

Microorganisms are the unseen pillars of mangrove biodiversity and ecosystem services

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Mangrove ecosystems are widely acknowledged in international policy and scientific literature for their crucial ecosystem services, including carbon sequestration, greenhouse gas regulation, food provisioning, and cultural value. Effective mangrove conservation and restoration should account for the biodiversity that underpins ecosystem functioning and services. However, one fundamental layer of this biodiversity remains underrepresented in restoration assessments and monitoring: the microbial world. Microorganisms represent the most abundant and taxonomically diverse components of mangrove sediments and rhizospheres, serving as key mediators of biogeochemical processes and, under certain conditions (e.g., pathogen outbreaks), as potential disruptors of ecosystem services. We propose a roadmap that includes: (i) establishing baseline reference datasets across biogeographic regions, vegetation zones, and tidal elevations to enable distinction between natural variability and anthropogenic degradation, (ii) shifting research focus from descriptive diversity surveys toward establishing causal mechanisms and developing standardized microbial functional indicators that can be scaled from plot-level measurements to landscape-level ecosystem service outcomes, and (iii) integrating microbial monitoring into national and international policy frameworks, supported by capacity-building initiatives, sustained funding mechanisms, and biosecurity protocols for any microbiome-based interventions.

MICROBIAL DIVERSITY: THE UNSEEN MAJORITY

The conventional view of mangrove biodiversity centers on visible flora and fauna. However, the highest biodiversity in mangroves is often found at the microbial scale. Tens of thousands of species of bacteria, archaea, fungi, viruses and protozoa coexist, forming intricate, interactive networks within sediments and the rhizosphere.¹ High-throughput sequencing continues to uncover a substantial fraction of microbial dark matter—referring to uncultured and unclassified lineages with unknown functions—in mangrove sediments, revealing a vast reservoir of taxonomic and phylogenetic novelty.² This taxonomic richness is underpinned by an immense and flexible genetic repertoire. Crucially, horizontal gene transfer enables genes to flow across species boundaries, creating a shared mobile gene pool within the community. This mechanism greatly accelerates microbial adaptation to environmental stressors characteristic of mangroves, such as salinity fluctuations, sulfide toxicity, and tidal redox oscillations.²

This immense genetic potential supports the critical functional diversity of mangrove ecosystems. Distinct microbial guilds perform specialized yet complementary metabolic processes, forming a web of interconnected functions. This intricate functional partitioning also establishes functional redundancy, which can stabilize key ecosystem processes against certain disturbances, although its effectiveness depends on disturbance type, intensity, and the specific functions involved. Importantly, this functional capacity is spatially organized by the complex physical structure of mangrove habitats. The root systems of mangroves create different micro-niches, ranging from oxygenated rhizosphere hotspots to anoxic bulk sediments, each selecting for different microbial assemblages and thereby sustaining microbial diversity across spatial scales. Microbial diversity is not static but varies dynamically across temporal scales, from tidal cycles that shift community composition to seasons that alter process rates and extending to long-term climate shifts that may reorganize functional guilds.² Together, these multi-scale dynamics maintain high levels of microbial diversity across taxonomic,

genetic, and functional dimensions. Despite serving as a foundational component of mangrove ecosystem functions, this microbial dimension remains largely overlooked in global conservation agendas and policy frameworks.³

