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Perspectives on the future of ecology, evolution, and biodiversity from the Council on Microbial Sciences of the American Society for Microbiology

Denise M. Akob,[1] A. Elizabeth Oates,[2] Peter R. Girguis,[3] Brian D. Badgley,[4] Vaughn S. Cooper,[5,6] Rachel S. Poretsky,[7] Braden T. Tierney,[8] Elena Litchman,[9] Rachel J. Whitaker,[10] Katrine L. Whiteson,[11] C. Jessica E. Metcalf,[12] Ecology Evolutionary and Biodiversity Retreat Participants

AUTHOR AFFILIATIONS See affiliation list on p. 12.

ABSTRACT The field of microbial ecology, evolution, and biodiversity (EEB) is at the leading edge of understanding how microbes shape our biosphere and influence the well-being of humankind and Earth. To that end, EEB is developing new transdisciplinary tools to analyze these ecologically critical, complex microbial communities. The American Society for Microbiology's Council on Microbial Sciences hosted a virtual retreat in 2023 to discuss the trajectory of EEB both within the Society and microbiology writ large. The retreat emphasized the interconnectedness of microbes and their outsized global influence on environmental and host health. The maximal potential impact of EEB will not be achieved without contributions from disparate fields that unite diverse technologies and data sets. In turn, this level of transdisciplinary efforts requires actively encouraging "broad" research, spanning inclusive global collaborations that incorporate both scientists and the public. Together, the American Society for Microbiology and EEB are poised to lead a paradigm shift that will result in a new era of collaboration, innovation, and societal relevance for microbiology.

KEYWORDS microbial ecology, evolutionary biology, biodiversity, interdisciplinary, Anthropocene, machine learning

Antonie van Leeuwenhoek's first observations of microorganisms helped launch the field of microbiology (1), and throughout the 17th, 18th, and 19th centuries, scholars worked to understand the origins and diversity of microorganisms, as well as the role they play in natural processes such as elemental cycles, weather, and erosion. These were the world's first environmental microbiologists, and their work laid the foundations for all of microbiology as we know it today.

Microorganisms are ecologically ubiquitous and critical to the homeostasis of their native biomes. Many soil microbes bolster the health and well-being of most plants on Earth (2, 3), while marine microbes play a major role in carbon dioxide and methane flux into the atmosphere (4). Microorganisms annually cycle at least an order of magnitude more carbon dioxide than produced contemporaneously by humans (5, 6). The digestive systems of most animals are inhabited by microbes that typically play a key role in their fitness (7). Microbes are arguably responsible for the habitability of Earth as they play an essential role in providing bioavailable nitrogen to the entire biosphere via nitrogen fixation (8). Microbial communities are incredibly diverse and are critical in all known ecosystems, with a (roughly) estimated one trillion microbial species on Earth (9). These observations have led to the proposed development of environmental probiotics for optimizing ecological homeostasis, for example, in coral, to mitigate deleterious impacts stemming from anthropogenic disruptions (10), and the application of microbes for

Editor Michael J. Imperiale, University of Michigan, Ann Arbor, Michigan, USA

Address correspondence to A. Elizabeth Oates, boates@asmusa.org.

Denise M. Akob, A. Elizabeth Oates, and Peter R. Girguis contributed equally to this article. Denise M. Akob and A. Elizabeth Oates are co-first authors and listed by seniority. Peter R. Girguis is the senior author of the article.

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contaminant remediation (as summarized in reference 11). Further, over the last several decades, massive advances in molecular biology, from high-throughput nucleic acid sequencing to CRISPR-based gene editing, have fundamentally altered our understanding of microbial functional diversity, providing insight into the mechanisms by which how microbes modulate their biosphere.

The American Society for Microbiology (ASM) is home to a vibrant community of ecology, evolution, and biodiversity (EEB) scholars engaged in cutting-edge research that furthers our understanding of how microbes shape our biosphere, including humankind. Today, the EEB community continues to unlock the secrets of the microbial world, finding new ways in which microbes fix carbon (12, 13), combat viruses (14), or "breathe" rocks (15). The EEB community is also at the leading edge of developing new tools to analyze massive, complex, transdisciplinary data sets that shed light on relationships between microbial activity, environmental and host health, and even climate change.

