nature communications

Perspective

https://doi.org/10.1038/s41467-025-62176-0

Aligning global mercury mitigation with climate action

Received: 13 April 2025

Accepted: 14 July 2025

Published online: 28 September 2025

Check for updates

Chengjun Li[1], Mengjie Wu[2], Wenli Tang[2], Ben Yu[3], Alfonso Saiz-Lopez[4], Alexandre Poulain[5], Michael S. Bank[6,7], Qinghua Zhou[2], Paul L. E. Bodelier[8], Zhen Yan[9], Beat Frey[10], Haiyan Hu[11], Jiaxing Chen[12], Yuelu Jiang[13] & Huan Zhong[2]

Environmental mercury (Hg) pollution affects microbial community structure and functions. Yet, whether and how this influence cascades through microbe-mediated cycling of major greenhouse gases (GHGs) remains poorly understood. This *Perspective* synthesizes emerging evidence on the Hg-microbe-GHG nexus, exploring the possibility that global Hg emission reductions, while critical for human and planetary health, may cause alterations to microbe-mediated GHG fluxes. Significant knowledge gaps persist, however, regarding the Hg-microbe-GHG nexus, particularly concerning the magnitude and direction of the nexus's net impact on climate and global environmental change. To bridge these gaps, we propose a three-step roadmap aimed at disentangling the potential impacts of global Hg emission mitigation strategies on microbial communities, associated GHG emissions, and subsequent climate change. Collectively, these joint efforts from scientists, industry, community stakeholders, and policymakers are critical to harmonizing global Hg mitigation efforts with climate action and to ensuring a sustainable future for Earth systems and their inhabitants.

The Earth's biogeochemical element cycles are complex and intricately interconnected[1]. Changes in one cycle, due to natural processes or human activities, can significantly impact others. This is the case for the cascading effects of altered carbon emissions on global mercury (Hg) cycling dynamics. Specifically, escalating anthropogenic activities —including deforestation and fossil fuel combustion—pump enormous amounts of greenhouse gases (GHGs) into the atmosphere, accelerating global warming and associated climatic shifts[2,3]. These changes subsequently drive large-scale environmental transformations such as biome shifts, permafrost thaw, and ocean stratification[2–4]. Such climate-driven changes can directly influence Hg cycling, e.g., accelerating the release of legacy Hg from thawing permafrost[5] and disrupting Hg accumulation in marine sediments through intensified ocean stratification[4]. Critically, these changes can also indirectly

[1]Nanjing Institute of Environmental Sciences, Ministry of Ecology and Environment, Nanjing, China. [2]State Key Laboratory of Water Pollution Control and Green Resource Recycling, School of Environment, Nanjing University, Nanjing, China. [3]National Research Center for Environmental Analysis and Measurement, Beijing, China. [4]Department of Atmospheric Chemistry and Climate, Institute of Physical Chemistry Blas Cabrera, Spanish National Research Council (CSIC), Madrid, Spain. [5]Department of Biology, University of Ottawa, 30 Marie Curie, Ottawa, ON, Canada. [6]Institute of Marine Research, Bergen, Norway. [7]University of Massachusetts Amherst, Amherst, MA, USA. [8]Department of Microbial Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Droevendaalsesteeg 10, Wageningen, The Netherlands. [9]Shandong Key Laboratory of Water Pollution Control and Resource Reuse, School of Environmental Science and Engineering, Shandong University, Qingdao, China. [10]Forest Soils and Biogeochemistry, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Zürcherstrasse 111, Birmensdorf, Switzerland. [11]State Key Laboratory of Environmental Geochemistry, Institute of Geochemistry, Chinese Academy of Sciences, Guiyang, China. [12]Institute of Environmental Research at Greater Bay Area, Guangzhou University, Guangzhou, China. [13]Technology Innovation Center for Marine Ecology and Human Factor Assessment of Natural Resources Ministry, Tsinghua Shenzhen International Graduate School, Tsinghua University, Shenzhen, China. e-mail: zhonghuan@nju.edu.cn

reshape Hg biogeochemistry by exerting impacts on microbes[6]. For instance, warmer temperatures and associated shifts in hydrology enhance microbial methylation, elevating concentrations of neurotoxic methylmercury (MeHg) in terrestrial and aquatic food webs[7,8]. This climate-microbe-Hg nexus amplifies exposure risks to wildlife and human health, undermining the effectiveness of global Hg mitigation efforts under the Minamata Convention (MC), which aims to reduce Hg pollution and exposure but now faces compounding pressures from rapid, global environmental change processes[9,10].

Growing evidence suggests a feedback process in which Hg contamination may affect GHG dynamics by altering microbial GHG metabolism[11]. Microbes serve as fundamental regulators of the global carbon (C) and nitrogen (N) cycles[12], driving GHG fluxes through the production and consumption of major GHGs—including carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O) (see details in Box 1). Key functional groups include decomposers (e.g., *Planctomycetota*[13] and *Actinomycetota*[14]), CH_4-producing methanogens (e.g., *Methanobacteria*[15]), CH_4-consuming methanotrophs (e.g., *Verrucomicrobiota*[16]), nitrifiers (e.g., ammonia-oxidizing bacteria[17]), and denitrifiers (e.g., *Pseudomonadota*[18]). However, Hg contamination elicits diverse, ecosystem-specific microbial responses that interfere with GHG-related microbial abundance or activities, potentially reconfiguring global GHG dynamics. For example, in forested ecosystems, Hg exposure reduces soil microbial diversity and activity[19], decreasing bacterial basal respiration by 11%–64% and compromising bacterial community structural integrity by 2%–3%[20]. Similarly, in paddy soils, Hg suppresses key microbial phyla such as *Planctomycetota and Actinomycetota*[21]—critical players in C and N cycling[13,14]—leading to a substantial 65.6% reduction in ecosystem multifunctionality[21]. Conversely, in pasture fields, long-term Hg exposure increases the abundance of *Verrucomicrobia* and fungi[22], potentially accelerating organic matter decomposition and CO_2 release[16,22,23].

Collectively, these findings, while potentially compounded by climate-mediated abiotic processes such as temperature-driven Hg remobilization[8] and temperature-disrupted Hg sedimentation[4], suggest that fluctuations in Hg inputs into ecosystems may impact microbial-mediated GHG emissions and cycling dynamics. However, the effects of Hg on microbial communities are complex and context-dependent, varying from negative to neutral or even positive (Table 1). This complexity could be further complicated by the effectiveness of global Hg mitigation efforts. For instance, while MC-aligned mitigation measures in a coal-heavy energy scenario offer promising regional Hg emission reductions, a global transition away from coal energy would ultimately yield a more substantial and widespread decrease in Hg emissions[24–26]. The uncertainties in both microbial response to Hg and the projected outcomes of mitigation strategies complicate our understanding and the predictability of climate-related consequences associated with global Hg mitigation efforts under the MC. Therefore, further research is essential to elucidate the complex Hg-microbe-GHG interactions across diverse environments. This will clarify whether ongoing Hg mitigation measures would cascade through GHG-regulating microbes, ultimately impacting net GHG emissions at local, regional, and global scales, particularly under climate conditions concurrently altered by persistent GHG emissions.

In this *Perspective*, we synthesize recent diverse findings to (1) highlight the urgency of elucidating the complex Hg-microbe-GHG

BOX 1

Microbes as fundamental GHG regulators

CO_2 and CH_4 regulators

- **Decomposers** (e.g., *Planctomycetota*[13], *Actinomycetota*[14], fungi[23]): These diverse microbial groups are crucial for the decomposition of organic carbon, acting as major producers of CO_2[83].
  - *CO_2 byproduct*: Through aerobic and anaerobic respiration, they break down complex organic matter (e.g., dead plant and animal tissues) into simpler compounds, releasing CO_2 back into the atmosphere. This process is fundamental for nutrient cycling and the long-term sequestration or release of carbon in soils and sediments[83].
- **Methanogens** (e.g., *Methanobacteria*[15]): These anaerobic archaea thrive in oxygen-deprived environments such as rice paddies[33] and are key players in the production of CH_4.
  - *CH_4 byproduct and CO_2 consumption:* Methanogens produce CH_4 as a metabolic byproduct through the reduction of CO_2 with hydrogen (hydrogenotrophic methanogenesis) or the cleavage of acetate (acetoclastic methanogenesis), the terminal step in the anaerobic decomposition of organic matter[84].
- **Methanotrophs** (e.g., *Verrucomicrobiota*[16]): In contrast to methanogens, methanotrophic bacteria and archaea act as natural CH_4 sinks.
  - *CH_4 consumption and CO_2 byproduct*: Methanotrophic bacteria consume CH_4 with CO_2 as the byproduct, in aerobic or anaerobic environments where they can utilize CH_4 as their sole source of carbon and energy, effectively mitigating CH_4 emissions from various sources before CH_4 can reach the atmosphere[85].

