

Editorial

# Safeguarding microbial biodiversity: microbial conservation specialist group within the species survival commission of the International Union for Conservation of Nature

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Microorganisms—including microscopic single-cell and multicellular life—form the biological foundation of life on Earth. They regulate biogeochemical cycles, control climate-relevant gas fluxes, and underpin the health of all multicellular organisms (1–4) (Fig. 1A and B). Microbial communities drive key functions such as carbon sequestration, nitrogen fixation, gas cycling, soil fertility, marine productivity, and host digestion and immunity, making them indispensable to ecosystems, economies, and public health (5) (Fig. 1). Despite their crucial roles, microbes and their impacts on visible life remain critically underrepresented in conservation science and policy (6). Global conservation frameworks, including the International Union for Conservation of Nature (IUCN) Red List of Threatened Species and the Convention on Biological Diversity (CBD), have focused overwhelmingly on visible macroscopic taxa, neglecting microbial diversity (except the recent inclusion of a fungal SSC) despite mounting evidence of its vulnerability (7–13) and importance for global conservation action (5, 14, 15). Similarly, major health frameworks such as One Health (16) have largely overlooked environmental microbial communities, especially those in soils and aquatic systems, despite their foundational importance for ecosystem stability and human well-being (17), Committee on Exploring Linkages (18). Furthermore, this knowledge gap poses a significant risk as the loss of microbial diversity may destabilize ecosystem functions and compromise the success of broader conservation strategies (7).

## The case for microbial conservation

Microbial ecosystems and individual taxa are increasingly imperiled by a range of anthropogenic pressures that disrupt their structure, function, and, in the case of host-associated taxa, intergenerational transmission. These losses threaten ecosystem stability, human health, food security, and the climate resilience of individual ecosystems and the planet. Given microbes' foundational roles in all life-supporting processes, the decline and/or disruption of microbiological communities may have as unpredictable and perilous consequences as macrobiological extinctions. Loss of certain microbial taxa could scale to community and food web disruptions and thereby potentially impact climate regulation, collapsing nutrient cycling and soil fertility, impairing essential ecosystem services, increasing the risk of disease outbreaks, and ultimately diminishing global biodiversity and evolutionary potential. Among the primary drivers of microbial richness decline are habitat destruction, climate change, pollution, and human-mediated homogenization of natural environments. We will briefly outline these threats here.

Processes causing large-scale habitat destruction include deforestation, agricultural intensification, glacial and permafrost melt, sea-ice melt, coral reef degradation, bottom