MICROBES: THE DUAL REGULATORS OF MANGROVE ECOSYSTEM SERVICES

The renowned capacity of mangroves to act as powerful blue carbon sinks is largely mediated by microbial processes. Although microbial communities are key mediators and regulators of critical ecosystem services (Figure 1), their role is dualistic: they sustain functions under stable conditions but can also destabilize services under stress (e.g., eutrophication, warming, pathogen invasion).⁴ In anoxic sediments, anaerobic decomposition—particularly under sulfate-reducing conditions—proceeds more slowly than aerobic decay, leading to the accumulation of organic carbon over millennia. Concurrently, microorganisms govern the net flux of key greenhouse gases. Methanogenic archaea produce methane (CH₄), which can be oxidized by methanotrophs; the balance is modulated by salinity, sulfate availability, and plant-mediated transport. Similarly, emission of nitrous oxide (N₂O) result from nitrification, denitrification, and dissimilatory nitrate reduction to ammonia, with the net flux depending on sediment redox and nutrient status. Understanding these competing microbial processes is essential for improving the accuracy of net climate benefit assessments of mangroves.⁵ Furthermore, mangroves function as efficient natural water treatment systems through a combination of physical trapping, sedimentation, plant uptake, and microbial metabolisms. Microbial processes such as denitrification convert nitrate into nitrogen gas (N₂), reducing nitrogen loads and helping to prevent eutrophication. Specialized microbes also degrade organic pollutants (e.g., petroleum hydrocarbons, pesticides) and contribute to heavy metal immobilization via sulfide precipitation, adsorption to organic matter, and redox-driven transformations. However, metals can be remobilized under changing redox conditions, highlighting the need for careful management.

Beyond regulation, microbes contribute indirectly to provisioning services by enhancing plant productivity through symbiotic nitrogen fixation and growth promotion. They also hold cultural value through their biotechnological potential (e.g., novel antibiotics, enzymes) and as subjects of scientific inquiry and education. For instance, biofilm-forming bacteria secrete extracellular polymeric substances (EPS), binding sediment particles and stabilizing shorelines. Furthermore, beneficial microbes, including nitrogen-fixing bacteria and plant-growth-promoting fungi, form symbiotic relationships with roots, enhancing nutrient acquisition and fueling productivity. Moreover, the extreme and fluctuating conditions of mangrove habitats select for microbes with unique metabolic pathways, making these sediments a hotspot for novel antibiotics and industrial enzymes. Preserving this genetic reservoir is therefore not only a matter of biodiversity conservation but also of safeguarding future biotechnological opportunities. However, the microbial influence holds an equally potent destructive capacity. Microbial community also includes pathogens and conditionally harmful taxa (e.g. *Alternaria alternata*) that can threaten mangrove plants (e.g. *Bruguiera gymnorhiza*) health.⁶ Pathogen outbreaks can lead to forest decline, directly undermining coastal protection and biodiversity. Therefore, a diverse and functionally balanced microbiome—characterized by stable process rates, low pathogen loads, and the capacity to maintain functions under stress—sustains and enhances mangrove ecosystem services. Conversely, a functionally degraded or