N_2O regulators

- **Nitrifiers** (e.g., ammonia-oxidizing bacteria[17]): Nitrifying bacteria and archaea are responsible for nitrification, a two-step process where ammonia (NH_3) is oxidized to nitrite (NO_2^-) by ammonia-oxidizing bacteria and archaea and then to nitrate (NO_3^-) by nitrite-oxidizing bacteria[86]. However, *Nitrospira* species have recently been discovered to be capable of complete oxidation of NH_3 to NO_3^- in one organism (i.e., comammox)[86].
  - *N_2O byproduct*: During NH_3 oxidation, especially under suboptimal oxygen conditions or high-nitrogen concentrations (e.g., fertilized agricultural soils), nitrifiers can produce N_2O as a byproduct[17]. Under certain low-nitrogen conditions, comammox organisms may outcompete ammonia-oxidizing bacteria and archaea[87], altering N_2O emissions due to different metabolic pathways and efficiencies.
- **Denitrifiers** (e.g., *Pseudomonadota*[18]): Denitrifying bacteria play a critical role in returning nitrogen gas (N_2) to the atmosphere by converting NO_3^- or NO_2^- under anaerobic conditions through a series of reductive steps, completing the N cycle.
  - *N_2O intermediate and consumption*: Nitrous oxide (N_2O) is often produced as an intermediate during this process ($NO_3^- \rightarrow NO_2^- \rightarrow NO \rightarrow N_2O \rightarrow N_2$)[88]. However, many denitrifiers, i.e., NO_2^- respiring bacteria with a complete denitrification pathway and/or stronger expression of the enzyme N_2O reductase (NosZ), such as *Cloacibacterium* sp. CB-01[88], can also consume N_2O and reduce it to N_2, thus serving as a natural sink for this GHG. The balance between N_2O production and consumption by denitrifiers is crucial for regulating atmospheric N_2O levels.

Table 1 | Hg impact on microbes and associated carbon and nitrogen cycling

Cycle	Process	Ecosystem	Microbe	Hg Concentration	Hg Impact	Ref
Carbon cycle	Methanogenesis	Rice paddy	*Methanobacteria*	0.25–990	Increased CH_4 emissions	33
	Organic matter decomposition	Pasture field	*Verrucomicrobiota;* Fungi	0.25–36.1	Increased CO_2 release due to Hg-tolerant decomposers	22
	Syntrophic interactions	Rice paddy*	Sulfate-reducing bacteria; *Geobacteraceae;* Methanogens	5–50	Altered syntropy, with an increased abundance of methanogens and enhanced CH_4 emissions	80
Nitrogen cycle	Nitrification	Vegetable field*	Ammonia-oxidizing bacteria	0–30	Significant reduction in abundance and nitrification rates	36
		Rice paddy	*Nitrospirota*	1.11–29.07	Reduced NO_3^- production due to Hg-induced abundance decline	18
		Rice paddy and upland	*Nitrospirota*	0.27–52.4	Relative abundance decreased with elevated MeHg concentrations	81
	Denitrification	Wheat-maize field*	Denitrifiers	0–100	Transient spikes in denitrification genes, *nirS* and *nosZ*	37
		Rice paddy	*Gemmatimonadota*	4.86–28	Increased abundance under Hg stress, altering nitrogen retention	18
Cross-cycle feedback	Microbial stress adaptation	Cropland	General microbial community	2.40–420.7	Increased abundance and diversity after Hg exposure	82
		Rice paddy	*Pseudomonadota*	1.11–29.07	Reduced microbial diversity at high Hg concentrations, notably *Pseudomonadota* for carbon/nitrogen cycling	18
		Rice paddy and upland	*Firmicutes; Bacteroidota*	0.27–52.4	Positive correlation with Hg; shifts in decomposition and nitrogen cycling	81
	Functional diversity loss	Forest*	General microbial community	0.03-32	High Hg basal respiration decreased; structural degradation	20
		Rice paddy	General microbial community	0.27–588	Reduced microbial diversity under Hg stress, e.g., *Planctomycetota* and *Actinomycetota*	21
	Community resilience	Tropical forest	General microbial community	3.20–32	Reduced microbial diversity under high Hg stress	19
		Agricultural floodplain	General microbial community	0.25–36	Increased basal respiration and nitrification rate at high Hg concentrations; carbon and nitrogen cycling were slightly hampered	47

"*" indicates spiked experiments. All Latin names listed above are updated following recent bacterial taxonomy revisions and thus may be slightly different from what they are in the original articles. Concentration unit: μg/g dry wt. in soils or sediments.

https://doi.org/10.1038/s41467-025-62176-0

nexus, (2) reveal critical knowledge gaps in identifying nexus hotspots and substantial uncertainties regarding the magnitude and direction of potential climate impacts, and (3) present a practical, three-step roadmap to navigate the complexities of global Hg mitigation strategies and their cascading effects on microbial communities, GHG emissions, and climate feedback loops. Importantly, the synthesis presented here adopts a baseline scenario of continuing anthropogenic Hg and GHG emissions. We recognize this baseline represents a normative choice reflecting current trajectories, rather than a steady-state natural system. The ongoing inputs of both Hg and GHGs themselves actively shape microbial communities and biogeochemical processes. Alternative baselines (e.g., stabilized or reduced emissions) would yield different perspectives on the interactions and potential impacts of mitigation efforts. This framing choice is critical for interpreting the dynamics discussed below and their policy implications. By doing so, we aim to increase awareness within the scientific community about the significance of the Hg-microbe-GHG nexus and to catalyze collaboration among industry, scientists, civil society, and policymakers. Such coordinated efforts are essential to foster synergies between global Hg mitigation and climate action, ensuring that progress in one does not inadvertently undermine the other.

A need to explore the microbe-mediated Hg-GHG nexus

Ongoing global Hg mitigation efforts under the MC, implemented during a period of increasing climate action, are yielding measurable decreases in atmospheric Hg concentrations[2,9,10]. For instance, Feinberg et al. documented a significant decrease in gaseous elemental Hg (Hg^0) concentrations in the Northern Hemisphere between 2005 and 2020, attributing this trend to an annual reduction of at least 140 megagrams (Mg) in anthropogenic emissions[27]. Regional studies also highlight similar progress, such as the observed 35% reduction in the Baltic Sea region between 1990 and 2017[28]. A particularly notable example is China's targeted Hg mitigation policies, implemented during the MC's active phase (2013–2022), which reduced atmospheric Hg^0 concentrations by 38.6% over the decade[29].

While these achievements signify crucial progress in Hg mitigation, they also raise critical questions about potential unintended interactions between Hg and CO_2 dynamics. These interactions are linked by the highly diverse microbes involved in carbon biogeochemistry and remain poorly understood at both regional and global scales. As highlighted earlier, microbes involved in carbon cycling—including those responsible for organic matter decomposition and CH_4 production—may respond to fluctuations in Hg concentrations, co-shaped by both Hg contamination and mitigation measures. This may lead to cascading impacts on CO_2 dynamics. An analysis of ice core data appears to show a concurrence of lower Hg with elevated CO_2 over the past 670,000 years[30]. Yet, whether and how they were mechanistically related to each other remains poorly understood, making causality difficult to establish. Clarifying this potential causal relationship is therefore a timely and critical research priority.