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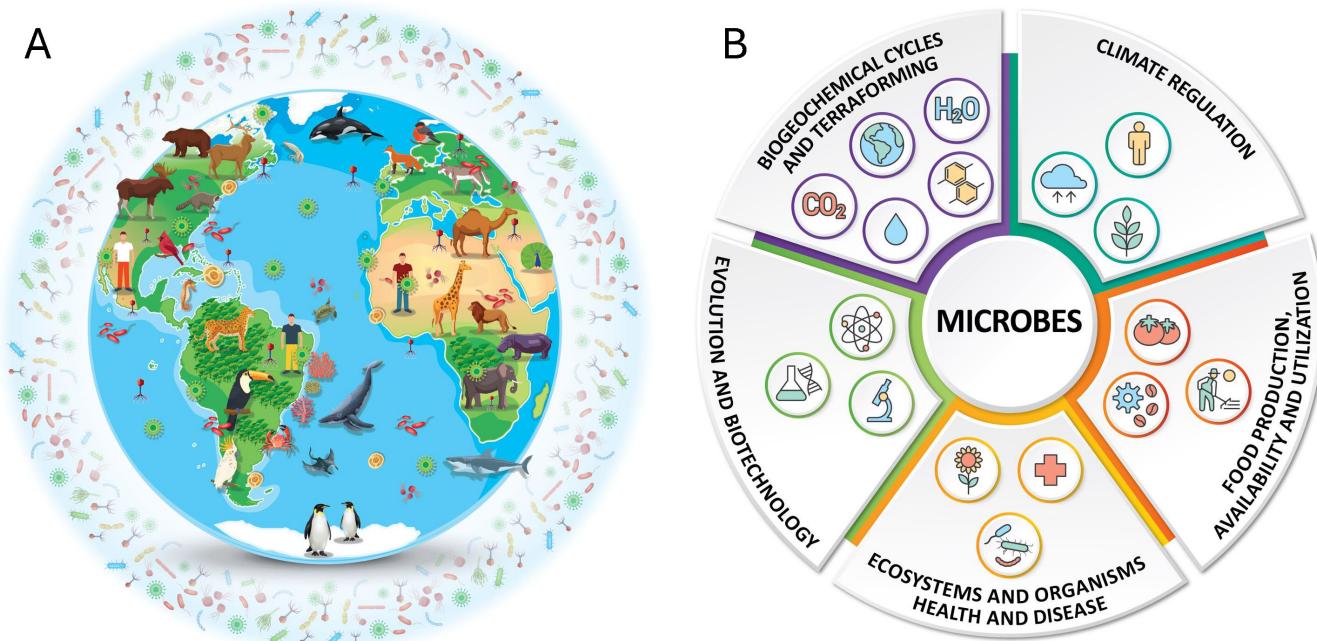
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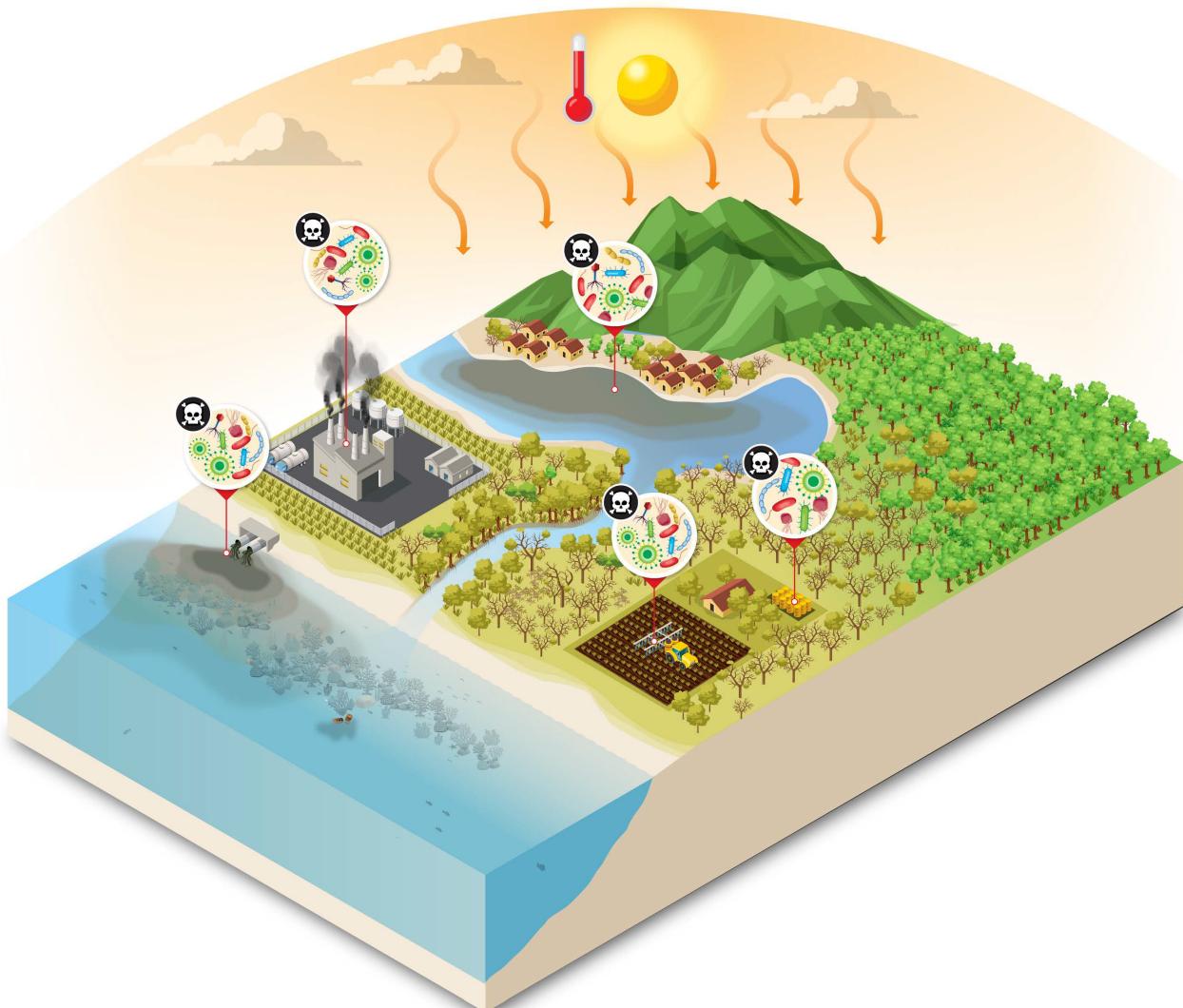
**FIG 1** We live in a microbial world. (A) Microbial distribution: microbes are ubiquitous, inhabiting every known ecosystem; from deep oceans, polar ice, and arid deserts to soils, freshwater, and the atmosphere, and forming intimate associations with all forms of life, including plants, animals, and humans—as well as among themselves. The figure illustrates the global distribution of microbial life across diverse environments and as symbionts. (B) The central role of microbes in planetary systems and human society. The ubiquitous distribution showed in panel A underscores the central importance of microbes in sustaining life on Earth and enabling future planetary habitability. They drive biogeochemical cycles and could be harnessed for terraforming; regulate climate through carbon sequestration, greenhouse gas production and consumption, and nutrient cycling; influence evolution and are engines of genetic innovation; and underpin biotechnology across health, industry, and environmental sectors. Microbes are essential for maintaining ecosystem and organism health, yet can also cause disease. They are critical to food production, availability, and utilization, from agriculture and aquaculture to fermentation and nutrient recycling. This interconnected network of microbial functions highlights their unparalleled importance in both natural processes and applied solutions for global challenges. Some of the vectors in panel A were designed by macrovector/Freepik.

