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Toward planetary microbial systems biology

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SUMMARY

Microorganisms underpin Earth's biosphere, sustaining life, shaping biogeochemical cycles, and maintaining ecosystem stability. In an era of scientific and geopolitical fragmentation, we advocate for a "planetary microbial systems biology" (PMSB) framework to uncover the mechanisms and organizational principles governing Earth's interconnected microbial systems across scales of matter, space, and time and in relation to underlying natural and anthropogenic drivers. PMSB combines molecular and cellular technologies, multi-omics data, artificial intelligence (AI), and integrated transdisciplinary research across ecosystems. By federating open data and combining field observations, experimentation, and modeling, PMSB enables predictive understanding of microbiome dynamics across planetary scales, thus filling a critical knowledge gap in our understanding of the co-evolution of life and the Earth-system.

INTRODUCTION

Microbes (viruses, prokaryotes, and micro-eukaryotes) have been the understudied architects of Earth's biosphere, driving its evolution through the emergence of an extraordinary diversity of metabolisms, cellular structures, and ecological interactions over billions of years.[1] They have colonized nearly all environments, and through their activities and interactions with biotic and abiotic components, they sustain ecosystems and drive essential planetary processes such as carbon and nitrogen fixation, sulfate reduction, methanogenesis, and the biological carbon pump that regulates ocean carbon sequestration and global climate.

At first glance, microbial dispersal appears limited by the wide and complex array of physical and biological boundaries within and across ecosystems, from host organism-associated barriers to shifts between distinct water masses or soil-plant-driven biomes. However, microbial life forms a planetary continuum. Microbes traverse the hydrosphere, soils, the atmosphere, and multicellular hosts, creating globally interconnected networks shaped by multiscale interactions. This planetary microbial connectedness is vividly illustrated in satellite observations of photosynthetic pigments from prokaryotic and eukaryotic phytoplankton in the world surface ocean (Figure 1A); Saharan dust storms transporting bioaerosols across the Atlantic Ocean to North America[2] (Figure 1B); or the intercontinental microbial links from the Amazon River's runoff reaching African coastlines (Figure 1C). Human activity further accelerates microbial dispersal and community coalescence at planetary scale[3] (Figures 1D–1F).

Today, this planetary microbial continuum is undergoing unprecedented, understudied, and thus unnoticed, changes as anthropogenic pressures intensify across ecosystems globally.[4] Documented biodiversity loss among macroscopic wildlife over the past 70 years has been staggering,[5,6] while a 2023 study found that six of the nine planetary boundaries that define the Earth's "safe operating space" have already been crossed.[7] It is therefore urgent to understand how these changes affect microbiomes.

Meeting this challenge requires extending our conceptual and methodological frameworks beyond their current boundaries and existing disciplines. To understand how microbial systems and functions evolve, how they respond to environmental change globally, and to predict their behavior, it is essential to build on the powerful tools of molecular and cell biology while moving beyond the traditionally reductionist focus of experimental life sciences. This means integrating microbial processes into ecological and evolutionary theory, which has largely been built upon studies of macroscopic organisms. A holistic framework is needed to

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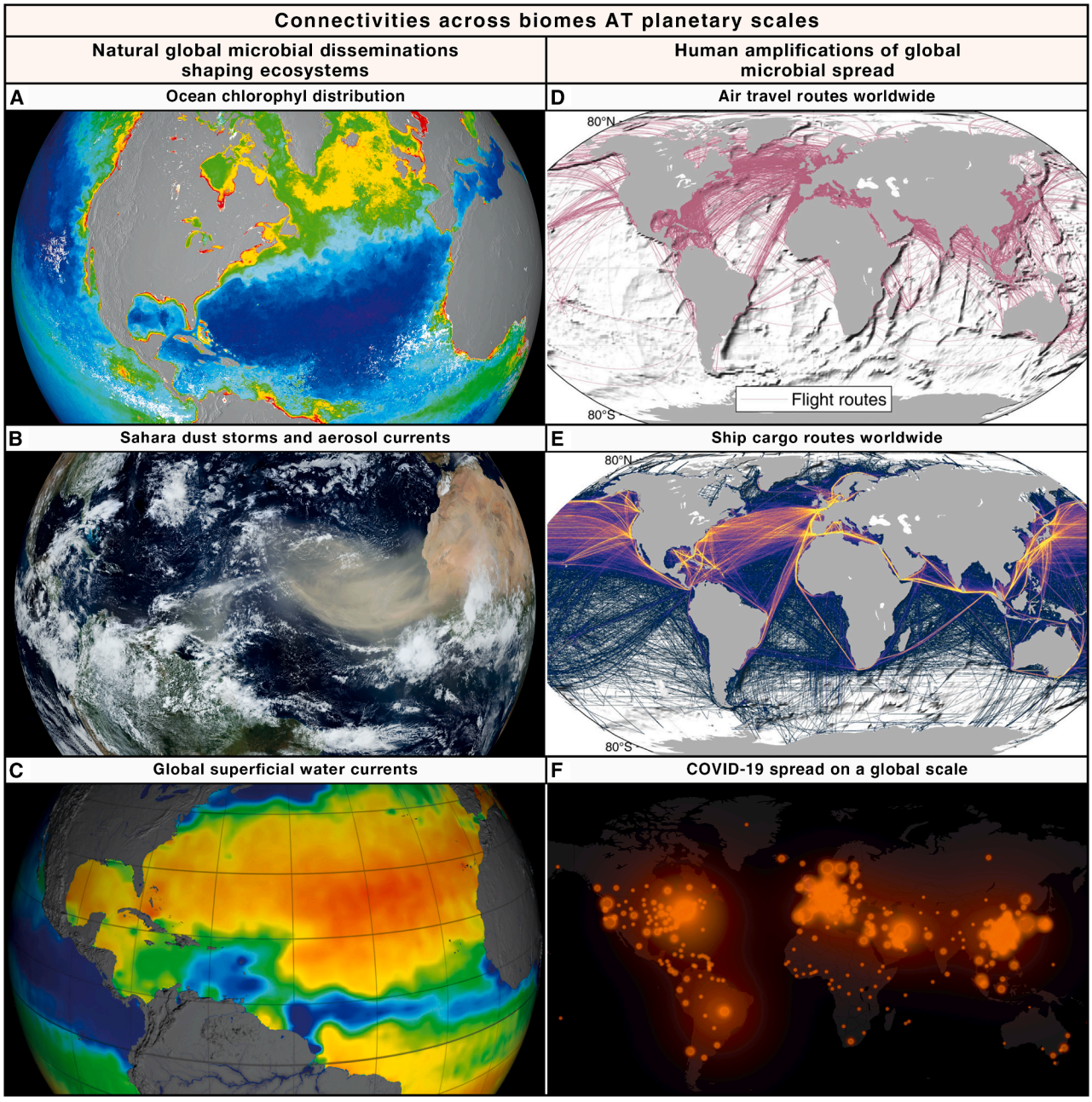


Figure 1. Microbes are shaping the biosphere across planetary scales

(A) Planetary-scale interconnectedness of photosynthetic prokaryotes and microbial eukaryotes in the world surface ocean, as revealed by satellite ocean color data from the Moderate Resolution Imaging Spectroradiometer MODIS, NASA. Image by Norman Kuring, acquired by the Suomi NPP satellite and licensed through Image Professionals GmbH.