The transdisciplinary focus of the EEB community affords us an opportunity to engage with other microbial science communities, such as host-microbe biology (HMB), molecular biology and physiology (MBP), antimicrobial agents and resistance (AAR), and applied and environmental science (AES), to tackle complex questions. Addressing questions such as how microbial data with associated physical and chemical data sets and how to consider community interactions and dynamics requires a team of diverse experts. For example, studies of gastrointestinal microbiomes have shown that microbial communities are associated with changes in human health (16–20). That said, while the shifts in human health and the diversity of gut microbes are well-documented, their mechanisms of action and modes of communication in response to ecological stressors (e.g., dietary shifts), are not well understood. However, these are experimental challenges that the EEB community has previously tackled with success. For example, fundamental studies of microbial ecology and evolution in extreme environments (21, 22) identified heat- and cold-shock proteins (23–25) which allow microorganisms to thrive across wide environmental temperature regimes. These discoveries from microbial ecology led to the discovery and application of *Taq* polymerase (26–29) which set the foundation for critical technological advancements across the microbial and biomedical sciences. Therefore, cross-discipline application of the tools and approaches of the EEB community may well provide a roadmap and even deeper understanding of how microbiomes in different human niches as well as in animal and environmental microbiomes respond to perturbations and evolve over time. In turn, the EEB community would benefit from learning about the methods and practices in gastrointestinal and clinical microbiology that offer opportunities to expand our understanding of the physiology and biochemistry of microbes. Through these collaborations with other microbiological sub-disciplines, it is our hope that, like our predecessors from centuries ago, EEB can play a role in laying the multidisciplinary foundation for the future of microbiology. A role that was highlighted during COVID-19 as evolutionary biologists were utilized to better infer the origins, evolution, and development of emerging infectious diseases.

The ASM is an ideal proving ground for building these collaborations. It is one of the oldest scientific organizations, founded in the 1890s, that aims to promote and advance the microbial sciences around the world. ASM's Council on Microbial Sciences (COMS) is the Society's "think tank," identifying the future directions of microbial sciences and providing ASM with recommendations to catalyze progress in the field. COMS is made up of over 90 ASM members who are recognized experts in their fields. These members self-affiliate based on their scientific interests into 8 Communities, which includes the EEB Community. Every 4 years, each COMS Community holds a retreat to identify scientific trends and opportunities.

The COMS EEB Community held their most recent retreat to identify the trajectory of ecology and evolution, both within the Society and within microbiology at large. We dedicated 2 days to the retreat and had visionary experts share insights on the future of biodiversity and the Anthropocene to stimulate discussions of opportunities in EEB. Here, we present the essence of the retreat, the key ideas discussed, and recommendations

resulting from the retreat that focus on the future of ecological and evolutionary microbiology.

RETREAT ORGANIZATION AND DEMOGRAPHIC DIVERSITY

The COMS EEB Community held a 2-day virtual retreat on 10–11 April 2023, with over 45 participants. The last retreat for the community was held on 19–20 December 2017. Over the preceding 5 years, significant advancements occurred in the EEB scientific community, and with that came new challenges and opportunities. The retreat was organized by ASM members, Dr. Peter Girguis (COMS EEB Community leader, interdisciplinary), Dr. Denise Akob (COMS vice chair), Dr. Vaughn Cooper (Division R, Evolutionary & Genomic Microbiology), and Dr. Vincent Young (COMS chair), and ASM staff of Dr. Beth Oates (staff lead, senior associate—governance), Allen Segal (chief advocacy officer), and Dr. Stefano Bertuzzi (ASM chief executive officer). Matt Loeb (Optimal Performance Seekers, LLC) served as a facilitator for the retreat. Half of the retreat participants were invited by the organizing committee, and to ensure a broad diversity of participants at-large ASM EEB members and other ASM groups like the ASM Young Ambassadors were invited to register. The open invitation was an important strategy to ensure that the participants represented the diversity of the EEB field with retreat attendees spanning the globe, specialties, and types of institutions (Fig. 1).

The objective of the EEB 2023 retreat was to envision the future of the entire EEB field, encompassing the wide range of research and researchers. Given that microbial ecology, evolution, and biodiversity are also well-represented in other professional societies, the retreat worked to define the frontiers of EEB that will have the greatest impact on microbiology and society and the role ASM can play within this research area. The retreat also aimed to foster deeper engagement within ASM EEB and across other ASM Communities as well as identify opportunities for ASM EEB to synergistically interact with other professional societies and the broader microbial science communities. The first day of the retreat focused on the topic of "Microbial Evolution and Ecology in the Anthropocene," whereas the second day of the retreat focused on the "The Ecology and Evolution of Polymicrobial Interactions." Each day also had two leading experts speak to each