The potential impacts of the Hg-microbe-GHG nexus may extend to nitrous oxide (N_2O) and CH_4, both potent GHGs with 300- and 80-fold warming potential of CO_2 over 100- and 20-year timescales, respectively[31]. Wetlands, which contribute ~25% of global CH_4 emissions[32], represent critical ecosystems where Hg contamination may affect CH_4 dynamics by altering the balance between methanogenic production and methanotrophic consumption[33,34]. For example, paddy soils with elevated Hg concentrations can enhance methanogen abundance (e.g., *Methanobacteria*)[33], potentially enhancing net CH_4 emissions. This aligns with observations in agricultural ponds where methanogen dominance drives higher CH_4 release[35]. Similarly, Hg also disrupts nitrogen cycling, with implications for N_2O emissions[36,37]. In vegetable fields, ammonia-oxidizing bacteria show a 50% reduction in potential nitrification rates at Hg concentrations >1.59 μg/g, while ammonia-oxidizing archaea remain resilient[36], skewing nitrogen retention toward NH_4^+. Wheat-maize soil exposed to elevated Hg doses exhibits transient spikes in denitrification enzyme activity, potentially increasing N_2O emissions[37]. These dose-dependent responses, while still lacking long-term exposure scenarios across low, medium, and high Hg concentrations in diverse environmental settings, highlight Hg's potential to destabilize interconnected carbon-nitrogen feedback, creating trade-offs between CH_4, CO_2, and N_2O emissions that depend on microbial adaptation and ecosystem status (Table 1).

Notably, even minor structural changes in microbial communities induced by Hg (e.g., a 2% change in microbial community structure in temperate forest soil[20]) may yield disproportionally large functional consequences for microbe-mediated GHG emissions at ecosystem and global scales. To illustrate the potential scale of this effect, consider a hypothetical 1% change in net CH_4 emissions in wetlands. This level of fluctuation is plausible given documented Hg impacts on microbial CH_4 cycling[33–35]. Based on 2023 wetland emission estimates (194 million tons)[38], this hypothetical change would increase the global CH_4 budget by 1.94 million tons. Such an increase equals 19% of the emissions from biomass burning, a major contributor to anthropogenic CH_4 emissions[38]. However, current observational data remain insufficient to predict the net climate impacts of Hg mitigation. Compounding factors, such as intensifying hurricanes, wildfires, and widespread forest decline, further complicate Hg-GHG interactions by altering redox conditions and microbial habitats[39,40]. Closing these knowledge gaps is essential to advance our understanding of the microbe-mediated Hg-GHG nexus, offering insights into aligning Hg and climate policies and ensuring that progress in one domain does not inadvertently undermine the other.

Elucidating the impacts of modern Hg

A key challenge in elucidating the impact of global Hg mitigation on climate change through the microbe-mediated Hg-GHG nexus lies in differentiating the distinct roles of "modern" and "legacy" Hg in reshaping microbial communities and their associated GHG emissions (see Box 2).

In nature, microbial communities are simultaneously exposed to modern Hg inputs and the large, but generally less bioavailable, legacy Hg reservoirs. While modern Hg inputs are smaller, especially in terrestrial ecosystems (e.g., <0.1% of Hg in global topsoil from annual atmospheric deposition[41]), they represent a more dynamic and bioavailable fraction to microbes (see Box 2). However, legacy Hg can be remobilized and spatially redistributed[42], particularly in historically contaminated sites, substantially affecting ecosystems far from the source, e.g., contributing 21%–82% of Hg in downstream marsh habitats in New Jersey, USA[43]. Furthermore, climate change and anthropogenic perturbations, such as farming and land use changes[42,44], can remobilize legacy Hg, thereby increasing its bioavailability and thus potential impacts on microbes[41,45]. For instance, the incorporation of rice straw into paddy soils, a common agricultural practice, has been shown to enhance the abundance/activity of microbial methylators and the transformation of refractory mercury sulfide (HgS)—a dominant species of legacy Hg in soils and sediments[44]—to organic matter-complexed Hg, increasing its bioavailability and subsequent microbial methylation to more mobile forms with higher toxicity like neurotoxin MeHg[46]. Consequently, the interplay between aging and remobilization (see Box 2) complicates the relationship between atmospheric Hg mitigation and microbial responses (Fig. 1). This complexity makes it difficult to pinpoint how reducing modern Hg inputs, the focus of global Hg mitigation efforts, affects microbial communities and GHG dynamics, and highlights the role of timing, severity, and frequency of ecological disturbances in mobilizing legacy Hg. Therefore, distinguishing individual and interactive roles of "modern" versus "legacy" Hg in the context of microbial GHG regulation is essential.

https://doi.org/10.1038/s41467-025-62176-0

BOX 2

Important concepts: Modern Hg vs. legacy Hg

Modern Hg

- *Definition*: Modern Hg in this work refers to the actively cycling Hg fraction within ecosystems, entering contemporarily via direct deposition (atmospheric wet/dry), indirect inputs (e.g., litterfall), and anthropogenic vectors (e.g., irrigation inflow and wastewater discharge[89]). Crucially, modern Hg encompasses Hg from both newly emitted (anthropogenic and natural) and re-emitted sources (from past emissions).
- *Bioavailability*: Modern Hg exhibits relatively high bioavailability. It primarily exists as reactive inorganic Hg, i.e., Hg(II). Its solubility enables uptake by organisms via passive diffusion or membrane transporters, as evidenced by bioavailable fractions of Hg(II) to fish reaching up to 51%[90].
- *Mitigation focus*: Global Hg mitigation efforts under the MC primarily target atmospheric deposition, a major form of modern Hg inputs, by emission reduction.

Legacy Hg

- *Definition*: Legacy Hg comprises Hg derived from geological sources and past emissions, now residing as a large, less immediately bioavailable pool in environmental reservoirs.
- *Aging*: Over time, modern Hg undergoes an aging process[91], becoming legacy Hg. This involves the transformation of modern Hg into stable complexes with organic matter (e.g., thiol-bound Hg in humic acids[92]) or into inorganic minerals, such as HgS[46], also known as cinnabar.
- *Bioavailability*: The aging process substantially reduces the mobility, availability, and immediate toxicity of Hg to microbes unless remobilized (Fig. 1, upper panel). A representative example is the sharp decrease in Hg mobility along the aging process, with legacy Hg exhibiting bioavailability of less than 5%[93].
- *Remobilization*: Legacy Hg can be remobilized and reactivated by environmental disturbances such as flooding (rewetting wetlands) and anthropogenic perturbations like straw incorporation[42,45]. These activities facilitate the anaerobic microbial transformation of legacy Hg, powered by the *hgcA* and *hgcB*—a pair of genes encoding proteins essential for Hg methylation[94].

Modern-to-legacy Hg ratio

- The modern-to-legacy Hg ratio represents the proportion of modern Hg compared to legacy Hg in a specific environmental reservoir or ecosystem. In essence, the modern-to-legacy Hg ratio fosters an understanding of the relative importance of newly introduced Hg versus Hg that has been residing in the environment for longer periods and accumulated in environmental reservoirs from geological sources and past emissions, with a distinct bioavailability fraction to microbes.

This challenge in linking fluctuations of modern Hg inputs to microbial GHG dynamics could be further complicated by microbes' complex and non-linear responses to Hg exposure. Microbial communities may initially react strongly to environmental changes, exhibiting significant shifts in structure and function. However, this initial sensitivity can be followed by a moderate response and even potential acclimation as the microbial community adapts to disturbance regimes and the altered environment[47]. Crucially, adaptation timescales vary substantially—from days to decades—depending on microbial species and environmental conditions. For instance, Zhou et al. found that microbial communities initially experienced a significant shift in gene expression patterns days after exposure to elevated Hg concentrations, followed by a gradual adaptation over time[37]. By contrast, a notable increase in the population size of microbes carrying the *merA* gene encoding the mercuric reductase enzyme, which is crucial for Hg detoxification, occurred approximately two decades into the Industrial Revolution[48]. This rise correlated with elevated atmospheric Hg concentrations and increased anthropogenic emissions. Bayesian relaxed molecular clocks identified a strong positive selection in the *merA* gene, highlighting microbial adaptation to increased modern Hg inputs[48]. However, we lack evidence for how rapidly microbes adapt to declining modern Hg inputs. Global Hg mitigation efforts have led to sharp reductions (e.g., a 70% decrease within four years on Chongming Island[49]), yet it remains unknown whether and how microbes can adjust to such rapid emission decreases.