(B) Massive Saharan dust clouds move microbes intercontinentally, from Africa into North America over the Atlantic Ocean in June 2020 (NASA's Scientific Visualization Studio [SVS]).

(C) Plume of Amazon River's fresh water extending from Brazil to Africa, revealed by satellite sensing of surface ocean salinity data (NASA's SAC-D Aquarius mission SVS).

(D) Reconstruction of the daily air travel routes worldwide over the ocean and (E) global maritime shipping routes, illustrating human-mediated connectivity between distant regions.

(F) Rapid spread of COVID-19 cases around the world in 2020. Image, Sebestyen Balint/stock.adobe.com; used under license.

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Box 1. Concepts and hypotheses underlying planetary microbial systems biology

PMSB extends the systems-biology paradigm from cells and individual organisms to the interconnected microbiomes of an entire planet. Its defining move is a shift in the unit of analysis: not the single cell, nor even the local community, but the continuum of microbiomes connected across planetary habitats. Its premise is that Earth's biosphere is an integrated biogeochemical system whose irreversible evolution is driven by the increasing complexification of life, and in which sensing, regulation, feedback, and emergent properties operate across planetary scales of matter, space, time, and environmental drivers. Yet, the principles governing its self-organization, homeostasis, and long-term evolution remain largely unknown. PMSB therefore aims to resolve the molecular and cellular mechanisms underlying microbiome interactions among microorganisms, their environments, and the associated macrobiota, and to explain how those interactions generate the ecosystem functions that sustain the Earth-system and underpin predictive understanding across ecosystems.

This conceptual framework builds upon five core pillars:

Interconnectivity: Earth's microbiomes do not exist as isolated systems but form an interconnected planetary continuum linked by biological, chemical, and physical exchanges.

Co-evolution: microorganisms and the Earth continuously shape one another, forming a co-evolving planetary system.

Emergent properties: planetary microbial functions emerge from the interactions across scales of biological organization, space, and time, and are shaped by natural and human-made drivers.

Underlying mechanisms: interaction networks between genes, proteins, metabolic pathways, and organisms drive the mechanisms of PMSB and should be explored together within their geophysical and chemical contexts.

Prediction: predictive understanding arises from the integration of field observations, ecosystem experimentation, and computational modeling to reveal planetary-scale mechanisms and predict ecosystems and Earth-system behaviors.

Why a dedicated framework is needed. The living component of the Earth-system is composed of cells whose molecular machineries have co-evolved with planetary geochemical processes and, through poorly understood eco-evolutionary feedbacks, have profoundly reshaped them over geological timescales. For more than three billion years, Earth's biosphere was shaped exclusively by unicellular and colonial organisms. Prokaryotes established the planet's major redox metabolic networks and actively transformed its initial matrices, water and rock. The subsequent emergence of eukaryotes generated an extraordinary diversity of cellular forms, subcellular and extracellular structures, and behaviors that far exceed the cellular diversity found in the relatively recent multicellular macroscopic lineages. From an Earth-system perspective, animals and plants are recent and exceptional rather than representative of life.

Yet, the conceptual tools available to us were built on precisely those exceptions. Ecological and evolutionary theory derives largely from observations of animals and plants, systems biology has concentrated on the molecular and cellular mechanisms of a small number of model organisms and organoids, and even integrative frameworks such as One Health remain centered on our own species and its immediate interactions with animals and the environment. Meanwhile, the molecular and cellular repertoire and complexity of the microorganisms that constitute the overwhelming, invisible majority of Earth's biodiversity is still largely unexplored. The mismatch is not only one of coverage. The eco-evolutionary rules of unicellular life appear to differ in kind: collective behavior, pervasive horizontal interaction, and symbiogenetic processes seem to be the norm rather than the exception, challenging the classical concepts of species, of discrete ecosystems, and of neo-Darwinian evolution driven by competition. Advancing beyond these limitations requires a new phase of integrated, planetary-scale exploration to uncover the fundamental functions, organizational principles, and scaling laws that emerge across microbial ecosystems.

Example questions that PMSB makes tractable. PMSB provides a roadmap for addressing questions that have remained largely inaccessible:

Which genes, molecules, cellular structures, and taxa dominate the different biomes of the planet, and which ones are core planetary functions versus biome-specific adaptations? What are the main modes and mechanisms of interactions between microbes across the competition-cooperation spectrum, and how redundant, plastic, and resilient are microbial interactomes? Which interactions mediate the transfer of matter, energy, and information across ecosystems and their interfaces? What are the self-organized patterns of interactomes across planetary spatial and physicochemical gradients and constraints (e.g., nutrient diffusion and light availability), and which scaling laws emerge from these patterns and constraints? How can these be translated into ecosystem and planetary functions, which drivers influence these functions, and at which spatiotemporal scales?

identify key components, map their interconnections, and investigate their spatiotemporal dynamics, while accounting for the emergent properties that span molecular, cellular, and organismal interactions through to ecosystem-level processes.[8–14]

We therefore advocate for a planetary microbial systems biology (PMSB) framework (see PMSB Box 1). PMSB builds on the achievements of planetary-scale initiatives that have transformed our understanding of global microbial diversity, distribution, and environmental associations, together with long-term local monitoring programs that have revealed seasonal and interannual microbiome dynamics. Rather than simply extending these efforts, PMSB asks a different class of biological questions aimed at uncovering the mechanistic and organizational principles that govern planetary microbiomes across ecosystems and organizational scales. Instead of asking which microorganisms are associated with particular environments or how microbial communities vary across the globe, PMSB asks whether common mechanistic principles govern the organization, functioning, and evolution of microbiomes across fundamentally different ecosystems. For example, do similar molecular and ecological mechanisms drive microbiome assembly, resilience, and adaptation across ecosystems? Do similar environmental perturbations elicit convergent microbial responses across soils, sediments, the atmosphere and the ocean, thus revealing principles that transcend individual ecosystems? Can these mechanisms then be used to predict ecosystem resilience, identify planetary boundaries that should not be crossed, and forecast microbial responses to future environmental change?