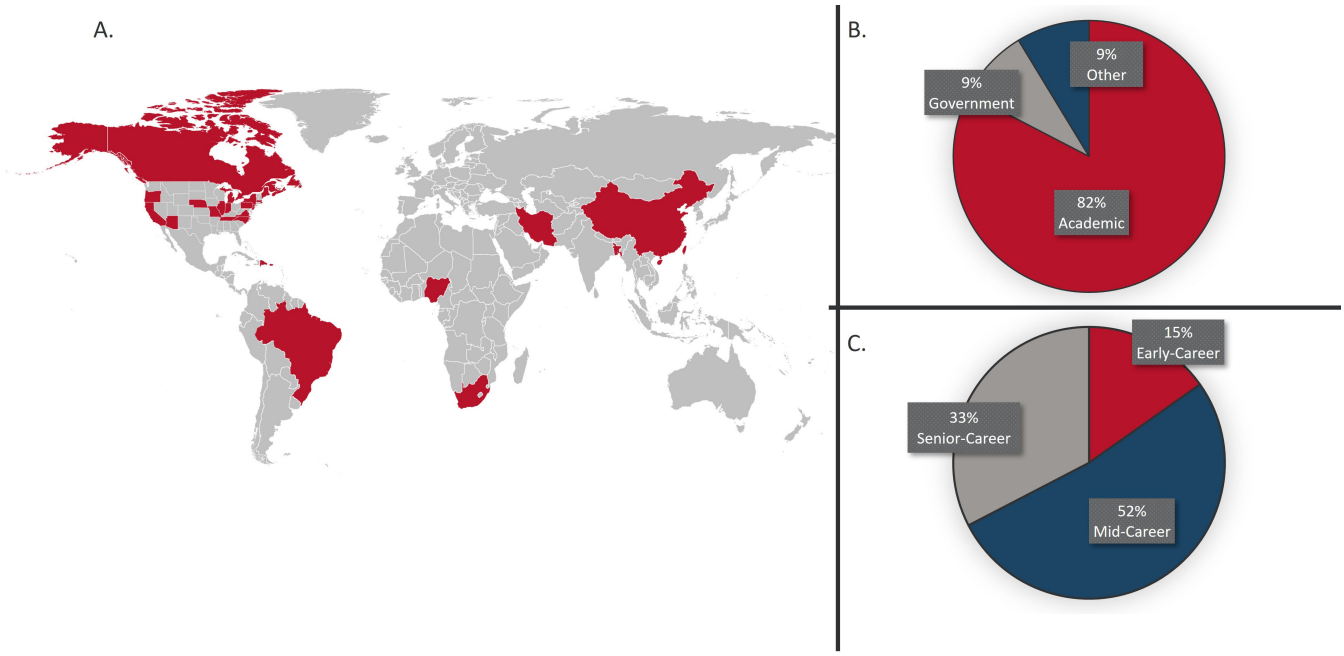

FIG 1 Retreat participant demographics. All retreat participants (n = 46, excluding ASM staff) registered to attend and participate in the retreat via an online form. (A) Retreat participants represented a wide geographical diversity of EEB scientists including participants from 10 different countries at the retreat. Participants included researchers from (B) universities, government agencies, and other institutions, and (C) spanned early-, mid-, and senior-career stages.

theme, and about the future of microbial ecology, evolution, and biodiversity (detailed below). Following the keynote presentations, participants engaged in small breakout sessions with a moderator and notetaker. Throughout the retreat, all participants were encouraged to share their input either in real time (by voice or by chat) or by e-mailing the organizers. A shared working document was also used to encourage asynchronous, post-meeting conversations, and gather additional perspectives outside of the retreat times.

HIGHLIGHTS FROM THE EEB RETREAT

Invited speakers from within the EEB field were asked to share their perspectives on two broad and contemporary science themes: "Microbial Evolution and Ecology in the Anthropocene" and "The Ecology and Evolution of Polymicrobial Interactions." The presentations emphasized the interconnectedness of microbes and their influence on human health and the environment. The keynote speakers provided a view on the complexity of polymicrobial communities in different environments, offering insight into the importance of interdisciplinary collaboration and challenging the EEB conventional scientific understanding of studying microbes in isolation. Speaker topics focused on the Anthropocene and influence of microbes and global climate changes on the health of environments. Talks highlighted the intricacies of microbial interactions, evolutionary dynamics, and their influence on human activity and the environments they inhabit.

"Microbial Evolution and Ecology in the Anthropocene": speakers and key outcomes

Dr. Elena Litchman (professor, Stanford University) presented on how we might better predict microbial community dynamics and resilience in the Anthropocene. Dr. Litchman alluded to Dr. Vladimir Vernadsky's theory of the noosphere, the development of the biosphere when human-and-nature interactions will be consciously balanced (30–33), as a potentially forthcoming stage in the evolution of Earth's biosphere. Dr. Litchman considered how microbial community responses to environmental shifts might be harnessed or supported to mitigate global changes. She discussed how improving our predictive capabilities in microbial ecology would help us gain insight into species-level ecophysiological responses to environmental changes by focusing on understanding the key mechanisms that shape these communities. Utilizing trait-based responses of microbial communities from long-term evolution experiments, Dr. Litchman posited that we could gain valuable insights into how traits, for example, thermotolerance, adapt to changing conditions. Dr. Litchman proposed cross-cutting topics for future exploration focused on increasing our ability to predict the resilience of microbial communities and functions in the Anthropocene.