Can reductions in modern Hg, the primary target of global mitigation efforts, reshape microbial communities and consequently shift the dynamic balance of microbial GHG production/consumption differently than the ongoing influence of continuous modern Hg deposition, or are these effects masked by legacy Hg dynamics? Resolving this requires disentangling the contributions of modern versus legacy Hg to microbial processes and elucidating the non-linear responses of microbial communities to changes in their environments. Besides, microbial responses to changes in modern Hg inputs likely depend on a range of properties, from the abundance and diversity of functional genes to global biogeochemical cycling patterns, that vary across spatiotemporal scales. Therefore, assessing how global Hg mitigation affects microbial GHG emissions also requires identifying ecosystems most sensitive to changes in modern Hg inputs, as detailed in the following section.

Hg mitigation and ecosystem sensitivity

It is important to recognize that the potential impacts of fluctuations in modern Hg on microbes and associated GHG emissions may vary considerably across ecosystems, leading to differences in ecosystem sensitivity to Hg mitigation (Table 1). Here, we propose that this sensitivity could largely be dependent on (1) the modern-to-legacy Hg ratio, which determines the bioavailable Hg pool accessible to microbes (see Box 2), and (2) microbial functional sensitivity, mediated by genetic profiles, physiology, and environmental factors that control Hg speciation, bioaccumulation, and toxicity. While ecosystem sensitivity involves complex feedback, we prioritize these two actionable parameters for global policy implementation, enabling the identification of terrestrial and aquatic hotspots where modern Hg fluctuations will most likely affect the Hg-microbe-GHG nexus.

The modern-to-legacy Hg ratio serves as a key indicator of an ecosystem's sensitivity to Hg contamination and its responsiveness and sensitivity to mitigation efforts. This significance in determining ecosystem sensitivity to Hg mitigation can be illustrated by contrasting marine and terrestrial environments. Specifically, the vast pool of legacy Hg in terrestrial surface soils—due to relatively fast aging as Hg can bind rapidly to organic matter/clays in soils/sediments[50]—may buffer the impacts of fluctuations in modern Hg inputs on microbes. This is because the larger pool of legacy Hg can act as a reservoir of bioavailable Hg, continuously remobilized under the impact of natural processes (including climate change) and ongoing anthropogenic activities like farming[45]. Consequently, a low modern-to-legacy Hg

https://doi.org/10.1038/s41467-025-62176-0

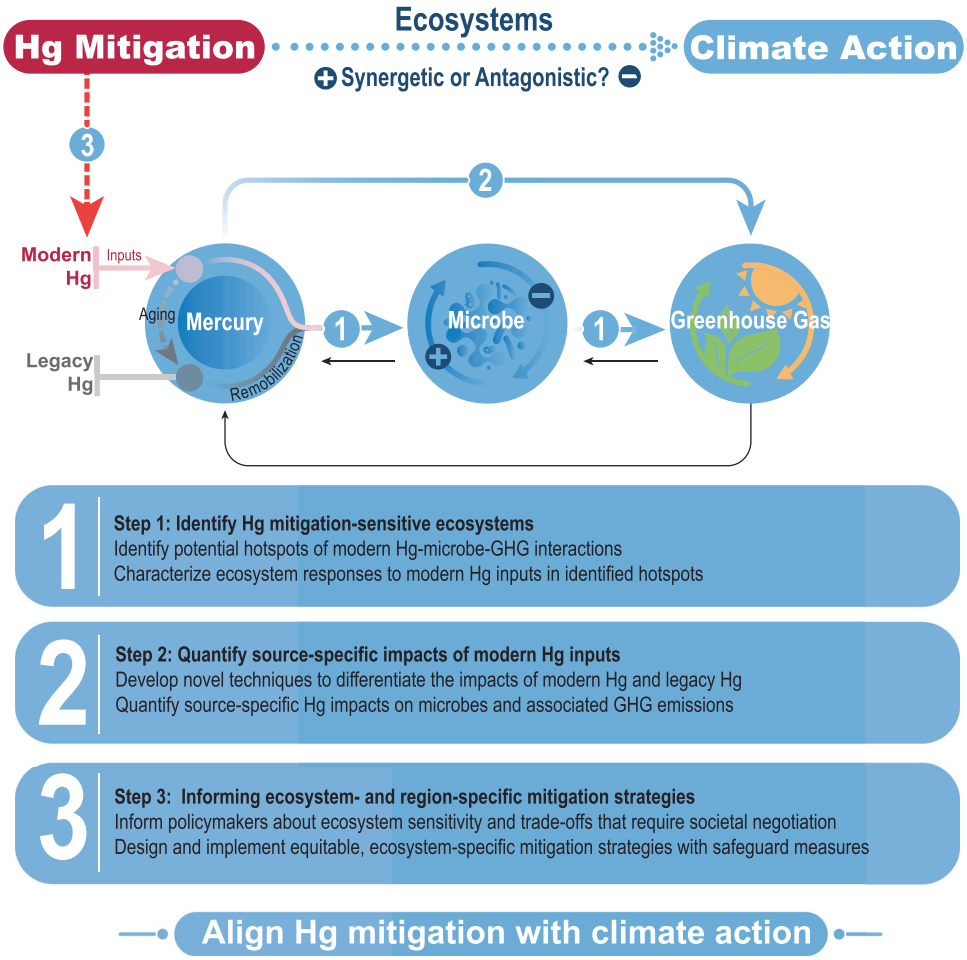

Fig. 1 | Proposed roadmap for aligning mercury (Hg) mitigation with climate action through the microbe-mediated Hg-microbe-GHG nexus. Modern Hg inputs (light red arrows) continuously deposit into ecosystems and convert to legacy Hg pools via aging (gray dashed arrow). Legacy Hg can be remobilized (gray solid arrow) by environmental disturbances. Both modern and remobilized legacy Hg impact microbial communities (see details in Box 2). Global Hg mitigation efforts (red arrow) substantially alter modern Hg inputs, potentially cascading through microbial communities to influence their greenhouse gas (GHG) emissions and thus climate change (blue arrow). Unlike the established climate feedback on microbes and Hg cycling (black arrow), ecosystem sensitivity to Hg mitigation—and its cascading GHG effects—remains poorly constrained. Therefore, we propose a three-step roadmap, aiming to identify these Hg mitigation-sensitive ecosystems and help align Hg mitigation with climate action.

ratio in terrestrial surface soils lessens the immediate ecosystem impacts of fluctuations in modern Hg inputs (and thus fluctuations in the ratio itself). By contrast, fluctuations in modern Hg inputs are highly likely to play a more pronounced role in marine ecosystems (covering 71% of Earth's surface) characterized by a higher modern-to-legacy ratio. On the ocean surface, the annual input of atmospheric Hg can be up to 1.5 times that of Hg residing in water[41] and can persist in bioavailable forms (e.g., MeHg) longer, partly because phytoplankton acts as a MeHg reservoir and produces organic matter that enhances MeHg production[51]. As a result, this higher ratio means marine ecosystems may exhibit greater sensitivity: reducing anthropogenic Hg emissions could have a more direct impact on marine bioavailable Hg pools, potentially leading to a higher sensitivity of marine ecosystems to global Hg mitigation strategies compared to systems dominated by legacy Hg.

Beyond the modern-to-legacy Hg ratio, the characteristics of microbial communities play a critical role in shaping the sensitivity of ecosystems to Hg mitigation. Different microbes may exhibit diverse responses to current Hg fluctuations (Table 1), leading to distinct changes in microbial GHG emissions. For example, methanogenic archaea show extreme sensitivity, with their CH_4 production strongly inhibited when exposed to 0.02 μg/mL inorganic Hg[52]. By contrast, some phototrophic microbes have been reported to benefit from the presence of inorganic Hg, an electrophilic element, to maintain redox homeostasis[53]. These diverse responses to Hg exposure could potentially result in positive, negative, or neutral consequences for overall microbe-mediated GHG emissions from various ecosystems. This point is exemplified in a recently published work highlighting a "see-saw" effect[31], wherein mitigating one could inadvertently elevate others due to the interconnectedness and complexity of microbial systems[11], such as increased N_2O emissions induced by methanotroph-mediated CH_4 mitigation[31,54]. This phenomenon directly parallels our investigation of Hg impacts on the microbial GHG nexus, underscoring how microbial functional interdependence governs biogeochemical feedback to Hg mitigation.