PMSB has become feasible only recently, through the convergence of high-throughput multi-omic technologies, quantitative environmental imaging, *in situ* and remote sensing, AI, and experimental ecosystems. Yet, technological advances alone

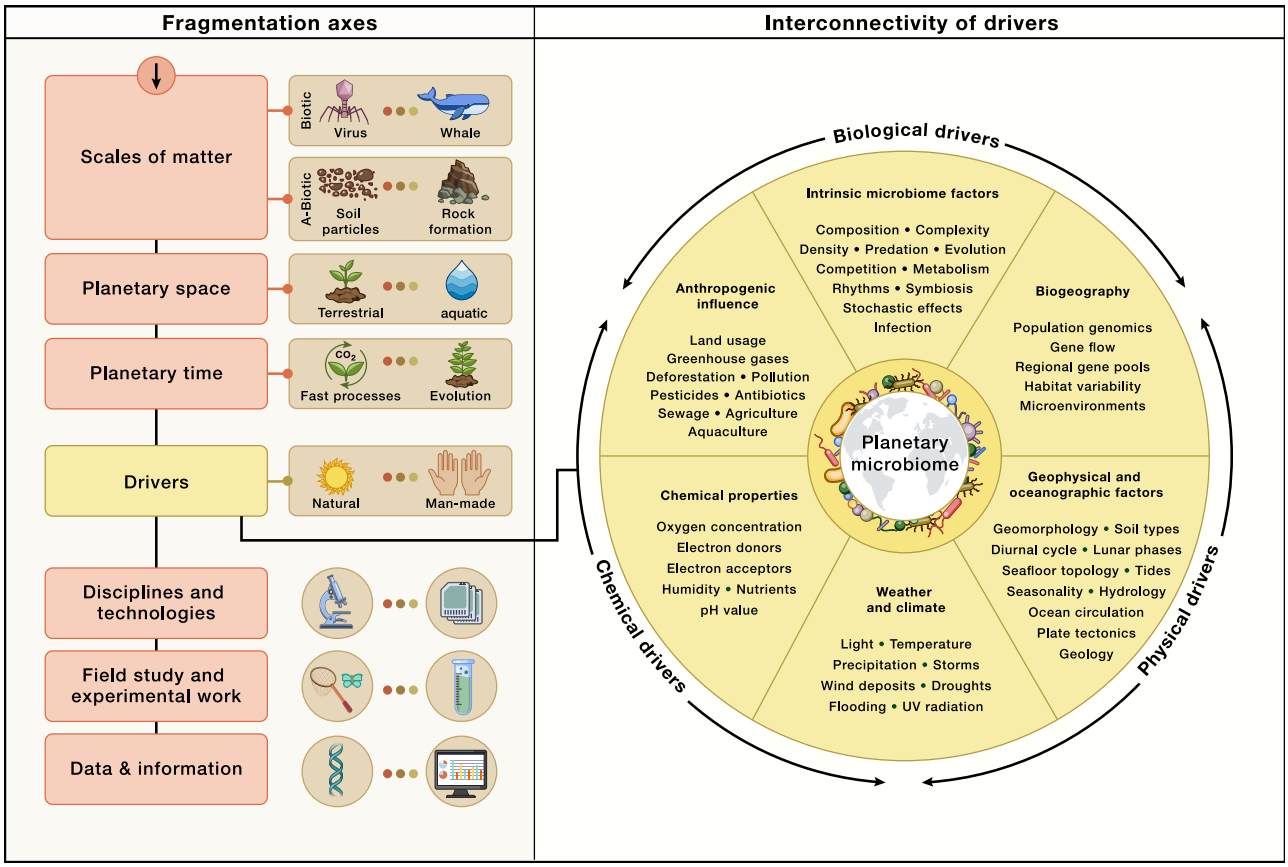


Figure 2. Fragmentation axes and interconnectivity of drivers of the planetary microbiome

(Left) The figure illustrates the major fragmentation axes in ecosystem research, including scales of matter, planetary space and time, environmental drivers, disciplines and technologies, the crosstalk of field and experimental approaches, and data integration.

(Right) This illustrates the complexity and interconnectivity of external factors shaping planetary microbiome structure and function, including environmental, biological, and human-made drivers. Most drivers remain unknown, even in confined and well characterized ecosystems such as the human gut.[23]

are insufficient to realize PMSB. Overcoming the long-standing fragmentation of environmental research, driven by technological constraints, disciplinary boundaries, geopolitical barriers, and short-term funding, also requires coordinated, long-term transdisciplinary research funding programs, interoperable datasets, and shared research infrastructures that integrate observations across biological and environmental scales. Together, these technologies and organizational advances create the conditions for a mechanistic understanding of the interactions that give rise to emergent properties across the Earth-system.

These conditions are no longer merely aspirational. In this perspective, we present the Traversing European Coastlines (TREC) Initiative as an empirical demonstration of how PMSB can be implemented in practice.

PMSB OVERCOMES FRAGMENTATION THROUGH AN INTEGRATIVE APPROACH

Understanding microbial systems at a planetary scale requires overcoming fragmentation across several interconnected axes: the scales of matter, space, and time; the drivers shaping microbial systems, scientific disciplines, and technologies; field observations and experimental approaches; and data and information (Figure 2). PMSB aims to overcome these divisions by integrating observations, experiments, technologies, and data to achieve a holistic understanding of planetary microbial systems.

Integrating across the *scales of matter* at various levels of biological complexity

Microbial systems are complex and adaptive,[14,22] forming vast, self-organized networks spanning from viruses to microbial eukaryotes that continuously interact with their biological, chemical, and physical environments. Understanding these systems requires observations across levels of biological organization, from the molecular and cellular mechanisms governing sensing, metabolism, and biogeochemical transformations to the interactions among organisms, communities, holobionts, and abiotic environments. Integrating observations across scales links molecular and cellular mechanisms with ecosystem and Earth-system processes.

Among the initiatives aligned with PMSB, relatively few investigate microbial systems across these scales of matter. This

reflects both the extraordinary diversity of microbiomes and the technical complexity of measuring the intricate, multi-layered nature of microbe-environment interactions. These challenges are further compounded by broader structural constraints, which include the complexity of coordinating large-scale operations and funding schemes that remain poorly suited to long-term transnational research efforts. As a notable exception, *Tara* Oceans[24] provides one of the first large-scale demonstrations of how this fragmentation axis can be overcome by investigating plankton communities across organismal size fractions from viruses to animals in the global ocean, while simultaneously measuring more than 200 (bio)chemical and physical parameters.

Exploring the *planetary space*

Microbes thrive, adapt, and evolve across habitats, ecosystems, and biomes, unconstrained by national borders. Each level of spatial granularity, from microscopic microbial communities in soil aggregates to global patterns in ocean microbiomes, reveals different aspects of the organization and function of life on Earth.[42] Only by integrating these spatial scales can we understand how microbial molecular and organismal interactions shape macroecological properties. However, multiscale exploration of different ecosystems (e.g., terrestrial and aquatic), biomes (e.g., temperate forests and deserts), and microscale habitats (e.g., sediment layers) are often constrained by national borders, funding structures, and regulatory frameworks within countries/regions.[43] Consequently, research has focused on a limited number of intensively studied locations, while vast regions, particularly those with limited research infrastructure, remain underexplored.