trawling, and potentially also deep-sea mining (Fig. 2). These processes all alter microbial communities and potentially eliminate niche-specialist taxa. These disruptions impair ecological functions such as nutrient cycling, carbon sequestration, and host–microbe interactions that determine holobiont form, function, and variation. For example, the disruption of human ancestral habitat toward urbanized environments can lead to disruptions in holobiont compositions and increases in inflammation and chronic stress of hosts (19). Also, deep-sea mining endangers microbial assemblages responsible for metal cycling and primary productivity in hydrothermal vents (20, 21).

Climate change further destabilizes microbial communities by altering temperature, moisture, and pH regimes across diverse systems (22). Melting glaciers, permafrost, and sea ice threaten cold-adapted microbes evolved over millennia. In soils, warming reduces microbial carbon storage and increases greenhouse gas emissions (5, 23). Marine warming and acidification, in turn, disrupt coral microbiomes, accelerating reef decline (24–26).

Pollution from antibiotics, pesticides, heavy metals, and plastics disturbs microbial networks in environmental and holobiont contexts (27–29). Such exposure potentially eliminates beneficial microbes while selecting for resistant and pathogenic strains, thereby undermining ecosystem services and host immunity.

Human-mediated homogenization via urbanization, industrial food systems, and erosion of indigenous lifeways is also collapsing microbial diversity (27, 30, 31). The shift from traditional microbiome-rich environments to sanitized lifestyles hampers intergenerational transmission and biocultural heritage (32, 33). Studies have documented



**FIG 2** There is no conservation without microbial conservation: anthropogenic stressors, and loss of microbial diversity drive ecosystem degradation and pathogen proliferation across connected biomes. In absence of diversity and beneficial microbiota, terrestrial, coastal, and marine habitats are increasingly linked by the spread of harmful microorganisms fueled by pollution, habitat destruction, and climate change. Deforestation, agricultural runoff, chemical contamination, and industrial waste disrupt microbial community balance, leading to the replacement of beneficial microbes by pathogenic taxa. These pathogens circulate among ecosystems and hosts, exacerbating biodiversity loss, impairing organism health, and threatening ecosystem services and, ultimately, human health. Some of the figure vectors were designed by macrovector/Freepik.

dramatic losses of keystone microbial taxa in industrialized populations, with lasting consequences for immunity, metabolism, and neurological health (27, 34, 35).

While it is true that microbes have demonstrated extraordinary genetic resilience through Earth's mass extinction events, this perspective overlooks several critical points. First, the current loss of microbial diversity is occurring at an unprecedented rate and is largely anthropogenic—driven by industrialization, land-use change, climate warming, antibiotic overuse, and pollution. Unlike past extinctions caused by natural cataclysms in the current era of the Anthropocene, human activity is the principal force behind microbial decline. Second, while microbial communities are naturally dynamic and can adapt and reorganize, the rapid erosion of diversity weakens ecosystem resilience, making systems more vulnerable to perturbations and less able to recover from stress. Functional redundancy exists, but only up to a point—continued loss reduces the pool of traits available to support ecosystem functions, especially under changing

environmental conditions. Finally, the notion that technological substitutes can replace microbial ecosystem services underestimates the complexity and interdependence of microbial networks in biogeochemical cycles, human and animal health, and climate regulation. These services are not easily replicable, and assuming we can engineer our way out of biodiversity loss risks complacency in the face of potentially irreversible ecological consequences.

It would seem axiomatic that preserving microbial ecosystems is not merely academic but is instead a prerequisite for achieving global conservation and restoration aims such as to protect 30% of Earth's ecosystems by 2030. This is especially true for interactions between microbes and macrobes (e.g., animals and plants). Therefore, while we must push for microbial conservation, we can also improve global conservation efforts through integrating microbial knowledge into existing conservation strategies. For example, microbial restoration holds promise for ecosystem resilience: probiotics are deployed to reduce bleaching of coral reefs (11), soil microbiomes are central to regenerative agriculture (23), and microbiota interventions are tested for the recovery of amphibians, bats, and pollinators impacted by microbial dysbiosis (36), and also in improving human health. Including microbiology as a category of living systems can also significantly improve the success in strategies proposed to address the UN sustainability goals (5).