These interconnected factors, including the modern-to-legacy ratio and variation in microbial fitness in the presence of Hg, can create microbial sensitivity hotspots within and across ecosystems where communities respond sensitively to modern Hg inputs, ultimately influencing global GHG emissions. For example, a potential hotspot where changes in modern Hg inputs are likely to affect microbial communities is the litter layer in topsoil environments. This layer,

characterized by frequent litterfall and active microbe-mediated litter decomposition, contributes to over 23% of global soil CO_2 emissions[55]. Simultaneously, efficient leaf uptake of atmospheric Hg^0, coupled with subsequent litterfall, concentrates atmospheric Hg within the litter layer. Quantitative assessments reveal substantial Hg loading through litterfall, with annual deposition fluxes reaching 40.5 μg/m^2 for total Hg and 0.10 μg/m^2 for MeHg in coniferous forests[56]. Even higher fluxes are observed in broad-leaved forests, where annual deposition reaches 90.9 μg/m^2 for total Hg and 0.34 μg/m^2 for MeHg, primarily attributed to greater litterfall biomass[56]. This combination could create potential hotspots in terrestrial ecosystems where modern Hg may exert a stronger effect on microbial GHG emissions in the specific layers, even though the concentrations of modern Hg inputs are generally lower than legacy Hg in bulk soil and may have only minimal effects on soil microbes.

Potential hotspots can also be found in aquatic environments. For example, algal blooms and their decomposition in the sediments of freshwater lakes create cycling regimes similar to those commonly observed in soil litter. During algal blooms, algae can scavenge high concentrations of Hg from both the atmosphere and the water column[57]. The subsequent decomposition of algal biomass in the sediments not only provides a rich source of organic carbon but also fosters anaerobic or anoxic conditions, facilitating the growth of methanogens and potentially leading to elevated CH_4 emissions[58]. While specific numbers on the direct inputs of Hg from algal blooms and the resulting increase in methanogens in sediments are highly variable and lake-specific, the general principle of concentrated Hg and organic matter leading to enhanced methanogenesis holds. Coastal zones similarly represent potential sensitivity hotspots due to land-sea exchange and river transport of terrestrial discharges[59,60]. The relatively high concentrations of modern, potentially more bioavailable Hg in the water column, combined with continuous inputs of nutrients and organic matter that boost microbial growth, organic decomposition, and GHG production, could create ecological hotspots where microbial activity and associated GHG production are more sensitive to changes in Hg loading. Likewise, constructed wetlands—increasingly deployed as nature-based solutions for wastewater treatment and flood control[61]—constitute another key hotspot category. These systems receive exceptional modern Hg loads from sewage and flood events, while dynamic water-level management[62] induces redox shifts that remobilize legacy Hg[63]. Such fluctuations may disproportionately alter microbial GHG fluxes compared to natural wetlands. It is thus urgent and necessary to confirm whether these hotspots exist, as well as their hidden impacts on global carbon cycling and climate change.

In addition to the aforementioned factors, ecosystem complexity itself modulates microbial responses and hotspot formation at broader spatiotemporal scales. For example, ecosystems like coastal Antarctica, where warming-induced glacial retreat increases Hg enrichment in sediments, may exhibit heightened sensitivity to modern Hg input fluctuations[64]. While microbial diversity in Antarctica might not be strictly lower than in other ecosystems, the microbial community composition, potentially with fewer Hg-resistant (*merA* gene-carrying) microbes due to historically low anthropogenic Hg concentrations[65], could lead to increased vulnerability. This aligns with evidence suggesting that ecosystems with lower microbial diversity or biomass generally show reduced resilience and greater responsiveness to external stresses like pollution[66,67]. Vegetation further complicates the Hg-microbe-GHG nexus. Plants can uptake atmospheric Hg, thus creating modern Hg inputs into soils via litterfall. Ecosystems with higher gross primary productivity, such as tropical forest soils with elevated atmospheric Hg contributions[68], may thus experience increased modern Hg inputs through this litterfall-driven pathway. Additionally, fungi, particularly arbuscular mycorrhizal fungi (AMF), play a critical role in Hg cycling. AMF form symbiotic relationships with plant roots, directly mediating Hg uptake and translocation in host plants[69]. Notably, their tolerance to Hg contamination varies, introducing variability into plant-Hg dynamics[70]. These multifaceted interactions underscore the complexity of predicting modern Hg's impacts on microbial communities and subsequent GHG emissions, likely creating hotspots of the Hg-microbe-GHG nexus. A thorough understanding of these interactions is essential for identifying sensitive ecosystems vulnerable to changing Hg concentrations under global mitigation scenarios.

In summary, our current understanding of how environmental Hg affects microbial communities is mechanistically limited and fragmented across Hg topical sub-disciplines and different spatiotemporal scales. These gaps hinder accurate estimations of microbe-mediated GHG emissions in response to fluctuating modern Hg inputs, which warrant further investigation and prompt attention from the scientific and public policy communities. Despite the complexity of these interactions, they offer opportunities for innovative solutions. Although global Hg mitigation and overall GHG emission reduction efforts might have unexpected consequences, region-specific strategies could leverage the unique characteristics of Hg-sensitive ecosystems to achieve synergistic benefits for both Hg mitigation and climate action. These complex relationships emphasize the critical role of microbial communities in climate mitigation and the need for careful planning in mitigation strategies at local, regional, and global scales (see **Roadmap** Step 3 in Fig. 1).

A roadmap to align Hg mitigation with climate action

Ensuring effective global Hg mitigation and its long-term benefits, in our opinion, requires navigating its complex interplay with climate change through the Hg-microbe-GHG nexus. We propose that integrating Hg mitigation strategies with climate action awareness is essential. However, we explicitly acknowledge that navigating potential trade-offs involves significant normative judgments. Prioritizing marginal GHG reductions could deprioritize Hg mitigation in sensitive ecosystems where conflicts arise. To enable transparent decision-making on these trade-offs, we propose a three-step roadmap (Fig. 1, lower panel):

Step 1: Identify Hg mitigation-sensitive ecosystems

Research efforts should be prioritized in regions with high natural GHG fluxes and substantial fluctuations in modern Hg inputs to identify potential hotspots of Hg-microbe-GHG interactions. Candidate ecosystems include terrestrial topsoil litter layers, algal-bloom lakes, coastal zones, and constructed wetlands (see "Hg mitigation and ecosystem sensitivity" Section).

- Remote sensing can be leveraged to monitor regions with high natural GHG emissions, such as wetlands and peatlands, and to track environmental variables acting as proxies for modern Hg inputs across broad spatiotemporal scales. Typical examples include soil organic carbon from Landsat 8/9 and Sentinel-2[71] for Hg sequestration, hyperspectral and multispectral imaging from the Moderate Resolution Imaging Spectroradiometer (MODIS) and Sentinel-5 Precursor for vegetation indices[72] like chlorophyll-a anomalies indicating algal blooms that reshape Hg methylation, and synthetic aperture radar of Sentinel-1[73] to track wetland inundation dynamics governing Hg methylation hotspots.
- Machine learning and deep learning (ML/DL) models can be employed to integrate remote sensing data with climate records, soil properties, hydrology data, and microbial functional trait databases, e.g., Integrated Microbial Genomes & Microbiomes (IMG/M) developed by the DOE Joint Genome Institute (JGI). This predicts potential sensitivity hotspots by estimating Hg-GHG coupling/decoupling probabilities, augmenting process understanding where direct data is scarce.

- Disentangle Hg-microbe-GHG interactions through both lab and field-based experiments in identified regions to characterize ecosystem responses to modern Hg inputs, be it synergetic (decreasing GHG emissions), antagonistic (increasing GHG emissions), or insignificant. Understanding the nature and scale of these interactions is crucial for predicting the impacts of global Hg mitigation on climate change. We emphasize that "sensitivity" reflects a policy-relevant framing, instead of an intrinsic ecosystem property.

Step 2: Quantify source-specific impacts of modern Hg inputs

Analytical methods, building upon existing techniques (e.g., Hg isotopes, metagenomics, remote sensing, and ML/DL), should be developed for Hg source fingerprinting. This is crucial for differentiating the impacts of modern Hg inputs from specific sources (e.g., atmospheric deposition, irrigation, and litterfall) on microbial GHG emissions across ecosystems.