Dr. Rachel Whitaker (professor, University of Illinois) focused on how multi-scale symbioses set the tempo and mode of evolutionary change in the Anthropocene. The traditional hierarchical understanding needs to be reconsidered, given the unique nature of microbial interactions and evolution. "Infectious" genetic elements such as viruses and plasmids play a critical role in driving evolutionary changes. However, these genetic elements have an evolutionary history of their own. The complex co-evolutionary relationships between hosts and infectious genetic elements are influenced by factors like the availability of resources and susceptible hosts. The co-evolution of infectious genetic elements and hosts goes beyond microbial interactions, playing a role in the broader ecological systems as well. Integration of molecular and organismal biology is critical to break down the isolation between fields to create a more holistic understanding of evolution and the interconnectedness of different biological components.

Key outcomes

The ecology and evolution of microbes in the Anthropocene is a complex and multifaceted issue that needs more comprehensive assessment. Prevailing studies often

hinge on model microorganisms that insufficiently represent the vast microbial diversity, resulting in biases favoring easily cultivable (often human-related) microbes over environmental counterparts. This bias can skew research outcomes, hindering the holistic understanding of how diverse microbial communities respond to our changing world. Through enhanced collaboration across microbial communities like environmental and medical microbiology, we could model more accurately the interplay between microbes, the environment and human influence. Encouraging interdisciplinary research will also promote advancements in techniques like immunosurveillance and creating "sensor networks," through which researchers can better understand the connectivity among microbial communities across different environments, to further understand the interactions between microbes and human health in the Anthropocene.

"The Ecology and Evolution of Polymicrobial Interactions": speakers and key outcomes

Dr. Katrine Whiteson (associate professor, University of California Irvine) focused on polymicrobial infections in humans to highlight the interconnectedness between microbial ecological processes and clinical treatments and challenges. The ecology of these communities goes well beyond their pathogenicity and includes the diversity and density of all microbes, including non-pathogens. The resulting ecological patterns represent the total, realized interactions among all microbes, including how non-pathogenic bacteria can shape the pathogenic community through competition for resources and other mechanisms. Using airway infections and cystic fibrosis as examples, she described how different microbes affect the physiology of one another through physical and molecular interactions. It is critical to consider ecological factors when analyzing microbial communities because of the complexity of such polymicrobial ecological interactions. Indeed, ecological processes are known to shape the microbial diversity in individuals, and techniques to "shape" these ecological interactions—for example, fiber-rich diets, antibiotics, fecal transplants, and probiotics—can have short- and long-term effects on microbial ecology and thus can be used to support treatments. The intersection of microbial and human ecology is an exciting area of research, but it still faces challenges with reproducibility and individual variation, establishing technical and methodological standards, and dealing with the many unknowns still present in microbiome research. Advancing our understanding of these complex dynamics requires broader, more-thorough collaboration and coordination among biomedical and environmental microbiological research communities.

Dr. Jessica Metcalf (associate professor, Princeton University) spoke about microbial immunity and the changes that occur across different environments and over time. Dr. Metcalf noted that vaccines are important for maintaining broad immunity among humans to control rampant outbreaks. That said, there are challenges in maintaining vaccination coverage and even more challenges in understanding the factors underlying an outbreak. The interactions among different microbial species often influence disease outcomes, can drive microbial (co)evolution, and ultimately affect the host immune response. We should recognize that characterizing the microbial/viral ecological dynamics within hosts is absolutely necessary to understand how these organisms shape human health, including autoimmune diseases. Microbes play a role in shaping host evolution, including dietary transitions and phenotypic adaptations, all of which can influence immune tolerance and long-term health of the host during a specific period of exposure. Predictive modeling that combines ecological and evolutionary principles with immune system dynamics can be used to better understand host-microbe interactions and disease outcomes. However, the modeling is dependent on comprehensive and diverse data on immunity, microbial communities, and human populations to advance the understanding of host-microbe interactions. Building robust data repositories would require establishing global observatory repositories and building upon interdisciplinary approaches to tackle the complex challenges posed by infectious diseases, immunity, and microbial evolution.

Key outcomes

Despite the progress made in understanding polymicrobial systems, there are specific areas where growth and development are needed. Studying polymicrobial systems requires the integration of rich contextual data sets, which encompass genomics, geochemical measurements, and physical data like flow rates and temperatures. The lack of adequate tools to enable the co-analyses of diverse data types and insufficient contextual data (metadata) limits the ability to fully utilize the vast publicly available databases. To this end, ASM could support efforts aimed at establishing "best practices" for polymicrobial community studies and involve collaboration with other scientific communities (e.g., anthropologists, public health scientists, and earth scientists) who have experience in developing theoretical and statistical approaches to utilize and assemble data from disparate sources. Furthermore, ASM could spearhead community workshops that focus on evaluating genotype-to-phenotype predictions, thus fostering innovation and collaboration within the scientific community.

The speakers all emphasized the inextricable relationships between microbes and humankind, highlighting the need for interdisciplinary approaches to tackle the complex challenges posed by unprecedented environmental change, the growing impact of humankind on the biosphere, and the rising threat of epidemics and pandemics. The speakers also emphasized the issue of addressing ongoing cultural, structural, and financial obstacles that hinder cross-disciplinary collaboration. This issue is especially acute with respect to international collaborations, as there is a scarcity of opportunities to support truly global partnerships to address our grandest challenges.