### The IUCN microbial conservation specialist group (MCSG)

In response to the growing recognition that microbial species and ecosystems are both foundational to life and increasingly imperiled, the IUCN Species Survival Commission (SSC) has formally established the MCSG, the first body within the IUCN dedicated to the stewardship of all microbial life forms. An existing fungal SSC has already led the charge by developing an IUCN red list with >1,000 fungal taxa. This group represents a critical expansion of the IUCN's mandate and technical competency, acknowledging that conservation cannot succeed without assessing and protecting the microbial communities that sustain biodiversity, ecosystem function, and human health. The MCSG has received funding from private foundations, Applied Microbiology International, and the International Society for Microbial Ecology to support the development of the following strategy over the next 18 months. The mission statement, strategic objectives, integration with other IUCN programs, and a call for engagement are mentioned as follows.

#### ***Mission statement***

To safeguard and foster microbial species and their function across Earth's ecosystems, recognizing microbes as the foundation of life and a cornerstone of planetary, microbial species, and human health.

#### ***Strategic objectives***

The MCSG aims to coordinate with all other relevant IUCN programs to fully integrate microbial perspectives into the IUCN Species Conservation Cycle through five core functions: Assessment, Planning, Action, Networking, and Communication & Policy:

1. **Assessment.** Microbial life has historically been excluded from conservation assessment frameworks due to taxonomic biases, challenges in taxonomy and in defining what constitutes a microbial species, its invisibility in ecosystems, the lack and complexity of baseline data for microbial communities, as well as of ecological concepts to measure the risk of loss. The MCSG will address this gap by pioneering tools and standards to evaluate the microbial conservation status:
  - Map microbial conservation hotspots and their threats, including unique and vulnerable microbial ecosystems such as Antarctic cryptoendoliths, hypersaline

mats, cryosphere, and animal- and plant-associated microbiomes, and define and identify endangered microbial populations (individual species) and communities (assemblages of different species), especially those most consequential for sustaining critical ecosystem services.

- Map the world's biobanks and culture collections and assess methods and technologies to advance baseline studies and time series of microbial communities, especially in undersampled areas, such as, for example, deep ocean, deserts, mountains, and aquifers.
  - Develop Red List-compatible assessment criteria for microbial communities, focusing on community integrity, functional collapse, and habitat specificity as well as vulnerability, and in certain circumstances on the extinction threat for keystone or specialist species.
  - Construct Community Integrity Indices to monitor the health and resilience of microbial ecosystems using metrics such as taxonomic and functional diversity, functional redundancy, and sensitivity to disturbance.
  - Map microbial conservation hotspots and their threats, including unique and vulnerable microbial ecosystems such as Antarctic cryptoendoliths, hypersaline mats, cryosphere, and animal- and plant-associated microbiomes, and define and identify endangered microbial populations (individual species) and communities (assemblages of different species), especially those most consequential for sustaining critical ecosystem services.
2. Planning. Robust microbial conservation requires actionable guidance rooted in both ecological science and practical implementation.
- Create microbial conservation planning templates including costing tools for *in situ* and *ex situ* interventions, from habitat restoration and rewilding to microbiome and species banking.
  - Co-develop risk–benefit economic frameworks for microbial interventions, including the use of probiotics, engineered microbes, and transplants in conservation programs. These frameworks should include holistic assessments of sustainability, feasibility, and potential unintended consequences, ensuring effective deployment that is aligned with safety, efficacy, and local context. It will be important to include environmental impact assessments, adaptive management frameworks, risk–benefit analyses, and life cycle assessments. Similar activities accounting for microbiome modifications could ensure actions are safe, effective, and context-appropriate. This will facilitate the development of microbial management recommendations for inclusion in protected area planning, especially where microbial ecosystems underpin host species viability and ecological resilience.
  - Co-develop ethical frameworks to coordinate the needs and priorities of multiple communities and stakeholders in conservation efforts, which can serve as templates for creating these collaborative networks, gathering their feedback, stimulating discussion and cooperation within the network, and creating an action plan which adheres to the best practices, similar to the ethos of codes of conduct for scientific and medical research.
3. Action. The MCG will serve as a catalyst for on-the-ground conservation and restoration efforts where microbial ecosystems are central to success.
- Develop pilot programs, coordinated with relevant existing IUCN efforts, that use microbial solutions to restore degraded ecosystems and threatened spe-

cies, such as managing microbiomes to protect and restore coral reefs, reduce methane emissions while maintaining livestock productivity, deploying microbes to improve plant resilience to drought and heat, bioremediating polluted soils and waters, and stabilizing carbon and other soil health metrics in degraded lands.

