacteria are represented as one of the foundational components of the microbial community. Numerous members of these groups, specifically *Bacillus* sp., have been found in both hot and cold deserts and are known for their wide variety of applications (Zhang *et al.*, 2021b). A similar microflora was reported by Bachran *et al.* (2019) and observed several halophilic domains of Bacteria and Archaea using polyphasic approaches. Among them, the major representative of the diversity of bacteria belongs to Salinimicrobium, Gammaproteobacteria and Firmicutes (Order-Bacillales). Smith *et al.* (2006) tested the mineral soil samples collected from Antarctic Dry Valleys and stated the dominant colonization of Bacteroidetes, Actinobacteria, and Acidobacteria. Gupta *et al.* (2015) documented a comparative analysis between the microbial community of Drass (Western Himalaya), Antarctica and Arctic region. The findings suggested that the order of dominance followed the appearance of Acidobacteria, Firmicutes and Proteobacteria in the Drass, Antarctica and Arctic region respectively. Further, some rare genus was found inhabiting Drass includes *Nitrospirae*, *Tenericutes*, *Planctomycetes*, *Chloroflexi*, *Armatimonadetes* (Gupta *et al.*, 2015). Williams *et al.* (2024) reported the presence of novel *Candidatus* spp., belonging to phylum Chloroflexota. Zakavi *et al.* (2022) documented that there is a directly proportional relationship between altitude and dominance of *Bacillus* species. Thus, suggesting the dynamic nature of microbial communities in response to altitude variation.

Evolutionary Cyanobacteria and Archaeobacteria

Cyanobacteria consist of a group of photosynthetic bacteria capable of harnessing sunlight to produce energy. This photosynthetic activity of cyanobacteria contributes to carbon fixation, further influencing the nutrient

dynamics of the ecosystem (Smith *et al.*, 2006; Barrón-Sandoval *et al.*, 2023). They are particularly known to survive in arid conditions and are essential nitrogen-fixing agents (Gupta *et al.*, 2015). It was noted that the radiation and desiccation tolerance follow a relationship when supporting the existence of cyanobacteria *Synechocystis* sp. and *Chroococcidiopsis* sp (Fagliarone *et al.*, 2017); thus, supports the growth of vegetation in nutrient-deprived cold desert environments. Choe *et al.* (2021) assessed the microbial diversity colonizing the Arctic rocks and their adjacent soil using omics approach. The microflora inhabiting the rocks was much distinct than that of the soil. The dominant microflora of rock was Cyanobacteria, Lecanoromycetes, Trebouxiphyceae, Ulvophyceae and Eurotiomycetes. While Acidobacteria, Latescibacteria, Pezizomycetes, Gemmatimonadetes, Rokubacteria, Sarcomonadea, Leotiomycetes, Spirotrichea and Mortierellomycetes were the most abundant in soil. The study of *Microcoleus* stated that morphological adaptations were responsible for the diversification of genomes (Skoupý *et al.*, 2024). Irit *et al.* (2023) isolated *Trichocoleus desertorum* from Negev desert, Israel. They were reported to possess DNA repair genes such as PhrB, mutS, mutL etc., as a survival source. Bahl *et al.* (2011) observed that geographical distance had no effect on the cyanobacteria *Chroococcidiopsis*. They possess an evolutionary legacy. However, Zhang *et al.* (2021b) focused on how shifting climate conditions impact cyanobacterial communities. Smith *et al.* (2006) reported prominent colonization of cyanobacteria in high-altitude conditions based on Antarctic soil samples. Although archaeobacteria are considered some of the toughest pioneer species capable of surviving the harshest conditions, making them ideal model organisms for studies on the 'existence of life,' there is a surprising scarcity of published reports on this subject. The Scopus database does not include any of the studies based on archaeobacteria (Fig. 4) while PubMed database include few reports. For example, Pointing *et al.* (2009) evaluated the samples from McKelvey Valley, Antarctica using culture independent approach; and found the absence of any archaeobacteria. However, the arid zone of Arava valley inhabits novel species belonging to *Haloparvum* and *Halorubrum* (Bachran *et al.* 2019). Kimble *et al.* (2018) also

reported for the presence of Thaumarchaeota from New Mexico, USA. It was demonstrated that the archae possess nitrogen cycling genes. Similar findings were observed from the Arctic valley's rock and soil that has marked the dominance of Thaumarchaeota (Choe *et al.*, 2021). Thermoprofundales were also explored from Siberian Kolyma-Indigirka permafrost through metagenome assembled genomes (MAG; Sipes *et al.*, 2021).