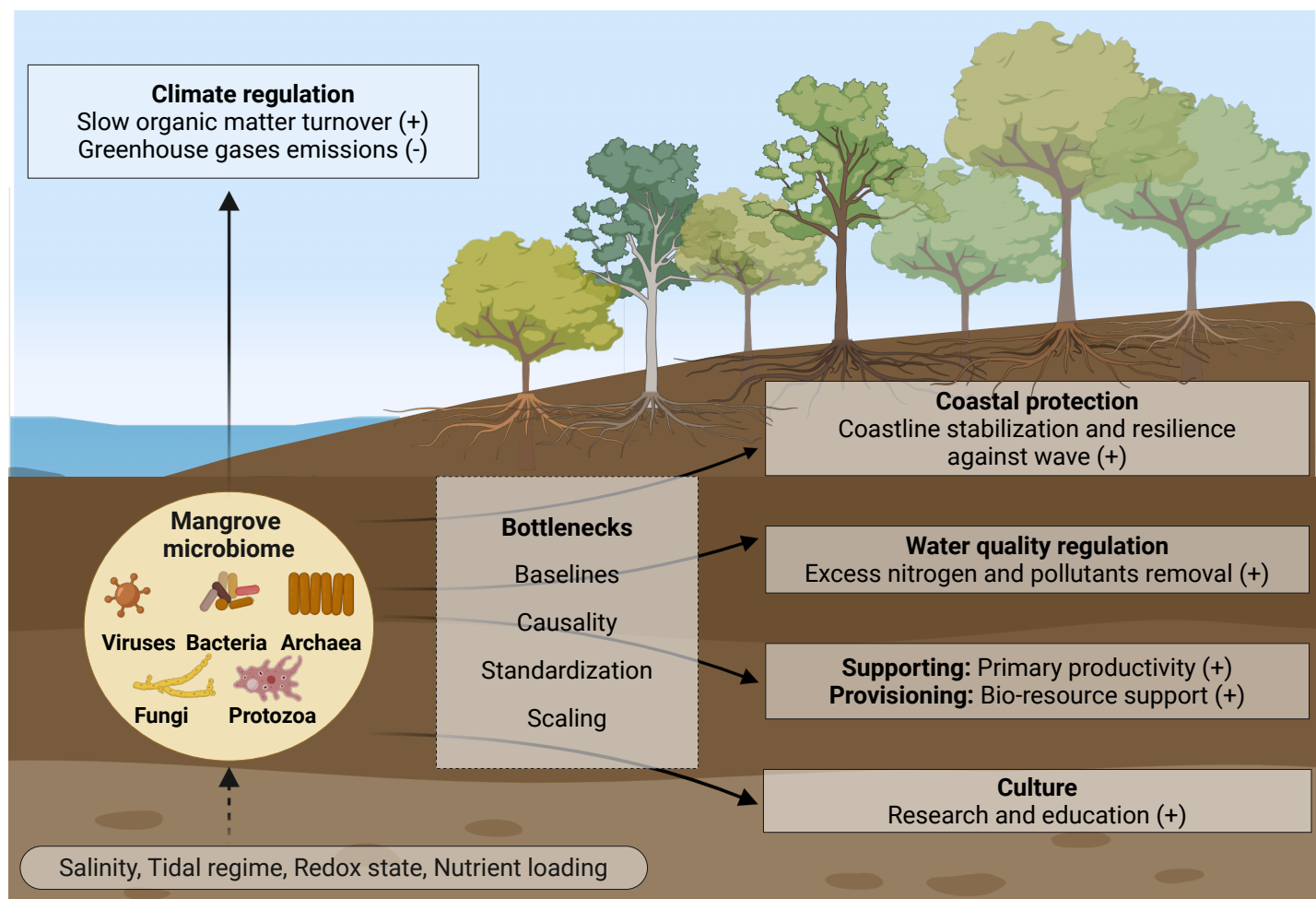


Figure 1. Integrative framework linking microbial diversity to ecosystem services in mangroves The diagram illustrates the pathway from microbial biodiversity to ecosystem services. Key research bottlenecks—including the need to generate baseline reference datasets, establish causal mechanisms, develop standardized indicators, and address scaling challenges—are explicitly indicated (dashed boxes) to highlight critical gaps that currently impede mechanistic understanding and effective management. The strength and direction of microbial contributions are modulated by environmental factors (e.g., salinity, tidal regime, redox state, nutrient loading). The plus (+) and minus (-) signs denote positive and negative impacts of microbial diversity on ecosystem services, respectively. The figure was created with www.biorender.com.

pathogen-dominated microbiome can precipitate the loss or reversal of these services. The conservation of mangrove ecosystem services is thus inextricably linked to the stewardship of microbial diversity and functional integrity. To ignore this unseen majority is to risk overlooking key microbial processes that determine the success of conservation and restoration efforts.

A ROADMAP FOR INTEGRATING MICROBIAL DIVERSITY INTO MANGROVE CONSERVATION

Despite their fundamental role, microorganisms are rarely mentioned in major policy instruments such as the Ramsar Convention guidelines or national mangrove management plans, reflecting a perception that they are too abstract or complex to integrate into conservation practice.³ Even within established conservation mechanisms such as World Heritage sites—which have been shown to deliver critical biodiversity co-benefits across ecosystem, species, and genetic levels—microbial dimensions are rarely considered.⁷ The recent establishment of the Microbial Conservation Specialist Group (MCSG) by the International Union for Conservation of Nature (IUCN) provides an institutional catalyst to bridge this gap.⁸ Concurrently, the newly established International Mangrove Center (IMC), as an intergovernmental organization dedicated to mangrove protection and restoration, offers a platform for global collaboration.⁹ While the IMC does not have direct regulatory authority, it can facilitate the development of technical guidelines, support pilot projects, and promote knowledge exchange among member states. Harnessing these complementary institutions—MCSG to set microbial conservation standards and IMC to support their implementation through

capacity building—offers a realistic pathway for integrating microbial considerations into mangrove management.