- Land use changes, vegetation indices related to litterfall, irrigation patterns, and other typical remote sensing products can be used in conjunction with ML/DL to map pathways of modern Hg inputs at scale. For example, light detection and ranging (LiDAR) topography and multispectral irrigation mapping[74] are promising for isolating agricultural Hg inputs. Likewise, nighttime lights [e.g., from the Visible Infrared Imaging Radiometer Suite (VIIRS)], alongside thermal anomalies from MODIS[75], have the potential to correlate artisanal and small-scale gold mining (ASGM) activities with Hg deposition gradients.
- Identified Hg source information and microbial data can be employed to develop ML/DL-enhanced models, considering factors like modern-to-legacy Hg ratios, microbial community characteristics, and other potential key factors identified in future studies to better predict ecosystem sensitivity related to post-deposition processes. To address data scarcity in such an underexplored area, ML/DL should augment—not replace—process-based techniques, including but not limited to Hg isotope apportionment and metagenomics. Such assemblies will be able to quantify how changes in modern Hg inputs from specific sources affect microbial communities and their associated GHG emissions. Model outputs should also include potential trade-off curves (e.g., ΔGHG fluxes vs. ΔHg exposure risks) at various scales. These outputs are crucial to inform policy by clarifying co-benefits and conflicts, not to predetermine choices.

Step 3: Inform ecosystem- and region-specific mitigation strategies

Knowledge from Steps 1–2 empowers policymakers to design equitable, ecosystem-specific strategies, acknowledging that trade-offs require societal negotiation informed by science. A one-size-fits-all approach will likely be ineffective. Herein, we recommend:

- In non-sensitive (i.e., Hg-GHG decoupled) ecosystems where there is low Hg-GHG feedback risk, standard Hg mitigation strategies should be implemented, as required under the MC.
- In sensitive (i.e., Hg-GHG coupled) ecosystems, strategies require careful balancing of Hg-GHG interactions and explicit consideration of equity.

  For synergistic zones, Hg mitigation measures can be implemented at a normal or higher-than-normal pace to co-benefit climate and health. These measures, including deploying advanced pollution control technologies and promoting clean energy adoption, would effectively reduce atmospheric Hg concentrations and modern Hg input into local ecosystems, as well as reduce microbe-mediated GHG emissions.
  For antagonistic zones, phased Hg mitigation strategies paired with robust equity safeguards can be considered. A more gradual pace allows microbial communities to adapt to changes in modern Hg inputs resulting from Hg mitigation, potentially avoiding sharp GHG emission spikes. Safeguards must include rigorous health monitoring of the immediate health and ecological risks of Hg pollution in the affected zone and tangible livelihood support, potentially funded via carbon credit mechanisms, to tackle the disproportionate burden potentially placed on local communities (e.g., subsistence fishers).

Crucially, this approach may inherently lead to a calculated delay in local Hg risk reduction to avoid counterproductive global climate impacts. This is a significant normative choice that must be made transparently by policymakers, weighing it against the precautionary principle and local impacts, equity and justice, and other sustainability goals such as impacts on biodiversity, food security, and cultural values. The choice between faster local Hg reduction and avoiding possible global GHG spikes involves competing values and risks. Science cannot resolve this choice; it can only illuminate the consequences. Policymakers must explicitly justify their prioritization, learning from analogous debates like sulfate aerosols[76], where prioritizing immediate local health protection over transient global cooling was deemed ethically necessary[15].

Conclusion

In this *Perspective*, we explore the Hg-microbe-GHG nexus, revealing how Hg mitigation strategies potentially influence microbe-mediated GHG dynamics in the face of the triple planetary crisis of environmental pollution, biodiversity loss, and climate change. Building upon these insights, we provide a science-based roadmap to identify sensitive ecosystems, quantify source-specific impacts, and inform—not prescribe—tailored strategies aimed at minimizing unintended consequences on ecosystems at local, regional, and global scales. Critically, it highlights the need for transparent societal deliberation on the normative trade-offs inherent in managing interconnected environmental crises.

More importantly, these advances will deepen our understanding of pollution-biodiversity-climate interactions and underscore microbes' vital role in connecting ecosystems, climate, and planetary health[77]. These insights provide essential scientific support and serve as the key interlinkage for the synergistic implementation of the MC and the Kunming-Montreal Global Biodiversity Framework[10], which is currently hindered by a lack of actionable frameworks and understanding of these critical interlinkages.

The proposed roadmap could potentially be adapted to explore the impact of other globally relevant pollutants within the context of the triple planetary crisis of environmental pollution, biodiversity loss, and climate change. Evidence increasingly suggests that pollutants, such as plastics, may alter microbe-mediated biogeochemical cycles of major elements[78,79]. Expanding our understanding of the Hg-microbe-GHG nexus to include a broader pollutant-biodiversity-climate nexus will significantly aid in combating the triple planetary crisis. This effort hinges on comprehending the interconnections among environmental pollution, biodiversity loss, and climate change.

References

1. Lyons, T. W. et al. Co-evolution of early Earth environments and microbial life. *Nat. Rev. Microbiol.* **22**, 572–586 (2024).
2. Change, I. P. o. C. AR6 synthesis report: Climate change 2023. *Climate change 2023: Synthesis Report. Contribution Of Working Groups I, II And III To The Sixth Assessment Report Of The Intergovernmental Panel On Climate Change*, 35-115 (2023).
3. Hu, Y., Wang, Y., Zhao, Z. & Zhao, B. Reconsidering gas as clean energy: Switching to electricity for household cooking to reduce NO_2-attributed disease burden. *Eco-Environ. Health* **3**, 174–182 (2024).