Fascinating fungi

Cold-adapted fungi display unique physiological mechanisms to withstand freezing temperatures and limited water availability. Jain *et al.* (2021) reported more than 30 fungi including majorly *Talaromyces*, *Apiotrichum*, *Phaeophlebiopsis*, *Candida*, *Microdiplodia*, *Penicillium*, *Naganishia*, *Xylaria*, *Periconia*, *Rhodotorula*, *Aspergillus*, *Cladosporium*, *Tausonia*. Sordariomycetes and ectomycorrhiza were more common in microhabitats that were accessible to light, despite the fact that the class Dothideomycetes dominated the fungal communities in both types of microhabitats (Lai *et al.*, 2024). These fungi often form symbiotic relationships with plant roots that enhance nutrient absorption and water uptake for both the fungi and the host plants. The presence of these fungal associations is crucial for the establishment and survival of plant species in cold desert ecosystems, as they facilitate the extraction of nutrients from the soil, contributing to the overall resilience of the vegetation. Li *et al.* (2024) collected a variety of dark septate endophytic (DSE) fungi including *Cladosporium subuliforme*, *Alternaria aspera*, *Curvularia buchloes*, *Wojnowiciella* sp., *Apodus* sp. etc., from Northwest desert, China. It was demonstrated that the drought resistant metabolites released by these DSE fungi were significantly affected by different water levels and thus could also serve as indicators of water scarcity.

Symbiotic eukaryotes: A captivating diversity of cold deserts

Lichens are well-adapted to withstand extreme temperature fluctuations, desiccation, and nutrient-poor conditions. These hardy organisms are often pioneers in colonizing bare surfaces, contributing to soil stabilization and preventing erosion. The intricate structure of lichens allows them to trap and retain

moisture, creating a microenvironment that supports other microorganisms and facilitates the establishment of higher plant species. The appearance of lichen-forming fungal diversity such as Verrucariales and Lecanorales was reported by Choe *et al.* (2021). *Buellia* sp., *Caloplaca regalis*, *Mastodia tessellate*, *Haematomma erythroma*, *Lecanora physciella*, *Rhizoplaca melanophthalma*, *Leptogium puberulum*, *Xanthoria elegans*, *Nostoc commune*, *Himantormia lugubris*, *Physconia muscigena*, and *Usnea* sp., were some of the lichens documented by Rautiainen *et al.* (2024) in Antarctica. Lange and Kappen (1972) observed that lichens inhabiting Antarctica photosynthesizes below 15°C by absorbing water vapors. It can be seen as an adaptive strategy for their resistance to frost and desiccation. Kumar *et al.* (2014) accessed the antioxidant and cytotoxic properties of saxicolous lichens reported in Ladakh. Further, it was suggested to utilize them as natural antioxidant and anti-cancer medicines. The studies on mosses are few in cold deserts yet significant. Spalzin *et al.* (2015) found various genera of mosses including *Philonotis*, *Tortella*, *Brachythecium*, *Anomobryum*, *Ptychostomum*, *Pohlia*, *Mnium*, *Cratoneuron*, *Gemmabryum*, *Mniobryum*, *Voitia*, *Haplocladium*, *Claopodium*, *Mielichhoferia*, *Drepanocladus*, *Lescuraea*, *Osterwaldiella*, *Anoetangium*, *Entosthodon*, and *Racomitricum* from Leh district, Ladakh. These mosses have a prominent literature signifying their role in ecological homeostasis, and nutrient uptake. Their role as environment pollution indicators and to develop Index of Atmospheric Purity (IAP) have been reported. For instance, Salih *et al.* (2024) documented the first ever report on the presence of ROS (Radical scavenging species) enzymes producing genes (CAT, POD, SOD etc.) isolated from a moss *Syntrichia caninervis*. ROS genes are functionally important in stress resilience; cold conditions induce their production more rather than desiccation.

As we delve deeper into the understanding of microbiome in cold deserts, we uncover a complex network of interactions that shape the ecological dynamics of these unique and fragile environments. The insights gained from studying the microbial communities in cold deserts not only broaden our understanding of life's adaptability but also hold implications for conservation and sustainable management of

these delicate ecosystems in the face of ongoing environmental changes.

Applications

Cold desert microbes, with their unique adaptations to extreme environmental conditions, hold immense potential for various applications across different categories, showcasing new achievements that have emerged through recent research endeavors. In recent years, research into the applications of cold desert microorganisms has expanded, revealing their potential in various fields. Microbial inhabitants of cold deserts are reported to play a significant role in developing plant-microbe interactions. Through these symbiotic connections, microorganisms play a critical role in boosting soil fertility and promoting crop output in harsh conditions (Mawar *et al.*, 2023). They are referred as plant growth-promoting rhizobacteria (PGPR) since they assist the plant in accessing critical nutrients like phosphorus, iron and nitrogen (Jain *et al.*, 2021). Arid microorganisms are capable of developing abiotic stress resilience (Alsharif *et al.*, 2020; Dhakar and Pandey, 2020). Thereby, promoting plant growth and sustaining various climatic stresses are offered by arid habitats.

Bioremediation efforts have benefited from the discovery of novel enzymes produced by these microorganisms, capable of degrading pollutants in cold environments, thus offering sustainable solutions for environmental cleanup (Zakaria *et al.*, 2021). Global warming causing the melting of permafrost and glacier has been a major concern resulting in the increase of spillage accidents over-the-years (Glanville *et al.*, 2020). A yearlong trial based report documented by Villalba Primitz *et al.* (2021) stated the efficiency of microbe-based consortia on the degradation of hydrocarbons. The consortia, along with the microorganisms include an inorganic salt, granular fertilizer and a commercialized bioremediation product. Another study using the microbial consortium for the successful degradation of diesel hydrocarbons was carried out by Roslee *et al.* (2021). The authors also employed optimization strategies to predict the optimal degradation conditions for their formulated microbial consortia.