KEY DISCUSSION OF SCIENTIFIC TRENDS

The 2023 EEB Retreat emphasized the need for more-inclusive representation in microbial ecological studies, reiterated the need for more-effective science communication, asserted that we as a community need to promote more inter- and transdisciplinary collaborations, and identified the boon in large language models and artificial intelligence as a potentially transformative opportunity for microbiology. The community also emphasized the importance of connecting microbial ecosystems to human health in our changing world. These insights and actionable items are set as recommendations to help shape the trajectory of the EEB Community, which includes deeper and broader interactions with other microbiological communities within the Society and beyond. The following recommendations from the retreat are of equal importance.

Advancing microbiology through artificial intelligence and machine learning

There is immense potential for artificial intelligence (AI) and machine learning (ML) to catalyze major advances in microbiology. AI, such as large language models, is advancing quickly, and several models already exist for molecular biology and biochemistry (e.g., Alphafold [34]). However, there are challenges in implementing these technologies that could, if left unchecked, diminish confidence in these tools. For example, there is currently a lack of data standards that can "benchmark" the output of any computational models. Moreover, not all investigators have ready access to the computing infrastructure needed to make best the use of such programs. Though there is an abundance of data that would benefit from such technologies, not all of them are inherently compatible with one another. Allying sparse data with expansive data sets can lead to inaccuracies in the output. Also, there is no straightforward way to differentiate high- and low-quality data, potentially resulting in erroneous outputs. For example, attempting to predict microbial gene function without well-annotated, mechanistically validated training data sets to begin with will yield low-quality output.

These issues underscore the need for a concerted effort to identify a "common scientific language" so that computational advances can be put to the best, most reliable use. Members of EEB work across scales from individual host to large-scale environmental microbiomes and they can provide their expertise in building data sets

for computational analysis. Developing robust data standards as well as ensuring open access to both model code and data output can help ensure the reliability of AI. In addition, there is a need for scientists to receive training in using machine learning and AI so that users understand the advantages and limitations of such computational tools. To this end, retreat participants proposed ASM-led training sessions, collaboration with other societies, such as the Society for Industrial and Applied Mathematics (SIAM), Institute of Electrical and Electronics Engineers (IEEE), and Applied Microbiology International (AMI), to develop data standards and to provide active support for AI-focused working groups.

Expanding ecological and environmental diversity

To date, microbial ecology studies are geographically biased to the Northern Hemisphere and primarily led by investigators based in North America, Europe, and Asia (Fig. 2)(35). This is further seen in an uneven distribution of soil microbial ecology studies to inform biodiversity and ecosystem functions across the globe (36). Accordingly, our understanding of microbial ecology at large—on the global scale—is limited. This bias is largely the result of structural and cultural impediments that prohibit broader, genuine international collaborations. As an example, in Africa, there are few science plans and policies for microbiome research which has led to a lack of coordinated research networks on the continent compared to other regions (35). Makhalanyane et al. highlighted a need for establishing research infrastructure linked to microbiome science including sequencing capabilities. Development of coordinated research networks in Africa and other Southern Hemisphere nations could allow researchers to leverage funding and access to emerging technologies like advanced sequencing capabilities. Such efforts have been proposed for expanding the understanding of soil biodiversity (36). EEB retreat participants also shared that the scientific community would benefit from enhanced opportunities to