To translate this institutional foundation into actionable conservation, we propose three priorities. First, establish baseline reference datasets. A critical obstacle is the lack of baseline datasets across mangrove habitats, making it difficult to distinguish natural variation from anthropogenic degradation or define meaningful restoration targets. Establishing baselines requires coordinated sampling across biogeographic regions, vegetation zones, and tidal elevations using standardized protocols.

Second, shift research focus and develop functional indicators. Research must move from describing diversity to uncovering causal mechanisms—clarifying how microbial diversity, together with hydrology and salinity, regulates blue carbon stability and nutrient removal. This transition is consistent with the aims of the Mangrove Microbiome Initiative (MMI), an international research network announced to advance the field by moving from descriptive studies to hypothesis-driven research that identifies microbial mechanisms underpinning ecosystem resilience and opens opportunities for microorganism-mediated restoration.¹⁰ This requires developing standardized microbial indicators of ecosystem health (e.g., denitrification rates, methane production potential, abundance of key functional genes like *nosZ*, encoding nitrous oxide reductase catalytic subunit, and *mcrA*, encoding methyl-coenzyme M reductase alpha subunit) and identifying functional hotspots for priority protection using spatial mapping and thresholds. A persistent challenge is scaling: can plot- or gene-level indicators reliably predict landscape- or national-scale service outcomes? This demands multi-

scale sampling designs and transfer functions linking microbial metrics to ecosystem processes. Concurrently, restoration ecology should move beyond planting-focused approaches toward microbiome stewardship—managing environmental conditions (e.g., hydrology, sediment quality) to naturally foster a resilient microbiome. Emerging interventions such as probiotics remain experimental and require rigorous risk assessment and biosecurity protocols. These scientific endeavors align directly with the MCSG's stated goal of developing microbial assessment frameworks and with the IMC's mission to translate research into practical conservation tools.⁸

Third, integrate microbial monitoring into policy frameworks with supporting mechanisms. The Kunming-Montreal Global Biodiversity Framework offers an opportunity to incorporate microbial functional indicators into national reporting alongside species-based metrics.³ Major mangrove-range states should pilot a minimal package: (a) denitrification and methane production rates using standardized protocols, (b) quantification of key functional gene abundances (e.g., *nosZ*, *mcrA*) via quantitative polymerase chain reaction (qPCR), and (c) low-cost sampling designs stratified by vegetation zone and tidal elevation, with capacity-building support for local laboratories. Organizations like the IMC can facilitate training, harmonise protocols, and support pilot projects. Ultimately, realizing this integration roadmap requires sustained funding for long-term monitoring and research, plus interdisciplinary capacity through regional training hubs, open-access data platforms, and the development of low-cost, field-deployable methods, with particular attention to experts from low- and middle-income countries. By 2030, success would see mangrove management plans incorporate microbial indicators alongside those of flagship species, signaling a profound transformation in how biodiversity is understood, valued, and safeguarded—provided that prior investments in standardization, validation, and capacity building are made.

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AUTHOR CONTRIBUTIONS

Cui-Jing Zhang: Literature Review, Writing – original draft, and Figure preparation. Rui Zhang: Conceptualization, Writing – review & editing, and Supervision. Meng Li: Conceptualization, Writing – review & editing, Supervision, and Funding acquisition. All authors contributed to the manuscript and approved the final version.

DECLARATION OF INTERESTS

The authors declare no competing interests.