- Analogous to successful global seed vaults (e.g., the Svalbard Global Seed Vault) and wildlife genetic repositories (such as the San Diego Zoo Wildlife Alliance's Frozen Zoo), microbial conservation efforts must align and accelerate activities that safeguard microbial diversity for future resilience and restoration. This includes the protection of natural microbial habitats, the systematic archiving of environmental and host-associated microbiome samples (especially those associated with threatened macroorganisms), and the expansion and integration of microbial biobanks and culture collections. These include leading facilities such as the Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, American Type Culture Collection, the Japan Collection of Microorganisms, the China General Microbiological Culture Collection Center, and the Belgian Coordinated Collections of Microorganisms. Complementing these, newer initiatives such as the Microbiota Vault (37) aim to store uncultured and cryopreserved microbiota from diverse populations and environments, focusing on preserving microbial functions and community structures. By coordinating across these repositories and linking them with global conservation goals, the microbial conservation community can build a robust infrastructure for the long-term stewardship of microbial life.
  - Build robust funding pipelines through philanthropy, public–private partnerships, and multilateral mechanisms, including the Global Environment Facility, the United Nations Soil Health Initiative, and bilateral conservation programs, to catalyze large-scale investment in microbial conservation and restoration as critical pillars of planetary, microbial species, and human health. Promote equity and benefit-sharing in accordance with the UN CBD and its Nagoya Protocol in recognition of countries' sovereign rights over their biodiversity as well as other UN instruments such as the Biodiversity Beyond National Jurisdiction and World Health Organization's Pandemic Agreement to ensure that microbial resources everywhere are accessed and used responsibly. This includes working with provider countries and indigenous communities and traditional knowledge holders to understand research priorities, guide methodological approaches, and shape the expected benefits of the work being returned to providers. This includes obtaining free, prior, and informed consent under mutually agreed terms in an effort to increase the diversity of sources and environments for microbial biobanking (human populations, traditional foods, under-represented environments, etc.). Work with Indigenous peoples and local communities includes respecting the right of peoples *not* to share microbial communities.
4. Networking. Microbial conservation must be a globally inclusive movement, rooted in interdisciplinary collaboration.
- Engage a diverse, global membership, with active recruitment across all IUCN Commissions and regions and strong representation from low- and middle-income countries, where many unique microbial ecosystems and indigenous and traditional stewardship systems reside.
  - Establish partnerships with professional societies (e.g., Applied Microbiology International, International Society for Microbial Ecology, American Society for Microbiology, and the International Union of Microbiological Societies), microbial biobank networks, and indigenous knowledge holders to coproduce knowledge and guide community-led conservation.

- Facilitate collaborations with other Conservation Specialist Groups of the IUCN, especially where microbes intersect with existing priorities—such as wildlife health, soil biodiversity, freshwater systems, and invasive species.
  - Provide expertise to policy frameworks addressing microbial biodiversity value, such as the new Biodiversity Beyond National Jurisdiction agreement, which will likely enter into force in 2026 and the further implementation of the Kunming-Montreal Global Biodiversity Framework (KMGBF).
5. **Communication and Policy.** Central to the MCSG's mission is the imperative to change the narrative and actions around microbial life, from invisible, unvalued, and irrelevant to indispensable.
- Launch the "Invisible but Indispensable" and "Tiny but Mighty" campaign, targeting conservation audiences, policymakers, and the general public to build awareness of microbial conservation imperatives.
  - Develop policy briefs and white papers aligned with major global frameworks, including the CBD, KMGBF, Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, and One Health initiatives.
  - Ensure microbial representation at international forums, including the CBD, UNFCCC COP, IUCN World Conservation Congress, High Seas Biodiversity Beyond National Jurisdiction negotiations, and regional biodiversity summits.
  - Facilitate the expansion of microbial discovery programs in undersampled regions, as well as on developing standards for monitoring microbial biodiversity in the environmental context (e.g., metagenomic/eDNA surveys).

Together, these objectives provide a roadmap for incorporating microbial life into biodiversity conservation. By protecting microbial communities, we secure the foundations of terrestrial and aquatic ecosystems, enable successful restoration, and safeguard the symbiotic microbiota that sustain plant, animal, and human life. The MCSG calls on the global conservation community to recognize that the microbial world is not a footnote; it is the foundation.