Cold arid environments on Earth are now more accessible than any time in past due to

cutting-edge tools and technologies. Hence, we can now gather excellent mineralogical, geochemical, and microbiological data (Antunes *et al.*, 2023). Metagenomics allows investigation of unculturable microbial communities, revolutionizing our understanding of microbial diversity. It not only identifies new genes with potential applications in biotechnology, agriculture, and medicine but also clarifies complex ecological relationships and sheds light on how microbial populations respond to environmental changes (Magnuson *et al.*, 2022). By encapsulating the genetic makeup of vast ecosystems, metagenomics enables us to explore the unexplored frontiers of microbial life and its significant effects on our planet. The Metagenome-Assembled Genome (MAG) analysis can also reveal the potential of arid microbiomes for heavy metal removal and detoxification. Additionally, certain MAGs encode characteristics like hemolysins, macroglobulins, and Tc-type toxin complexes, suggesting potential interactions with other species (Sipes *et al.*, 2021; Williams *et al.*, 2024). MAGs also contain uncommon genes responsible for cellulose breakdown, trehalose synthesis, thymine metabolism, and mevalonate biosynthesis. They play a pivotal role in adaptation to membrane stability and osmotic stress and are known to contain high-quality DNA, indicating long-term survival strategies (Sipes *et al.*, 2021). These informations can serve as a strong foundation for understanding the cycles of water and other elements essential for life, the effects of harsh environments on biodiversity and habitability, the limits of life, and the preservation and identification of biosignatures (Davila *et al.*, 2021; Magnuson *et al.*, 2022).

Conservation and Management

Conservation strategies and restoration efforts play a crucial role in mitigating the negative impacts of anthropogenic activities and promoting the resilience of microbial communities (Tewari and Kapoor, 2016; Sharma and Samant, 2019). Protected areas and conservation reserves can serve as havens for cold desert microflora, providing undisturbed habitats where natural processes can unfold. These areas play a critical role in safeguarding the unique biodiversity of cold deserts, including the intricate microbial communities that underpin ecosystem functioning (<https://>

whc.unesco.org/en/tentativelists/6055/; Sharma and Samant, 2019). Replanting native vegetation, implementing sustainable land management practices, and controlling invasive species help restore ecological balance and support the recovery of microbial diversity (Tewari and Kapoor, 2016). Soil stabilization measures, such as the use of bioengineering techniques and planting native vegetation with extensive root systems, can prevent erosion and enhance soil quality. Moreover, research and monitoring programs focused on understanding the ecology of cold desert microflora contribute valuable insights for effective conservation and management strategies (van Dorst *et al.*, 2017). Identifying key microbial species, understanding their roles in nutrient cycling, and assessing their responses to environmental changes are essential steps in designing conservation interventions that target the specific needs of cold desert ecosystems. Advances in molecular biology and sequencing technologies enable researchers to unravel the genetic diversity of microbial communities, providing a deeper understanding of their functional capabilities and adaptive mechanisms. In summary, the integration of scientific research, conservation efforts, and community engagement becomes imperative for ensuring the long-term health and sustainability of cold desert ecosystems and their microbial inhabitants.

Conclusion and Future perspective

The realm of cold desert microbial ecology faces both challenges and exciting opportunities for exploration. Recent studies employing advanced molecular techniques have expanded our understanding of microbial diversity, interactions, and responses to environmental changes in cold deserts. However, substantial research gaps persist, including limited knowledge of specific microbial functions, discovery and challenges of archaeobacteria, interactions with higher organisms, and the long-term impacts of climate change. Although, the use of advanced sequencing technologies have enabled researchers to analyze microbial communities at a finer taxonomic resolution, uncovering hidden biodiversity and potential keystone species critical for ecosystem stability; nevertheless, challenges persist, especially in deciphering the functional roles of these newly discovered microbes and understanding their contributions to ecosystem processes.

Furthermore, recent studies have started to unravel the intricate relationships within microbial communities and their influence on plant-microbe and animal-microbe interactions. For instance, investigations into mycorrhizal associations between cold-adapted fungi and plants have highlighted the importance of these symbiotic relationships in nutrient uptake and stress tolerance. Further exploration of these interactions is crucial for comprehending the ecological dynamics of cold deserts and designing effective conservation strategies. Additionally, the impact of climate change on cold desert microbial communities represents a critical area for future research. Latest studies have provided evidence of shifts in microbial community composition and activity in response to climate change-induced alterations in temperature and precipitation patterns. Understanding these changes is essential for predicting the resilience of cold desert ecosystems to ongoing climatic shifts and formulating strategies to mitigate potential consequences. Incorporating long-term monitoring studies and experimental manipulations can enhance our understanding of how cold desert microbes respond to climate change, facilitating the development of proactive conservation and management measures.

Conflict of interest

Authors declare no conflict of interest in this study.

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