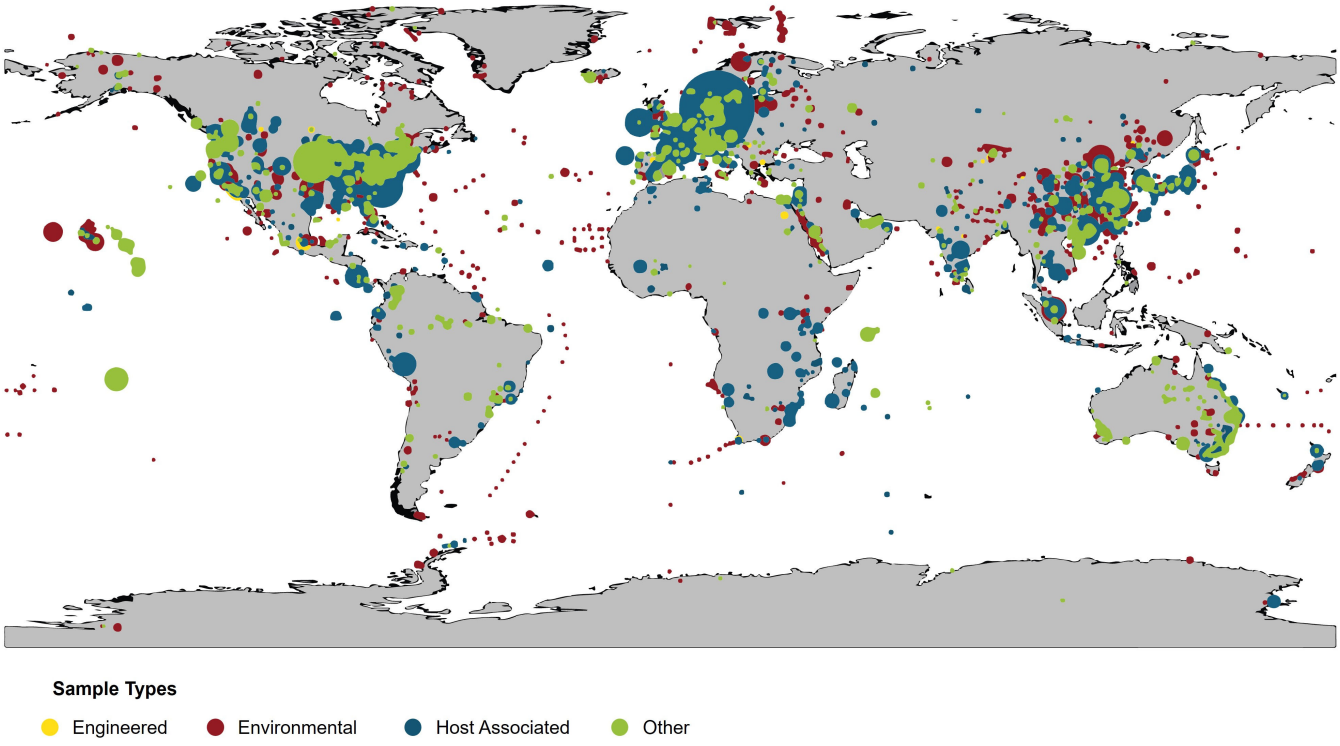

FIG 2 Distribution of microbiome research studies across the globe. Reproduced from Makhalanyane et al. (35). The world map shows metagenomic data retrieved from the National Center for Biotechnology Information (NCBI) BioSample database. The circle colors correspond to the sample types and the size the number of studies. Sample types include engineered systems such as wastewater treatment plants, terrestrial and marine environmental datasets, host-associated microbiomes (human and animal), and other metagenomic sequences.

work with scholars in Southern Hemisphere nations. Participants shared that most funding opportunities prohibit the distribution of funds to international scholars, and that funds that promote international collaborations are usually restricted to fostering collaboration among resource-replete nations. The retreat called for increased, broader, and more-earnest engagement across the global microbiology community. ASM has a unique and timely opportunity to promote and advance such global scientific collaborations. In addition, ASM could directly provide financial support for selecting international microbiology researchers to partner with currently funded scientists, which is a cost-effective solution to fostering research and training in the global South and beyond.

With respect to microbial ecology studies, there was broad agreement that the community needs more longitudinal studies to better understand biodiversity changes and microbial adaptations. Understanding how microbial diversity changes over time and in response to environmental change provides critical baseline information that is key to the future of microbial EEB. This is especially critical given the myriad of ways that microorganisms can be affected by climate change from shifts in pathogens and microbially mediated ecosystem functions. Lennon et al. (37) highlighted several case studies where long-term studies revealed the ties between microbial ecology and climate change in the context of pathogens, water quality, and microbial function. However, studies are still limited by a lack of globally distributed and temporally explicit observational data of biodiversity and function (e.g., references 35, 36). By investing scientific effort in longitudinal studies of microbial ecology, for example, EEB can identify trends in microbial biodiversity changes and adaptations in a changing climate.

There was additional discussion of the critical need to improve extant cultivation methods. With the majority of microbes currently eluding cultivation (including numerous phyla without any cultivated representatives), we cannot rely solely on existing culture-based methods to expand our knowledge of EEB in the short term. Moreover, there are a number of biases that favor the use of easily cultivable microbes, often from humans, in lieu of cultivating more-challenging environmental microbes. This bias can skew research outcomes, hindering the holistic understanding of how diverse microbial communities respond to our changing world. ASM has an opportunity to promote these efforts by supporting coordination and communication among a community of scholars who raise support to undertake large-scale longitudinal studies. Specifically, ASM could use its existing communication channels to enable such efforts. In addition, ASM could make a significant impact by helping to create a set of "best practices" among major databases such as the National Center for Biotechnology Information (NCBI), the American Type Culture Collection (ATCC), and the Genome Taxonomy Database (GTDB). Collaborations among these essential resources would streamline data management and accessibility, ultimately benefiting researchers and the broader scientific community by facilitating seamless access to critical information and enhancing the efficiency of scientific endeavors.