4. Bowman, K. L., Lamborg, C. H. & Agather, A. M. A global perspective on mercury cycling in the ocean. *Sci. Total Environ.* **710**, 136166 (2020).
5. Schaefer, K. et al. Potential impacts of mercury released from thawing permafrost. *Nat. Commun.* **11**, 4650 (2020).
6. Walker, T. W. N. et al. Microbial temperature sensitivity and biomass change explain soil carbon loss with warming. *Nat. Clim. Change* **8**, 885–889 (2018).
7. Tsz-Ki Tsui, M., Kwon, S. Y., Li, M.-L. & Bishop, K. Revisiting the relationship between mercury emission and bioaccumulation. *Eco-Environ. Health* **2**, 1–2 (2023).
8. Sonke, J. E. et al. Global change effects on biogeochemical mercury cycling. *Ambio* **52**, 853–876 (2023).
9. Conference of the Parties to the Minamata Convention on Mercury. MC-5/14 - First effectiveness evaluation of the Minamata Convention on Mercury. (https://minamataconvention.org/sites/default/files/documents/decision/UNEP-MC-COP.5-Dec.14_First-Effectiveness-Evaluation_English.pdf, 2023).
10. Conference of the Parties to the Minamata Convention on Mercury. MC-5/17: Mercury and the Kunming-Montreal Global Biodiversity Framework. (https://minamataconvention.org/sites/default/files/documents/decision/UNEP-MC-COP.5-Dec.17_KM-Biodiversity_Framework_English.pdf, 2023).
11. Stein, L. Y. The long-term relationship between microbial metabolism and greenhouse gases. *Trends Microbiol.* **28**, 500–511 (2020).
12. Song, Y. et al. Soil metabolomics: deciphering underground metabolic webs in terrestrial ecosystems. *Eco-Environ. Health* **3**, 227–237 (2024).
13. Fuerst, J. A. in *Microbial Resources* (ed Ipek Kurtböke) 1–27 (Academic Press, 2017).
14. Bhatti, A. A., Haq, S. & Bhat, R. A. Actinomycetes benefaction role in soil and plant health. *Microb. Pathog.* **111**, 458–467 (2017).
15. Lv, Z. et al. Isolation of a novel thermophilic methanogen and the evolutionary history of the class methanobacteria. *Biology* **11**, 1514 (2022).
16. Schmitz, R. A. et al. Verrucomicrobial methanotrophs: ecophysiology of metabolically versatile acidophiles. *FEMS Microbiol. Rev.* **45**, https://doi.org/10.1093/femsre/fuab007 (2021).
17. Di, H. J. et al. Nitrification driven by bacteria and not archaea in nitrogen-rich grassland soils. *Nat. Geosci.* **2**, 621–624 (2009).
18. Liu, Y.-R., Wang, J.-J., Zheng, Y.-M., Zhang, L.-M. & He, J.-Z. Patterns of bacterial diversity along a long-term mercury-contaminated gradient in the paddy soils. *Microb. Ecol.* **68**, 575–583 (2014).
19. Frossard, A., Hartmann, M. & Frey, B. Tolerance of the forest soil microbiome to increasing mercury concentrations. *Soil Biol. Biochem.* **105**, 162–176 (2017).
20. Frey, B. & Rieder, S. R. Response of forest soil bacterial communities to mercury chloride application. *Soil Biol. Biochem.* **65**, 329–337 (2013).
21. Pu, Q. et al. Mercury drives microbial community assembly and ecosystem multifunctionality across a Hg contamination gradient in rice paddies. *J. Hazard. Mater.* **435**, 129055 (2022).
22. Frossard, A. et al. Long-and short-term effects of mercury pollution on the soil microbiome. *Soil Biol. Biochem.* **120**, 191–199 (2018).
23. Lustenhouwer, N. et al. A trait-based understanding of wood decomposition by fungi. *Proc. Natl Acad. Sci.* **117**, 11551–11558 (2020).
24. Giang, A., Stokes, L. C., Streets, D. G., Corbitt, E. S. & Selin, N. E. Impacts of the Minamata Convention on mercury emissions and global deposition from coal-fired power generation in Asia. *Environ. Sci. Technol.* **49**, 5326–5335 (2015).
25. Oberschelp, C., Pfister, S., Raptis, C. E. & Hellweg, S. Global emission hotspots of coal power generation. *Nat. Sustainability* **2**, 113–121 (2019).
26. Geyman, B. M. et al. Projecting global mercury emissions and deposition under the shared socioeconomic pathways. *Earth's Future* **12**, e2023EF004231 (2024).
27. Feinberg, A. et al. Unexpected anthropogenic emission decreases explain recent atmospheric mercury concentration declines. *Proc. Natl Acad. Sci.* **121**, e2401950121 (2024).
28. Jędruch, A. et al. Mercury in the Polish part of the Baltic Sea: A response to decreased atmospheric deposition and changing environment. *Mar. Pollut. Bull.* **186**, 114426 (2023).
29. Feng, X. et al. Combating air pollution significantly reduced air mercury concentrations in China. *Natl Sci. Rev.* **11**, https://doi.org/10.1093/nsr/nwae264 (2024).
30. Gao, J. et al. Can mercury influence carbon dioxide levels? Implications for the implementation of the Minamata Convention on Mercury. *Environ. Sci. Technol.* **58**, 6077–6082 (2024).
31. Stein, L. Y. & Lidstrom, M. E. Greenhouse gas mitigation requires caution. *Science* **384**, 1068–1069 (2024).
32. Saunois, M. et al. Global methane budget 2000–2020. *Earth Syst. Sci. Data Discuss.* **2024**, 1–147 (2024).
33. Vishnivetskaya, T. A. et al. Microbial community structure with trends in methylation gene diversity and abundance in mercury-contaminated rice paddy soils in Guizhou, China. *Environ. Sci.: Process. Impacts* **20**, 673–685 (2018).
34. Bārdule, A. et al. Variation in the mercury concentrations and greenhouse gas emissions of pristine and managed hemiboreal peatlands. *Land* **11**, 1414 (2022).
35. Liu, H. et al. Methanogens dominate methanotrophs and act as a methane source in aquaculture pond sediments. *Ecotoxicol. Environ. Saf.* **288**, 117317 (2024).
36. Liu, Y.-R., Zheng, Y.-M., Shen, J.-P., Zhang, L.-M. & He, J.-Z. Effects of mercury on the activity and community composition of soil ammonia oxidizers. *Environ. Sci. Pollut. R.* **17**, 1237–1244 (2010).
37. Zhou, Z. et al. Responses of activities, abundances and community structures of soil denitrifiers to short-term mercury stress. *J. Environ. Sci.* **24**, 369–375 (2012).
38. IEA. Global methane tracker 2024, IEA, Paris https://www.iea.org/reports/global-methane-tracker-2024, Licence: CC BY 4.0 (2024).
39. Feinberg, A., Jiskra, M., Borrelli, P., Biswakarma, J. & Selin, N. E. Deforestation as an Anthropogenic Driver of Mercury Pollution. *Environ. Sci. Technol.* **58**, 3246–3257 (2024).
40. Liu, B. et al. Disturbance impacts on mercury dynamics in northern Gulf of Mexico sediments. *J. Geophys. Res.: Biogeosci.* **114**, https://doi.org/10.1029/2008JG000752 (2009).
41. UNEP. Global Mercury Assessment 2018. *UN Environment Programme, Chemicals and Health Branch Geneva* (UNEP, 2019).
42. Li, C., Li, S., Zhou, Q., Tang, W. & Zhong, H. Remobilized metals threaten urban wetlands. *Science* **388**, 922–923 (2025).
43. Reinfelder, J. R. & Janssen, S. E. Tracking legacy mercury in the Hackensack River estuary using mercury stable isotopes. *J. Hazard. Mater.* **375**, 121–129 (2019).
44. Gilli, R. S. et al. Speciation and mobility of mercury in soils contaminated by legacy emissions from a chemical factory in the Rhône Valley in Canton of Valais. *Switz. Soil Syst.* **2**, 44 (2018).
45. Zhong, H. et al. Mercury supply limits methylmercury production in paddy soils. *Sci. Total Environ.* **927**, 172335 (2024).
46. Tang, W. et al. Increased methylmercury accumulation in rice after straw amendment. *Environ. Sci. Technol.* **53**, 6144–6153 (2019).
47. Frey, B., Rast, B. M., Qi, W., Stierli, B. & Brunner, I. Long-term mercury contamination does not affect the microbial gene potential for C and N cycling in soils but enhances detoxification gene abundance. *Front. Microbiol.* **13**, 1034138 (2022).
48. Ruuskanen, M. O., Aris-Brosou, S. & Poulain, A. J. Swift evolutionary response of microbes to a rise in anthropogenic mercury in the Northern Hemisphere. *ISME J.* **14**, 788–800 (2020).