The composition of microbial communities in terrestrial, freshwater, and marine environments varies dramatically, thus reflecting adaptations to temperature, salinity, anoxic/oxic conditions, pressure, and the complexity of their environmental matrices.[44] Comparing microbial life across these contexts will help to distinguish the universal microbial processes at the core of the Earth-system from those adapted to specific environments and habitats. Furthermore, ecosystems are connected through continuous physico-chemical gradients rather than discrete entities. Ecotones, therefore, provide unique opportunities to investigate microbiome transitions,[45] to identify environmental thresholds and tipping points, and to assess the vulnerability of keystone microbes and microbial communities to local and global change.

To date, the spatial dimension is arguably the best-resolved fragmentation axis in PMSB, with several projects achieving a truly planetary scale (Table 1). These include the Global Ocean Survey (GOS), which in 2007 was the first expedition to gather global metagenomics data across the Pacific[46]; the Malaspina 2010 expedition[23]; and the first planetary-scale topsoil metagenomic study, which revealed regional and global patterns in fungal-prokaryote interactions, mainly shaped by antibiotic resistance.[47] While impressive in scope, these projects generally focused on a single biome (marine or terrestrial) or lacked temporal depth. Other initiatives have explored microbial gradients and biome interactions at more local or regional scales, including the Crete Island Sampling Day[48] and the Microflora Danica[49] projects, which provide valuable cross-biome insights at spatially restricted areas.

Incorporating biological *time*, from past to future

Biological timescales span picoseconds for macromolecular changes, milliseconds for immediate behavioral responses, hours and days for rapid acclimatization, and months for seasonal cycles. They stretch further to years and decades for ecological shifts, and thousands to millions of years for evolutionary processes. These timescales shape the biological rhythms that synchronize microbial metabolism, physiology, growth, reproduction, and behavior in response to environmental cycles. Linking processes across timescales is essential to understand how microbial systems function, adapt, and coevolve with the Earth-system.

Currently, different biological timescales are rarely studied in connection with one another. Although biological time series are increasingly being established to assess ecosystem rhythmicity, synchrony, and long-term dynamics, observations often remain fragmented, misaligned (e.g., due to protocol variations or time-stamp differences), or limited in temporal resolution. Additionally, overlapping cycles, such as shifting tides and diurnal rhythms, can obscure microbial responses to environmental change, particularly during extreme events such as floods and marine heatwaves. These challenges highlight the need for high-resolution time-series observations tailored to the temporal resolution required to answer specific biological questions.

Long-term perspectives are equally essential for understanding the macro-evolutionary processes and microbial responses to climate change, pollution, biodiversity loss, and environmental adaptation. Traditionally, phylogenomics and extinction-speciation models[50,51] have been the principal tools. However, paleogenomics methods provide new opportunities for hindcasting. These methods leverage environmental samples, such as soil, sediment, and ice cores, to help with reconstructing ancient ecosystems. Paleogenomic analyses have successfully reconstructed ecosystem diversity from two million years ago,[52] shedding light on microbial evolution over geological timescales. At shorter timescales, they can also reveal human impacts on microbial communities during the Anthropocene.[53] Environmental archives can also enable the revival of microbial resting stages (microbial "resurrection"), which provides a unique opportunity to investigate how microorganisms adapted to past environmental conditions respond to contemporary and future environmental change (e.g., through performance curve experiments[54]).

Encouragingly, a growing number of time-series programs employ molecular monitoring with increased temporal resolution and standardization (e.g., European Marine Omics Biodiversity Observation Network [EMO-BON], Long Term Ecological Research Network [LTER], and BioGeoSCAPES).[55,56] Some of these initiatives generate observations from specific ecosystems spanning multiple biome layers over decadal time frames, providing insights into the rates of ecosystem dynamics.[57] At the same time, there is growing recognition of the value of environmental archives and paleogenomic analyses for extending the temporal perspective of microbial ecology, thus creating new opportunities to integrate contemporary observations with reconstructions of past ecosystems.

Integrating timescales within PMSB requires coupling high-frequency *in situ* observations, long-term monitoring programs, sediment archives, and computational models. Computational

Table 1. A selection of multinational, multiscale projects that have overcome at least some of the research fragmentation challenges

Project	Highlights	Data access
Long Term Ecological Research Network (LTER)[25]: Since 1980. A network of research sites across diverse ecosystems (e.g., forests, grasslands, freshwater, marine, and urban). Focused on long-term ecological phenomena, studying processes such as climate change, biodiversity, and ecosystem dynamics. Collects extensive data on ecological variables, including biotic and abiotic factors, across temporal and spatial scales.	exemplary data repository, availability of long-term data.	central data repository with almost 10,000 data packages of diverse measurements and data types[26] Most recent data submission in 2025.
ForestGEO[27]: Since 1981. Established to advance the long-term study of the world's forests, encompassing 78 research sites across 29 countries. Data collection includes comprehensive tree censuses, species identification, growth measurements, environmental variables, and molecular data such as DNA barcoding.	long-term data collection.	data partially available upon request[28] and also via R packages.
Eurostat LUCAS Survey (land use/cover area frame survey)[29]: Since 2006. *In situ* surveys conducted every three to four years, covering the entire European Union. Collects harmonized data on land use, land cover, and environmental parameters through direct field observations. Partially also includes data on soil chemistry.	providing standardized data on the level of a whole continent across 18 years.	data available from website and data repository,[30] including metagenomic sequencing data for 658 samples. Most recent dataset from 2024.
GEO BON (Group on Earth Observations Biodiversity Observation Network)[31]: Since 2007. Coordinating global efforts to monitor and assess biodiversity changes as a collaborative network of scientists and institutions. Developing essential biodiversity variables (EBVs) and supporting national, regional, and global biodiversity monitoring systems. Focusing on terrestrial, marine, and freshwater ecosystems. Delivering open access data to inform policy, conservation, and sustainable management.	development of standardized indicators for various aspects of biodiversity.	central data repository[32] with 48 datasets of diverse data types. Most recent dataset from 2024.
***Tara* Oceans**[33]: Since 2009. Sampling campaigns on board the schooner *Tara*. Covering the open oceans around the world. Measuring metagenomes, metatranscriptomes, metabarcodes, as well as morphologies, across 11 plankton size fractions from viruses to animals, together with 216 contextual (bio)physical and chemical parameters. Ongoing expeditions, e.g., in the context of TREC.	large number of contextual parameters.	sequencing data,[34] quantitative imaging, and contextual data.[35]

(*Continued on next page*)