Fostering civic engagement

Broadly speaking, there has long been distrust, as well as a lack of microbial science literacy, among the general populace (38, 39). The retreat participants noted that the validity and importance of the work from the EEB community have—at times—become a politicized point of contention. This can impede progress toward addressing global ecological and evolutionary challenges. Amidst these challenges, it is critical to foster more-effective engagement between the scientific community and the broader public. For example, ASM could further invest in public communication by creating content that emphasizes the role of microbes in maintaining our planet. Working with the EEB Community, ASM could create additional content about the role of microbes in everyday life that can be found in home gardens home septic systems, and the role of microbes in maintaining air and water quality, and so on (Fig. 3). ASM has a wealth of engagement and education materials, additional support in distributing these materials, and development of newer materials, to our membership and to the broader public

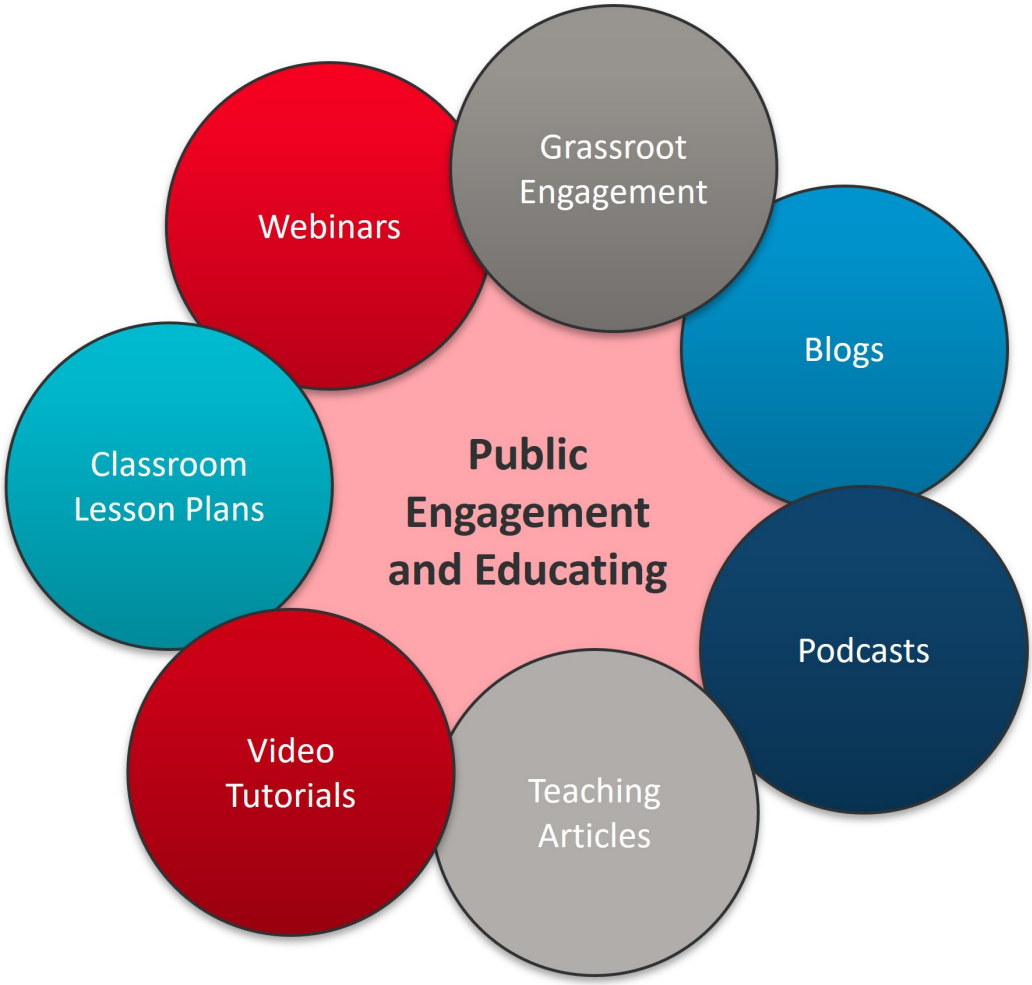

FIG 3 Leverage engagement with the public. ASM uses various means to engage with the community of microbial scientists. Each type of engagement can be leveraged for different uses for different audiences, all of which aim to make understanding microbes, specifically environmental microbes, easier to comprehend and associate with day-to-day life.

can help bridge the aforementioned gap. In addition, ASM can bolster its ongoing efforts to represent microbial sciences to policymakers. Increasing the number of EEB community members who engage with policymakers is an effective way to emphasize the role of microbes in environmental health, including the importance of understanding microbial responses to natural/anthropogenic disasters as well as climate change (40, 41). Notably, engaging scientists from a diversity of social, economic, and professional backgrounds is important for these efforts. Moreover, ASM could consider co-sponsoring webinars that guide researchers on how to be more closely connected to their local communities. Finally, ASM could lead the charge in demonstrating the importance and impact of microbial ecology and evolution in primary schools, which is key to advancing microbiology literacy in the broader public. Through these and other activities, ASM would play a pivotal role in strengthening the bridge between scientific knowledge and public understanding. This is a key step toward building a shared understanding of the critical nature of microbes in the health and well-being of our world (42).