49. Tang, Y. et al. Impacts of anthropogenic emissions and meteorological variation on hg wet deposition in Chongming, China. *Atmosphere* **11**, 1301 (2020).
50. Sanei, H. & Goodarzi, F. Relationship between organic matter and mercury in recent lake sediment: The physical–geochemical aspects. *Appl. Geochem.* **21**, 1900–1912 (2006).
51. Lei, P. et al. Algal organic matter drives methanogen-mediated methylmercury production in water from eutrophic shallow lakes. *Environ. Sci. Technol.* **55**, 10811–10820 (2021).
52. Wood, J. M., Kennedy, F. S. & Rosen, C. G. Synthesis of methylmercury compounds by extracts of a methanogenic bacterium. *Nature* **220**, 173–174 (1968).
53. Grégoire, D. S. & Poulain, A. J. A physiological role for HgII during phototrophic growth. *Nat. Geosci.* **9**, 121–125 (2016).
54. Rinne, J. et al. Nitrous oxide emissions from a municipal landfill. *Environ. Sci. Technol.* **39**, 7790–7793 (2005).
55. Fan, Y., Zhang, Y., Osborne, B. & Zou, J. Global patterns of soil greenhouse gas fluxes in response to litter manipulation. *Cell Rep. Sustainability* **1**, 100003 (2024).
56. Zhou, J., Wang, Z. & Zhang, X. Deposition and fate of mercury in litterfall, litter, and soil in coniferous and broad-leaved forests. *J. Geophys. Res.: Biogeosci.***123**, 2590–2603 (2018).
57. Pickhardt, P. C., Folt, C. L., Chen, C. Y., Klaue, B. & Blum, J. D. Algal blooms reduce the uptake of toxic methylmercury in freshwater food webs. *Proc. Natl Acad. Sci.* **99**, 4419–4423 (2002).
58. Wang, T. et al. Variable promotion of algae and macrophyte organic matter on methanogenesis in anaerobic lake sediment. *Environ. Res.* **237**, 116922 (2023).
59. Liu, M. et al. Rivers as the largest source of mercury to coastal oceans worldwide. *Nat. Geosci.* **14**, 672–677 (2021).
60. Jonsson, S. et al. Terrestrial discharges mediate trophic shifts and enhance methylmercury accumulation in estuarine biota. *Sci. Adv.* **3**, e1601239 (2017).
61. Babatunde, A. O., Zhao, Y. Q., O'Neill, M. & O'Sullivan, B. Constructed wetlands for environmental pollution control: A review of developments, research and practice in Ireland. *Environ. Int* **34**, 116–126 (2008).
62. Rooney, R. C. et al. Replacing natural wetlands with stormwater management facilities: Biophysical and perceived social values. *Water Res.* **73**, 17–28 (2015).
63. Liu, J. et al. Inorganic sulfur and mercury speciation in the water level fluctuation zone of the Three Gorges Reservoir, China: The role of inorganic reduced sulfur on mercury methylation. *Environ. Pollut.* **237**, 1112–1123 (2018).
64. Zhou, C. et al. Warming-induced retreat of West Antarctic glaciers weakened carbon sequestration ability but increased mercury enrichment. *Nat. Commun.* **16**, 1831 (2025).
65. Luo, Y., Zhong, H., Li, C. & Sonne, C. Regulate to protect fragile Antarctic ecosystems from growing tourism. *Nature* **631**, 275–275 (2024).
66. Osburn, E. D., Yang, G., Rillig, M. C. & Strickland, M. S. Evaluating the role of bacterial diversity in supporting soil ecosystem functions under anthropogenic stress. *ISME Commun.* **3**, 66 (2023).
67. Christel, A. et al. Differential responses of soil microbial biomass, diversity and interactions to land use intensity at a territorial scale. *Sci. Total Environ.* **906**, 167454 (2024).
68. Ma, H. et al. Distribution of mercury in foliage, litter and soil profiles in forests of the Qinling Mountains, China. *Environ. Res.* **211**, 113017 (2022).
69. Janeeshma, E. & Puthur, J. T. Direct and indirect influence of arbuscular mycorrhizae on enhancing metal tolerance of plants. *Arch. Microbiol.* **202**, 1–16 (2020).
70. Solís-Ramos, L. Y., Coto-López, C. & Andrade-Torres, A. Role of arbuscular mycorrhizal symbiosis in remediation of anthropogenic soil pollution. *Symbiosis* **84**, 321–336 (2021).
71. Castaldi, F. Sentinel-2 and Landsat-8 multi-temporal series to estimate topsoil properties on croplands. *Remote Sens.* **13**, 3345 (2021).
72. Doughty, R. et al. Global-Scale Consistency of Spaceborne Vegetation Indices, Chlorophyll Fluorescence, and Photosynthesis. *J. Geophys. Res.: Biogeosci.***126**, e2020JG006136 (2021).
73. Sellaperumal, P. et al. Time series analysis of Sentinel 1 A SAR data to retrieve annual rice area maps and long-term dynamics of start of season. *Sci. Rep.* **15**, 8202 (2025).
74. Pak, J. & Son, H. I. 3D LiDAR-based semantic SLAM for intelligent irrigation using UAV. *IEEE J. Sel. Top. Appl. Earth Observations Remote Sens.* **18**, 7495–7508 (2025).
75. Song, J. et al. Characterization of Urban Heat Islands Using City Lights: Insights from MODIS and VIIRS DNB Observations. *Remote Sens.* **13**, 3180 (2021).
76. Löndahl, J., Swietlicki, E., Lindgren, E. & Loft, S. Aerosol exposure versus aerosol cooling of climate: what is the optimal emission reduction strategy for human health. *Atmos. Chem. Phys.* **10**, 9441–9449 (2010).
77. Banerjee, S. & Van Der Heijden, M. G. Soil microbiomes and one health. *Nat. Rev. Microbiol.* **21**, 6–20 (2023).
78. Li, C. & Zhong, H. The world must move forwards with plastics treaty. *Nature* **638**, 39 (2025).
79. Zhao, X. et al. Protect wetlands from legacy plastics. *Science* **384**, 1414–1415 (2024).
80. Liu, C., Ning, Y. & Liu, J. Geochemical mercury pools regulate diverse communities of hgcA microbes and MeHg levels in paddy soils. *Environ. Pollut.* **334**, 122172 (2023).
81. Liu, Y.-R., Delgado-Baquerizo, M., Bi, L., Zhu, J. & He, J.-Z. Consistent responses of soil microbial taxonomic and functional attributes to mercury pollution across China. *Microbiome* **6**, 1–12 (2018).
82. Li, D., Li, X., Tao, Y., Yan, Z. & Ao, Y. Deciphering the bacterial microbiome in response to long-term mercury contaminated soil. *Ecotoxicol. Environ. Saf.* **229**, 113062 (2022).
83. Mustafa, G. et al. Microbiology of wetlands and the carbon cycle in coastal wetland mediated by microorganisms. *Sci. Total Environ.* **954**, 175734 (2024).
84. Mesquita, C. P. B. d, Wu, D. & Tringe, S. G. Methyl-based methanogenesis: an ecological and genomic review. *Microbiol. Mol. Biol. Rev.* **87**, e00024–00022 (2023).
85. Kalyuzhnaya, M. G., Gomez, O. A. & Murrell, J. C. in *Taxonomy, Genomics and Ecophysiology of Hydrocarbon-Degrading Microbes* (ed Terry J. M.) 245–278 (Springer International Publishing, 2019).
86. van Kessel, M. A. H. J. et al. Complete nitrification by a single microorganism. *Nature* **528**, 555–559 (2015).
87. Rodriguez, J. et al. Nutrient-limited enrichments of nitrifiers from soil yield consortia of nitrosocosmicus-affiliated AOA and nitrospira-affiliated NOB. *Front. Microbiol.* **ume 12**, 2021 (2021).
88. Hiis, E. G. et al. Unlocking bacterial potential to reduce farmland N_2O emissions. *Nature* **630**, 421–428 (2024).
89. Guédron, S. et al. (Methyl)Mercury, arsenic, and lead contamination of the world's largest wastewater irrigation system: the Mezquital Valley (Hidalgo State—Mexico). *Water, Air, Soil Pollut.* **225**, 2045 (2014).
90. Bradley, M. A., Barst, B. D. & Basu, N. A review of mercury bioavailability in humans and fish. *Int. J. Environ. Res. Public. Health* **14**, 169 (2017).
91. Yuan, C. et al. A meta-analysis of heavy metal bioavailability response to biochar aging: importance of soil and biochar properties. *Sci. Total Environ.* **756**, 144058 (2021).
92. Song, Y. et al. Thermodynamics of Hg(II) bonding to thiol groups in suwannee river natural organic matter resolved by competitive ligand exchange, Hg LIII-Edge EXAFS and 1H NMR spectroscopy. *Environ. Sci. Technol.* **52**, 8292–8301 (2018).

93. Hintelmann, H. et al. Reactivity and mobility of new and old mercury deposition in a boreal forest ecosystem during the first year of the METAALICUS study. *Environ. Sci. Technol.* **36**, 5034–5040 (2002).
94. Lin, H. et al. Mercury methylation by metabolically versatile and cosmopolitan marine bacteria. *ISME J.* **15**, 1810–1825 (2021).

Acknowledgements

This work was financially supported by the National Natural Science Foundation of China (Grant Nos.: 42525710 and 42107223).

Author contributions

C.L. and H.Z. conceived the study. C.L., H.Z., M.W., and W.T. led the writing of the manuscript. M.W. and Q.Z. collected the data. C.L., H.Z., M.W., W.T., B.Y., A.S.L., A.P., M.S.B., Q.Z., P.L.E.B., Z.Y., B.F., J.C., Y.J., and H.H. contributed to data analysis and interpretation, reviewed and edited the manuscript. W.T. and H.Z. secured funding.

Competing interests

The authors declare no competing interests.

Additional information

Correspondence and requests for materials should be addressed to Huan Zhong.

Peer review information *Nature Communications* thanks Junjiong Shao and the other, anonymous, reviewer(s) for their contribution to the peer review of this work.