### Integration with existing structures of the IUCN species survival commission

The MCSG will adopt a hub-and-spoke model, maintaining liaison officers within other SSC groups (e.g. Climate Change, Wildlife Health, and Coral Specialist Group). This will allow for the integration of microbial dimensions into broader conservation planning, ecosystem health assessments, and restoration monitoring. Moreover, the MCSG will work with Red List Authorities and the IUCN Red List of Ecosystems to adapt assessment criteria appropriate for microbial communities and functional ecosystems. We will also partner with foundations and NGOs already addressing threats to microbial biodiversity. In parallel, we will engage with IUCN's World Commission on Environmental Law to explore the legal dimensions of microbial conservation, linking with existing initiatives such as the Rights of Nature and emerging efforts to recognize the Rights of Microbes (<https://repository.graduateinstitute.ch/record/320234?v=pdf>).

### Conclusion and call for participation

The creation of the IUCN MCSG represents a necessary and overdue step in global conservation. Without microbes, no conservation goal, from reforestation to species survival, can be sustainably achieved. Recognizing microbial diversity as an integral part of biodiversity is not only scientifically valid but practically essential for securing the ecological, health, and economic futures of our planet. We welcome microbiologists, ecologists, conservationists, healthcare professionals, citizen scientists, indigenous

communities, and policy stakeholders to support and collaborate with us in this transformative mission.

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## REFERENCES

1. Cavicchioli R, Ripple WJ, Timmis KN, Azam F, Bakken LR, Baylis M, Behrenfeld MJ, Boetius A, Boyd PW, Classen AT, et al. 2019. Scientists' warning to humanity: microorganisms and climate change. *Nat Rev Microbiol* 17:569–586. <https://doi.org/10.1038/s41579-019-0222-5>
2. Lennon JT, Abramoff RZ, Allison SD, Burkhardt RM, DeAngelis KM, Dunne JP, Frey SD, Friedlingstein P, Hawkes CV, Hungate BA, Khurana S, Kivlin SN, Levine NM, Manzoni S, Martiny AC, Martiny JBH, Nguyen NK, Rawat M, Talmey D, Todd-Brown K, Vogt M, Wieder WR, Zekem EJ. 2024. Priorities, opportunities, and challenges for integrating microorganisms into Earth system models for climate change prediction. *mBio* 15:e00455-24. <https://doi.org/10.1128/mbio.00455-24>
3. Lennon JT, Frost SDW, Nguyen NK, Peralta AL, Place AR, Treseder KK. 2023. Microbiology and climate change: a transdisciplinary imperative. *mBio* 14:e03335-22. <https://doi.org/10.1128/mbio.03335-22>
4. Peixoto R, Voolstra CR, Stein LY, Hugenholtz P, Salles JF, Amin SA, Häggblom M, Gregory A, Makhalaanyane TP, Wang F, Agbodjato NA, Wang Y, Jiao N, Lennon JT, Ventosa A, Bavoil PM, Miller V, Gilbert JA. 2024. Microbial solutions must be deployed against climate catastrophe. *Sustain Agric* 2:qvae029. <https://doi.org/10.1038/s44264-024-00033-1>
5. Crowther TW, Rappuoli R, Corinaldesi C, Danovaro R, Donohue TJ, Huisman J, Stein LY, Timmis JK, Timmis K, Anderson MZ, et al. 2024. Scientists' call to action: microbes, planetary health, and the sustainable development goals. *Cell* 187:5195–5216. <https://doi.org/10.1016/j.cell.2024.07.051>
6. Redford KH. 2023. Extending conservation to include Earth's microbiome. *Conserv Biol* 37:e14088. <https://doi.org/10.1111/cobi.14088>
7. Redford KH, Segre JA, Salafsky N, del Rio CM, McAloose D. 2012. Conservation and the microbiome. *Conserv Biol* 37:195–197. <https://doi.org/10.1111/cobi.14088>
8. Averill C, Anthony MA, Baldrian P, Finkbeiner F, van den Hoogen J, Kiers T, Kohout P, Hirt E, Smith GR, Crowther TW. 2022. Defending earth's terrestrial microbiome. *Nat Microbiol* 7:1717–1725. <https://doi.org/10.1038/s41564-022-01228-3>
9. Battin TJ, van Wijngaarden A, Sattler B, Anesio AM, Cook J, Huss M, Edwards A. 2025. Glaciers are not just blocks of ice - plans to save them mustn't overlook their hidden life. *Nature* 639:861–863. <https://doi.org/10.1038/d41586-025-00897-4>
10. Chiarello M, Auguet J-C, Graham NAJ, Claverie T, Sucré E, Bouvier C, Rieuvilleeneuve F, Restrepo-Ortiz CX, Bettarel Y, Villéger S, Bouvier T. 2020. Exceptional but vulnerable microbial diversity in coral reef animal surface microbiomes. *Proc Biol Sci* 287:20200642. <https://doi.org/10.1093/rspb.2020.0642>
11. Peixoto RS, Voolstra CR, Baums IB, Camp EF, Guest J, Harrison PL, Montoya-Maya PH, Pollock FJ, Smith DJ, Wangpraseurt D, Banaszak AT, Chui APY, Shah N, Moore T, Fabrício KE, Vardi T, Suggett DJ. 2024. The critical role of coral reef restoration in a changing world. *Nat Clim Chang* 14:1219–1222. <https://doi.org/10.1038/s41558-024-02202-z>
12. Sonnenburg JL, Sonnenburg ED. 2019b. Vulnerability of the industrialized microbiota. *Science* 366:eaaw9255. <https://doi.org/10.1126/science.aaw9255>
13. Zucconi L, Fierro-Vásquez N, Antunes A, Bendia AG, Lavin P, González-Aravena M, Sani RK, Banerjee A. 2025. Advocating microbial diversity conservation in Antarctica. *NPJ Biodivers* 4:5. <https://doi.org/10.1038/s44185-025-00076-8>
14. Trevelline BK, Fontaine SS, Hartup BK, Kohl KD. 2019. Conservation biology needs a microbial renaissance: a call for the consideration of host-associated microbiota in wildlife management practices. *Proc Biol Sci* 286:20182448. <https://doi.org/10.1093/rspb.2018.2448>
15. West AG, Waite DW, Deines P, Bourne DG, Digby A, McKenzie VJ, Taylor MW. 2019. The microbiome in threatened species conservation. *Biol Conserv* 229:85–98. <https://doi.org/10.1016/j.biocon.2018.11.016>