Table 1. *Continued*

Project	Highlights	Data access
Earth Microbiome Project[36]: Since 2010. Global collaborative effort to catalog microbial diversity across a wide range of environments. Collecting and analyzing 16S rRNA gene sequences from environmental samples. Leveraging standardized protocols for DNA extraction, sequencing, and bioinformatics. Covering ecosystems including soil, oceans, freshwater, air, and host-associated habitats. Generating comprehensive datasets to map microbial distribution, diversity, and ecological functions worldwide.	breadth of sampling across planetary space.	sequencing and contextual data available.[37]
Global Soil Mycobiome Consortium[38]: Since 2015. Sampling campaigns conducted across 108 countries, collecting 3,200 composite soil samples. Analyzing full-length internal transcribed spacer (ITS) regions and 18S rRNA gene V9 regions to achieve high taxonomic resolution. All samples collected and processed using standardized protocols, with molecular analyses performed in a single laboratory.	global, land-based sampling campaign across all continents.	sequencing and contextual data available.[39]
Earth BioGenome Project[40]: Since 2018. A global initiative to sequence, catalog, and analyze the genomes of all eukaryotic species on Earth within a decade. Prioritizing reference-quality genomes across taxonomic groups, with a focus on species of ecological, evolutionary, and societal importance. Generates genomic data to advance understanding of biodiversity, evolution, and ecosystem functionality, addressing over 1.5 million known eukaryotic species.	serves as an umbrella for many eukaryotic sequencing projects.	data portal for sequencing progress and data.[41]

modeling, increasingly supported by AI models, can serve as a bridge across timescales, thus linking molecular and ecosystem-level processes and generating projections of microbial ecosystem responses to climate change. While microbial processes are increasingly incorporated into Earth-system models, including those used in the Intergovernmental Panel on Climate Change simulations,[58] predictive capacity remains constrained by our limited understanding of microbiome functional diversity, adaptation, and evolution. Addressing this gap requires standardized paleocore sampling and paleogenomic analyses to link microbial dynamics across time with planetary "space"-scale patterns. Connecting observations across timescales will be essential for uncovering the eco-evolutionary mechanisms governing microbial resilience, adaptation, and planetary change.

Deciphering drivers that underpin microbial networks

Microbial communities are shaped by a multitude of internal and external drivers, defined here as measurable biotic and abiotic factors that influence microbial communities, their interactions, dispersal, adaptation, evolution, and ecosystem-level functions. Intrinsic drivers, such as metabolic byproducts or symbiotic interactions, determine the capacity of microbial communities to self-regulate and respond to environmental change. In parallel, extrinsic factors, such as physical and chemical conditions, geomorphology, and climate, shape microbial ecosystems. Together, these drivers influence global biogeochemical cycles, ecosystem resilience, and human health. Understanding how these drivers interact across biological and environmental contexts is essential for explaining ecosystem function and change.

In today's world, human activities, such as the release of metals, oil spills, the use of pesticides and fertilizers, and wastewater discharge, are substantially changing planetary microbiomes,[59] often at rates that exceed our capacity to disentangle natural variability from anthropogenic impacts. Disentangling these drivers is therefore essential for predicting microbiome dynamics and designing effective interventions across agriculture, medicine, and environmental sustainability.

PMSB requires systematically identifying, quantifying, and disentangling intrinsic and extrinsic, biotic and abiotic, and natural and anthropogenic drivers. Field programs should characterize these variables using advanced technologies. This

requires careful planning of field research initiatives: sampling strategies should be designed according to the climatic, ecological, and anthropogenic gradients to maximize statistical power and enable robust variance analyses.[60] Comprehensive *in situ* measurements increase the likelihood of identifying key drivers behind observed variation, including their non-linear synergistic and antagonistic effects, thereby strengthening the mechanistic basis for predictive modeling.

Despite their central role, only a limited number of environmental and biological drivers are typically measured in microbial ecosystem studies. Some PMSB-aligned initiatives illustrate how expanding the range of measured drivers can reveal the mechanisms underlying ecosystem dynamics. *Tara* Oceans, for instance, systematically measured a broad range of (bio)physical and chemical parameters at each sampling station, thus revealing water temperature as the dominant extrinsic driver shaping global ocean microbiomes.[24] At a more local scale, an eight-year plankton time series[61] revealed intrinsic drivers of microbial systems, such as complex self-organization within microbial interactomes that contributed to observed community dynamics. Longer-term studies also provide valuable insights. The Global Change and Terrestrial Ecosystems (GCTE) project explored how plant productivity, soil carbon dynamics, and biodiversity were affected by anthropogenic drivers such as rising temperatures and land exploitation. It highlighted the sensitivity of terrestrial carbon sinks such as soil to temperature, moisture, and land-use changes, revealing feedback loops that amplify climate change.[62] Even in the well-studied human gut, where more than 100,000 gut microbiomes have been sequenced, less than 20% of the inter-individual variation in microbiome composition is explained by drivers such as lifestyle, diet, or medication, whereas the contribution of host genetics and disease remain actively debated (for review see Schmidt et al.[63]). Together, these examples illustrate both the progress made and the remaining challenges in disentangling the interacting drivers underpinning microbial systems across biological and environmental contexts, thus highlighting a central objective of PMSB.

Bridging *scientific and technical frameworks*

One of the greatest challenges facing PMSB is the continued fragmentation of scientific disciplines. Different disciplines focus on complementary aspects of microbial systems while relying on distinct conceptual frameworks, methodologies, and technologies and even terminology. Overcoming this fragmentation requires a shared technical framework that enables observations generated using different methodologies and technologies to be compared, integrated, and interpreted within a common analytical framework. PMSB should therefore rely on harmonized sampling strategies, intercalibration exercises, and comprehensive metadata standards. Together, these elements ensure interoperability despite the continuous evolution of technologies. Standard operating procedures (SOPs) remain particularly valuable for preservation and biobanking (including legacy samples), metadata collection and data management, and integration and sharing, especially when long-term data comparability is required. Together, these approaches make datasets findable, accessible, interoperable, and reusable (FAIR) across projects and scales.

The technology and protocols used to study life, especially at molecular and (sub)cellular levels, are extremely diverse and rapidly evolving. Biomolecular technologies such as genomics, metabolomics, and proteomics often evolve faster than complementary analytical approaches in other disciplines. As a result, maintaining stable protocols and ensuring long-term comparability is challenging. PMSB should therefore incorporate hindcasting-compatible components and preserve legacy samples that can be reanalyzed as new methods and technologies emerge. Public documentation of protocols, analytical pipelines, and metadata also supports intercalibration and integration across projects.[64]

One of the main limitations of implementing PMSB is the limited accessibility of cutting-edge technologies and expertise across many parts of the world. These tools often remain prohibitively expensive and capacity-building efforts to make them available more broadly remain inadequate. As a result, many large-scale projects aligned with PMSB concepts have primarily been led by teams based in the Northern Hemisphere (Table 1). Developing affordable, open source technologies that can be deployed directly in the field represents one promising strategy to expand PMSB globally.[65]

PMSB will, therefore, require a coordinated research community that enables sustained collaboration across disciplines, institutions, and geographical regions. Beyond technical interoperability, establishing PMSB as a coherent research field will depend on long-term international coordination, equitable access to technologies, and sustained support for collaborative research initiatives capable of addressing fundamental questions about planetary microbiomes.