16. FAO, UNEP, WHO, World Organization for Animal Health (WOAH) (founded as OIE). 2022. One Health joint plan of action, 2022–2026. FAO, UNEP, WHO, WOAH
17. Singh BK, Yan Z-Z, Whittaker M, Vargas R, Abdelfattah A. 2023. Soil microbiomes must be explicitly included in One Health policy. *Nat Microbiol* 8:1367–1372. <https://doi.org/10.1038/s41564-023-01386-y>
18. Committee on Exploring Linkages Between Soil Health and Human Health, Board on Agriculture and Natural Resources, Food and Nutrition Board, Division on Earth and Life Studies, Health and Medicine Division, National Academies of Sciences, Engineering, and Medicine. 2024. Exploring linkages between soil health and human health. National Academies Press, Washington, DC.
19. Flandroy L, Poutahidis T, Berg G, Clarke G, Dao M-C, Decaestecker E, Furman E, Haahtela T, Massart S, Plovier H, Sanz Y, Rook G. 2018. The impact of human activities and lifestyles on the interlinked microbiota and health of humans and of ecosystems. *Sci Total Environ* 627:1018–1038. <https://doi.org/10.1016/j.scitotenv.2018.01.288>
20. Orcutt BN, Bradley JA, Brazelton WJ, Estes ER, Goordial JM, Huber JA, Jones RM, Mahmoudi N, Marlow JJ, Murdock S, Pachiadaki M. 2020. Impacts of deep - sea mining on microbial ecosystem services. *Limnol Oceanogr* 65:1489–1510. <https://doi.org/10.1002/lo.11402>
21. Vonnahme TR, Molari M, Janssen F, Wenzhöfer F, Haeckel M, Titschack J, Boetius A. 2020. Effects of a deep-sea mining experiment on seafloor microbial communities and functions after 26 years. *Sci Adv* 6:eaaz5922. <https://doi.org/10.1126/sciadv.aaz5922>
22. Jansson JK, Hofmockel KS. 2020. Soil microbiomes and climate change. *Nat Rev Microbiol* 18:35–46. <https://doi.org/10.1038/s41579-019-0265-7>
23. Beattie GA, Edlund A, Esiobu N, Gilbert J, Nicolaisen MH, Jansson JK, Jensen P, Keiluweit M, Lennon JT, Martiny J, Minnis VR, Newman D, Peixoto R, Schadt C, van der Meer JR. 2025. Soil microbiome interventions for carbon sequestration and climate mitigation. *mSystems* 10:e01129-24. <https://doi.org/10.1128/msystems.01129-24>
24. Fan L, Liu M, Simister R, Webster NS, Thomas T. 2013. Marine microbial symbiosis heats up: the phylogenetic and functional response of a sponge holobiont to thermal stress. *ISME J* 7:991–1002. <https://doi.org/10.1038/ismej.2012.165>
25. Peixoto RS, Voolstra CR. 2023. The baseline is already shifted: marine microbiome restoration and rehabilitation as essential tools to mitigate ecosystem decline. *Front Mar Sci* 10. <https://doi.org/10.3389/fmars.2023.1218531>
26. Pita L, Rix L, Slaby BM, Franke A, Hentschel U. 2018. The sponge holobiont in a changing ocean: from microbes to ecosystems. *Microbiome* 6:46. <https://doi.org/10.1186/s40168-018-0428-1>
27. Gilbert JA, Hartmann EM. 2024. The indoors microbiome and human health. *Nat Rev Microbiol* 22:742–755. <https://doi.org/10.1038/s41579-024-01077-3>
28. Gomes IB, Maillard J-Y, Simões LC, Simões M. 2020. Emerging contaminants affect the microbiome of water systems—strategies for their mitigation. *NPJ Clean Water* 3:1–11. <https://doi.org/10.1038/s41545-020-00086-y>
29. Lindell AE, Zimmermann-Kogadeeva M, Patil KR. 2022. Multimodal interactions of drugs, natural compounds and pollutants with the gut microbiota. *Nat Rev Microbiol* 20:431–443. <https://doi.org/10.1038/s41579-022-00681-5>
30. McCall L-I, Callewaert C, Zhu Q, Song SJ, Bouslimani A, Minich JJ, Ernst M, Ruiz-Calderon JF, Cavallini H, Pereira HS, Novoselac A, Hernandez J, Rios R, Branch OH, Blaser MJ, Paulino LC, Dorrestein PC, Knight R, Dominguez-Bello MG. 2020. Home chemical and microbial transitions across urbanization. *Nat Microbiol* 5:108–115. <https://doi.org/10.1038/s41564-019-0593-4>
31. Vinogradova E, Mukhanbetzhanov N, Nurgazihev M, Jarmukhanov Z, Aipova R, Sailybayeva A, Bekbosynova M, Kozhakhmetov S, Kushugulova A. 2024. Impact of urbanization on gut microbiome mosaics across geographic and dietary contexts. *mSystems* 9:e00585-24. <https://doi.org/10.1128/msystems.00585-24>
32. Ecklu-Mensah G, Choo-Kang C, Maseng MG, Donato S, Bovet P, Viswanathan B, Bedu-Addo K, Plange-Rhule J, Oti Boateng P, Forrester TE, Williams M, Lambert EV, Rae D, Sinyanya N, Luke A, Layden BT, O'Keefe S, Gilbert JA, Dugas LR. 2023. Gut microbiota and fecal short chain fatty acids differ with adiposity and country of origin: the METS-microbiome study. *Nat Commun* 14:5160. <https://doi.org/10.1038/s41467-023-40874-x>
33. Ramaboli MC, Ocvirk S, Khan Mirzaei M, Eberhart BL, Valdivia-Garcia M, Metwaly A, Neuhaus K, Barker G, Ru J, Nesengani LT, et al. 2024. Diet changes due to urbanization in South Africa are linked to microbiome and metabolome signatures of westernization and colorectal cancer. *Nat Commun* 15:3379. <https://doi.org/10.1038/s41467-024-46265-0>
34. Sonnenburg ED, Sonnenburg JL. 2019a. The ancestral and industrialized gut microbiota and implications for human health. *Nat Rev Microbiol* 17:383–390. <https://doi.org/10.1038/s41579-019-0191-8>
35. Zuo T, Kamm MA, Colombe J-F, Ng SC. 2018. Urbanization and the gut microbiota in health and inflammatory bowel disease. *Nat Rev Gastroenterol Hepatol* 15:440–452. <https://doi.org/10.1038/s41575-018-0003-z>
36. Peixoto RS, Voolstra CR, Sweet M, Duarte CM, Carvalho S, Villela H, Lunshof JE, Gram L, Woodhams DC, Walter J, Roik A, Hentschel U, Thurber RV, Daisley B, Ushijima B, Daffonchio D, Costa R, Keller-Costa T, Bowman JS, Rosado AS, Reid G, Mason CE, Walke JB, Thomas T, Berg G. 2022. Harnessing the microbiome to prevent global biodiversity loss. *Nat Microbiol* 7:1726–1735. <https://doi.org/10.1038/s41564-022-01173-1>
37. Dominguez-Bello MG, Steiger D, Fankhauser M, Egli A, Vonaesch P, Bokulich NA, Lavrinenko A, Hoffmann C, Zimmermann P, Muhammed A, Sayasone S, Larbi A, Padonou SW, Zinsstag J, Tschopp R, Santivarangkna C, Albertos Torres D, Li YY, Benvenega V, Teo Y, Houngbédji M, Kwarteng A, Knight R, Gilbert JA, Blaser MJ. 2025. The microbiota vault initiative: safeguarding Earth's microbial heritage for future generations. *Nat Commun* 16:5373. <https://doi.org/10.1038/s41467-025-61008-5>