Combining data-driven *field studies* with hypothesis-driven *controlled experiments*

A central feature of PMSB is the iterative integration of large-scale field observations, controlled experimentation, and computational modeling. Field observations reveal patterns and scaling laws and generate new hypotheses. Controlled experiments then test those hypotheses, establish causal relationships, and uncover the underlying mechanisms. Finally, computational models evaluate whether these mechanisms can be generalized across habitats, ecosystems, and biomes while projecting future scenarios. Together, these complementary approaches move PMSB beyond correlations toward identifying causal mechanisms and predicting microbial responses to environmental changes.

It is notoriously difficult or impossible to culture many microbes in the lab, and even in cases where they can be cultured, they may not exhibit the cellular processes that take place in their natural environment. Therefore, PMSB must fill the gap between observational and experimental approaches. To achieve this, mobile research infrastructures such as mobile laboratories, modular containers, and field-deployable Ecotrons should be strategically deployed.[66] These infrastructures bring advanced analytical technologies and multidisciplinary expertise directly into ecosystems, thus enabling researchers to monitor and manipulate microbial communities under near-natural conditions while identifying ecological interactions, adaptive microbial traits, and responses to environmental stressors, which are often

difficult to reproduce in conventional laboratory environments. Importantly, such setups also allow for *in situ* cultivation of rare or previously uncultured microbes, which deepens our functional understanding of microbial roles in planetary systems.

PMSB also relies on controlled ecosystem experimentation facilities, such as macrocosms (Ecotrons), which enable more complex, multiparameter simulations of environmental conditions. These systems embrace ecosystem complexity while enabling the automatic measurement of ecosystem processes.[67] To maximize their impact, research infrastructures must coordinate across national borders and be federated to support PMSB efforts. An example is the Analysis and Experimentation on Ecosystems (AnaEE) European research infrastructure consortium, a legal entity that provides access to Ecotrons across Europe and fosters collaboration through shared access to advanced experimental research facilities.

The power of this iterative field-experiment-model framework has already been demonstrated across multiple microbial systems. For marine microbes, the interplay between laboratory-based model system experiments informing and being informed by field studies has been critical for establishing: (1) the limitations of single-gene markers for resolving microbial diversity and ecological function, and the importance of genome streamlining in shaping microbial lifestyles[68,69]; (2) genome-guided cultivation strategies[70,71]; (3) new approaches to global ocean biogeochemical modelling[72–75]; and (4) the effects of virus-infected cells on ecosystem outputs.[76–80] A concrete example of an approach that generated predictive insight is (3): physiological optima measured in cultured *Prochlorococcus* and *Synechococcus* strains were used to parameterize a model ocean in which community structure was allowed to self-assemble rather than being prescribed, and the emergent biogeography recovered the ecotype partitioning observed in the field[75]; the same trait-based approach underpinned projections of how these populations will redistribute under future warming.[74]

In gut microbiome research, diverse human populations are characterized through clinical phenotyping, followed up by *in vitro* and *ex vivo* studies. This results in new hypotheses and models that are then tested, an example being the identification of drug combinations that reduce the effect of antibiotics on commensal microbes, which were first identified *in vitro*, then validated *in vivo* in mice, and then elaborated by *ex vivo* cultivation in humans.[81–84] Together, these examples illustrate how continuous iteration between field observations, controlled experimentation, and computational modeling creates a virtuous cycle of discovery, thus transforming descriptive observations into mechanistic understanding and predictive capability.

Federating *data* and centralizing *information*

The continuous iterations between field observations, experimentation, and modeling generate enormous and heterogeneous datasets that must remain linked to samples, environmental data, and metadata to enable their preservation, integration, and reuse. Achieving this requires interoperable data flows across public databases, a major challenge for complex field studies generating multiple data types distributed across specialized repositories. Project-level data hubs can serve as useful intermediaries, provided they incorporate robust data-management systems capable of linking diverse datasets and metadata. To be effective, these hubs also require standardized metadata annotation and clear strategies for making derived datasets publicly accessible once geo-referenced raw data have been submitted to specialized public repositories. Long-term data stewardship that extends beyond the initial lifetime of a project is important, as only original data submitters may be able to revise or update datasets. To ensure the maximal utilization of analytical toolboxes, including machine learning, the consistent taxonomic and functional annotation of derived data from heterogeneous sources ideally generated through standardized sampling and sample processing, is crucial. This will also facilitate AI approaches by reducing biases and inconsistencies within training datasets.

Open access to the data of each project is essential, but discovering and integrating all the relevant data remains challenging when conducting research across scales from molecular to planetary scale. Many repositories hosting microbial data are habitat- or taxa-specific, store only certain data types, use heterogeneous metadata standards, or contain information that is not computer-readable. Furthermore, some valuable microbial data never reach public data resources, for example, remaining hidden in supplementary material in publications that are not openly accessible.

Encouragingly, many widely used data resources in the life sciences are broadening their mandate and extending their metadata and contextual data. For example, EMBL-EBI's molecular archives increasingly allow the archiving of additional layers of information alongside core data.[85] The European Nucleotide Archive (ENA) now integrates various annotations, some within its system, others with links to other resources.[86] At the ecosystem level, microbial species are receiving increased attention, and international collaborations, such as those between the Ocean Biodiversity Information System (OBIS[87]) and the Global Biodiversity Information Facility (GBIF[88]), are helping to overcome habitat-specific limitations by expanding biodiversity databases and incorporating genomic information.

Despite this progress, substantial challenges remain in ensuring equitable data access and usability, particularly in the Global South. Sustained investment in open data initiatives, standardized workflows, and large, international scientific consortia will be key to making high-quality biological data more accessible, interoperable, and reusable. Federating microbial data across repositories, scales, and disciplines will ultimately be indispensable for transforming fragmented observations into predictive knowledge of planetary microbial systems (Table 1).

OUTLOOK: A CALL FOR A COORDINATED INITIATIVE OF INTERCONNECTED PMSB PROJECTS

Throughout this perspective, we have argued for a shift beyond the disease-centered view of microbes, from Koch's etiology to modern frameworks such as One Health, toward recognizing microorganisms as ancestral, interconnected, and co-evolving drivers of planetary function. The reframing is urgent. The invisible living majority with whom we share the planet is being transformed by human activity, and these transformations could drive abrupt ecosystem shifts and the loss of unique microbial

Box 2. Traversing European coastlines

The TREC initiative was designed as one of the first large-scale efforts to test PMSB hypotheses by combining harmonized field observations, controlled experiments, and predictive modeling across interconnected terrestrial, coastal, marine, and atmospheric ecosystems. The TREC flagship expedition traversed European coastlines from Finland to Greece, thus providing an empirical framework for implementing PMSB principles at a continental scale. The expedition aimed to characterize how life is organized across coastal ecosystems where terrestrial and marine environments meet. These critical habitats, home to over 40% of the world's population, face significant pressures.[15,16] The expedition considered both natural and anthropogenic factors shaping the structure and function of life as an interconnected whole, transcending national boundaries and integrate observations from molecules to ecosystems and from microbes to plants and animals, so as to investigate how life responds and provide feedback to physical, chemical and biological drivers.

Involving more than 90 institutions from 30 countries, most of them in Europe, the TREC-*Tara* Europa expedition brought together experts from molecular biology to Earth sciences. To address the complexity of coastal ecosystems, more than 200 protocols enabled the study of local and global ecological gradients and drivers. Systematic sampling and processing combined molecular, cellular, and organismal observations, reducing fragmentation among research areas. After four years of preparation, TREC established standardized protocols drawing on previous initiatives such as EMOBON for sediments[17] and *Tara* Oceans for offshore and coastal waters.[18] From 115 land-sea transects, selected based on habitat, climate, land use, and human impact, more than 70,000 samples were collected, including sediment cores from 15 areas spanning the Anthropocene, providing a paleogenomic approach aimed at tracing and quantifying historical human impacts on microbiomes.

Customized ship- and land-based mobile labs were employed at the sampling sites for on-site characterization of life in its natural environment, thus enabling real-time imaging, advanced sample processing, and targeted follow-up analyses of selected organisms and communities. For example, by applying on-site automated high-resolution 3D fluorescence imaging and cell sorting[19] on fresh samples with community- and single-cell metagenomics, TREC enables the assignment of morphogenetic features to genomic information, including those resulting from symbioses, and the quantification of these features within and between microbial populations. Live samples collected during the first TREC expedition are also being used in meso- and macrocosm experiments, under partially controlled conditions over both short and the long term timescales. For example, experiments may replicate the concentration curves of harmful pesticides detected in specific sampling areas. These experiments establish a feedback loop between observation and experimentation, thus allowing hypotheses generated from field patterns to be tested under controlled conditions and refining mechanistic explanations of ecosystem responses, such as their resilience to chemical pollutants through dose-response analyses. A central sample hub was set up at EMBL Heidelberg to handle storage, post-expedition shipping, and legacy samples. It is linked to a data hub that centralizes data handling and facilitates federated analysis. It performs quality-control on stores metadata as well as derived information on genes, (sub)cellular structures, and their interactions along with contextual data that will be openly shared as will be the raw data via dedicated public archives.[20] These resources are designed to be linked with other PMSB initiatives, and TREC envisions making its expertise, data infrastructure, and open access approaches available to future projects that follow PMSB standards.

One of the aims of the TREC initiative is to quantify direct human impacts on ecosystems. Samples were collected to assay for more than 4,000 relevant compounds, including pesticides, antibiotics, synthetic hormones, and forever chemicals, among many others. Another goal is to advance our mechanistic understanding of antibiotic resistance spread in natural settings, with relevance for human health, as the respective genes disperse between land and sea locally, although only very few microbes can thrive in both biomes. Generalists may resolve this apparent paradox as the likely vehicles of transfer, but their role has so far been inferred from co-occurrence in archived data.[21] TREC's land-sea transects allow the hypothesis to be tested where the transfer occurs: whether resistance determinants cross at the interface, in which direction, and at what rate. Other scientific pillars, with more than 150 sub-projects (https://www.embl.org/about/info/trec/projects/), center around quantification and the consequences of microbial biodiversity decline as well as delineation of keystone microbial metabolic processes, e.g., for carbon fixation, with potential impact on nutrient cycling and climate models.

(Continued on next page)

functions, many of which may hold solutions to the very crises that threaten them.

The scientific case for PMSB is straightforward: we still cannot quantify microbial functions at planetary scale, let alone predict them. For example, the contributions of photosynthetic and diazotrophic microbes to global carbon and nitrogen inventories are well recognized, yet the diversity and functional roles of microbes in terrestrial and marine ecosystems remain poorly constrained, thus impeding our understanding of even the most fundamental biogeochemical processes.[89] Supported by AI-enabled analyses of increasingly large, FAIR quantitative datasets, PMSB aims to move beyond describing diversity and function toward understanding the rules by which microbiomes assemble, adapt, interact with their environment, and together shape planetary processes.

Achieving this vision will require addressing three methodological challenges. The first is "granularity": systems biology's high-resolution tools were largely developed for biomedical settings, and their cost and infrastructure demands constrain their use elsewhere, so sampling strategies and analysis pipelines must be designed to the resolution a given question actually requires, which is a design problem that will increasingly benefit from AI support as studies accumulate publicly. The second is "process rates": assessing microbial transformation rates and the transfer of matter and energy between microbial processes and trophic/symbiotic levels, for which enabling technologies are only beginning to emerge.[90] The third is "extrapolation": new remote-sensing capacity such as NASA's PACE hyperspectral mission, coupled with *in situ* multi-omics and interpreted through machine learning, offers a route to interpolate between sampling sites and extend global coverage. Together these approaches could transform large-scale inventories into a predictive understanding of planetary microbial dynamics.

Box 2. *Continued*

To raise awareness for such topics and overcome fragmentation between research and the general public, the first TREC-*Tara* Europa expedition incorporated citizen science projects. It further took advantage of bringing science to many places and included an ambitious outreach and public engagement program, which targeted the general public and, more specifically, pupils, students, educators, and policymakers.



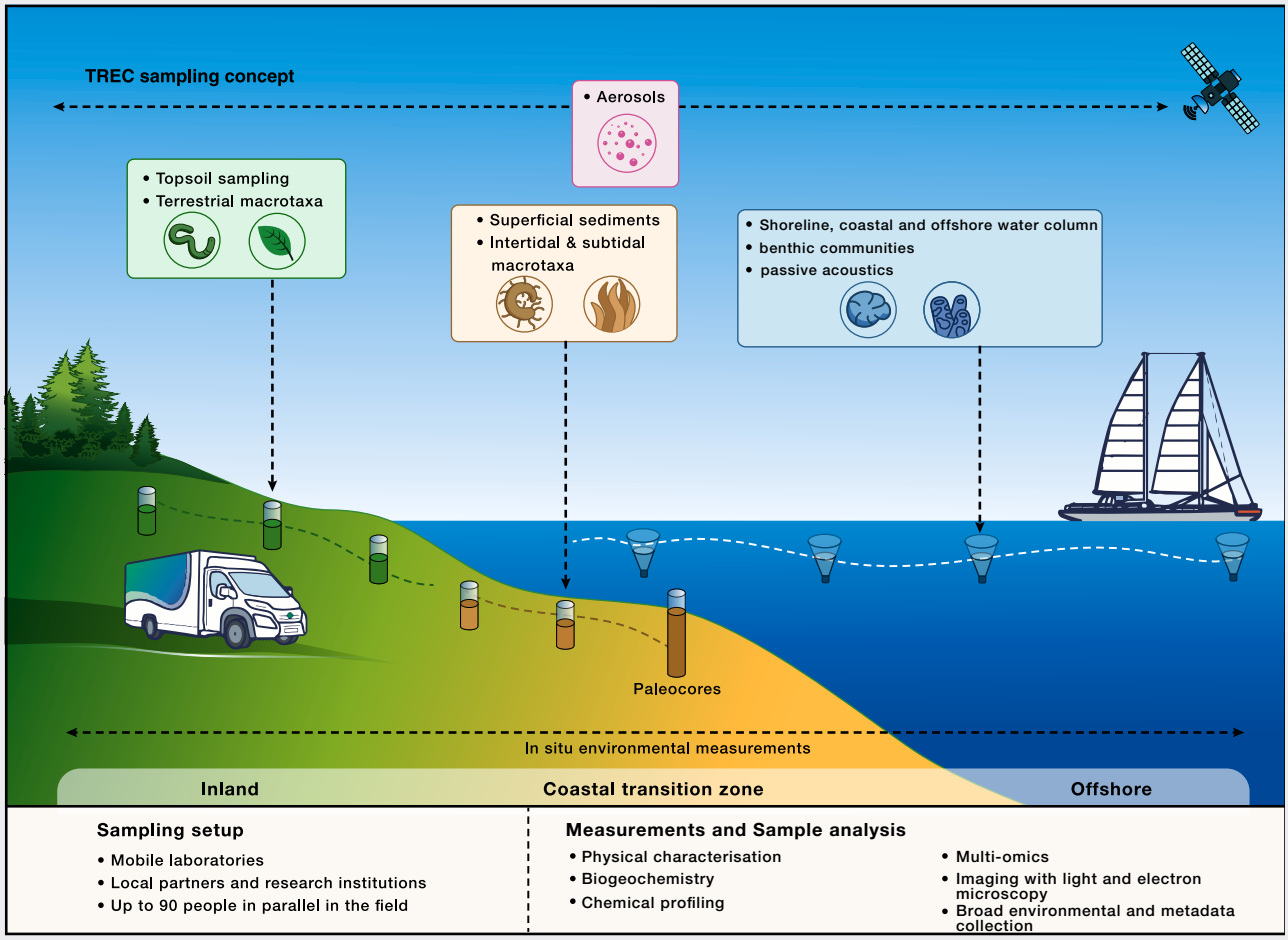
Mobile labs for studying microbiomes at the land-sea interface while engaging the public
A fleet of mobile labs on land (A) and on the sea. The research vessel Tara (D) supported fieldwork by enabling sampling (B) and on-site experiments with freshly collected samples (E). Scientific services and education were combined with public engagement activities involving the general public (C) and policymakers, including high-level political figures. Here is the then-president of Estonia (F).

(Continued on next page)

The infrastructure and policy case follows from these scientific challenges: no single project, discipline, or nation can answer these questions, which makes coordination a scientific requirement rather than an administrative one. This calls for internationally coordinated research infrastructures that bridge field observations and controlled experimentation across ecosystems and scales. Mobile laboratories bring experimentation and analysis to fresh samples, thus capturing transient dynamics and rare biosignatures that would be lost in transport, and are the practical means of extending PMSB into remote or logistically challenging environments; they should be paired with controlled-environment facilities such as Ecotrons, where mechanisms can be isolated and causality established. Both need to be federated across borders, made accessible through collaborative networks, and integrated with existing platforms such as Long-Term Ecological Research sites. The parallel challenge is harmonizing evolving methodologies and embedding them in everyday practice, so that data generated by different technologies remain interoperable as those technologies change. We therefore call for dedicated international programs, coordinated through an international center or hub that develops and disseminates standardized protocols for sampling, data acquisition, annotation, and open access, with research undertaken both within the hub and by the wider community to ensure inclusivity, scalability, and equitable participation beyond well-resourced regions. This depends in turn on funding instruments that sustain long-term international efforts rather than short project cycles.

The Traversing European Coastlines (TREC) initiative, through its large-scale TREC-*Tara* Europa expedition, provides a concrete example of how several of these principles can be implemented in practice. Bringing together international partners, harmonized methodologies, and an integrative sampling strategy, the expedition combines molecular, cellular, organismal, and environmental observations across Europe's coastal land-sea-air interfaces to investigate how physically connected yet biologically distinct ecosystems interact across boundaries and respond to natural and anthropogenic drivers. By generating interoperable, openly accessible datasets and enabling interdisciplinary research across biological and environmental scales, TREC lays the groundwork for mechanistic and predictive studies of microbial systems and offers a model for future internationally coordinated PMSB initiatives (see Box 2).

Box 2. *Continued*



TREC sampling concept

The TREC-*Tara* Europa expedition implements an integrative sampling strategy along land-sea transects extending from inland terrestrial areas to offshore marine waters. Broad *in situ* environmental measurements and comprehensive molecular, cellular, and chemical analyses enable the investigation of the interface of ecosystems across scales. The integration of paleoenvironmental records provides an additional temporal perspective.

Beyond the scientific and organizational challenges, the societal value of PMSB lies in translating predictive knowledge of microbial systems into actionable strategies for monitoring, protecting, restoring, and managing ecosystems. A mechanistic understanding enables the identification of bioindicators that remain informative despite the variability and noise inherent to biological systems, nature-based bioremediation strategies that work with, rather than against, the sensitivity of living systems. These applications span climate regulation, nutrient cycling, ecosystem restoration, and environmental monitoring. Some benefits are already visible in outline: a better account of microbial photosynthesis sharpens climate mitigation estimates, and a better account of the nitrogen cycle clarifies how human activity is perturbing it. Responding to environmental change requires a deeper appreciation of ecosystem services, both for their intrinsic value and for what they provide to humanity, and that appreciation must extend to microbes, which policymakers should recognize as allies in confronting these challenges rather than as agents to be eliminated. With vision, coordination, and sustained commitment, PMSB can establish the foundation for a new understanding of microbial life as a central component of the Earth-system and contribute to global sustainability.

CONSORTIA

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DECLARATION OF INTERESTS

The authors declare no competing interests.

DECLARATION OF GENERATIVE AI AND AI-ASSISTED TECHNOLOGIES IN THE MANUSCRIPT PREPARATION PROCESS

During the preparation of this work, the authors used ChatGPT (OpenAI) and Claude (Anthropic) to assist with language editing, improving clarity, and refining the presentation of the manuscript. After using these tools, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

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