Role of EEB within the ASM organization

For over a century, microbiologists have been studying the relationships among processes that occur at the cellular, community, and ecosystem scales. The EEB community is inherently inter- and transdisciplinary and is well positioned to play

a pivotal role in supporting other communities in allying biological observations to exogenous chemical and physical factors. As microbiology continues to become more inter- and transdisciplinary, all communities continue to see an increase in the diversity of methods and technologies being used to advance our understanding of microbiological processes (37, 43–45). However, different technologies emerge in different communities yet the frequency and extent of interactions amongst ASM communities is limited. As such, we are not fully realizing the benefits of technology sharing across ASM's many Communities. For example, the EEB Community could share the latest approaches to cultivating challenging organisms, or to genetically modifying non-model organisms. This could be of benefit to our colleagues in other communities. Naturally, the converse is also true, and the EEB Community could benefit from many of the technologies that are used in biomedical and clinical microbiology. ASM could work to further encourage technology exchanges among the different communities. For example, ASM could promote the use of techniques such as immunosurveillance to bridge the gap between disease-specific epidemiology and microorganism-specific surveys. By creating such "sensor networks" researchers can better understand the connectivity among microbial communities across different environments, to further understand the interactions between microbes and human health in the Anthropocene. These actions have the potential to enhance knowledge and inform strategies for promoting One Health, optimizing the health of humans, animals, and environment in a rapidly changing world.

The retreat participants identified two other primary barriers to interdisciplinary microbiology: communication and funding. As such, a number of actionable items were identified to further engagement across ASM Communities. First, ASM could support training opportunities for ASM members on the strengths and challenges of inter- and transdisciplinary research. A key activity would be sharing our discipline's cultural norms (e.g., jargon, typical practices within each discipline); that could help overcome the challenges that arise from our disciplinary "language barriers." These workshops could also catalyze collaboration between EEB scientists and other, more biomedically oriented scientists. Cross-collaboration among ASM journals could further enhance cross-community exchange. Finally, the introduction of an EEB mixer at ASM meetings, in particular the ASM Microbe meeting, could provide a vibrant platform for showcasing the research and skills of the EEB Community and afford an information and networking opportunity to foster engagement across the ASM. These in-person mixers can be complemented by virtual meetups throughout the year which will provide an additional, inclusive platform for members to engage and network.

Retreat participants noted that EEB Community members' attention is frequently divided among numerous societies and organizations, which can sometimes dilute their focus on engaging with other ASM Communities. It was suggested that ASM be more proactive in elevating the profile of EEB and underscore this community's value in driving advances in ecological, evolutionary, and environmental microbiological research. Moreover, there is an opportunity to have the EEB Community lead the effort to engage with other professional societies that could contribute to advancing microbiology. For example, organizing workshops with engineering, physics, and earth science societies could foster collaborations across these communities and help bridge gaps between research areas. These actions could use the ASM *mSystems* journal collaboration with the American Geophysical Union's (AGU) *GeoHealth* journal as an example to build more similar efforts.

It was also noted that while ASM is an international organization, engagement globally by the Society remains limited. ASM leadership could focus attention and financial support on promoting engagement among ASM's international microbiology community. For example, ASM could provide seed funding for international meetings that address urgent topics. Equally important, ASM could curate a list of international funding opportunities. There are several philanthropic entities that could support international collaborations (there are also few federal agencies in any nation that would fund an international group of investigators), though it is time-consuming for

individual investigators to identify these funding opportunities. We suggest that ASM could lead the effort to compile and maintain a list of such opportunities, as that is a cost-effective way to enable the ASM international community to further work together on global-scale issues.

CONCLUSION

The ecology and evolution of microbes in the Anthropocene is, put succinctly, complex and multifaceted. The discussions stimulated by the EEB retreat highlight the intricate challenges facing the community and emphasize the need for greater inclusivity, more effort in implementing new technologies and assessing its efficacy, fostering more global collaborations, promoting greater public engagement, and furthering the integration of interdisciplinary approaches (Fig. 4). The retreat repeatedly emphasized the future of science is through transdisciplinary collaboration, echoing the essay by Lennon et al. (37) that highlighted the need for diverse collaborations to address the role microbes play in climate change. Building diverse collaborative teams can help to address the complex challenges facing the microbial sciences. The majority of the challenges and recommendations posed throughout the retreat hinge on interdisciplinary collaborations like enhancing the utility of diverse data sets, creating and implementing robust data standards and accessible AI-driven tools. However, the full utilization of the collaborative effects requires an understanding and foundation of a "common scientific language" (46).

Science is inherently international and requires inclusive representation and equitable access to resources for advancement of the understanding of the microbial world. Increasing international collaborations by empowering researchers from

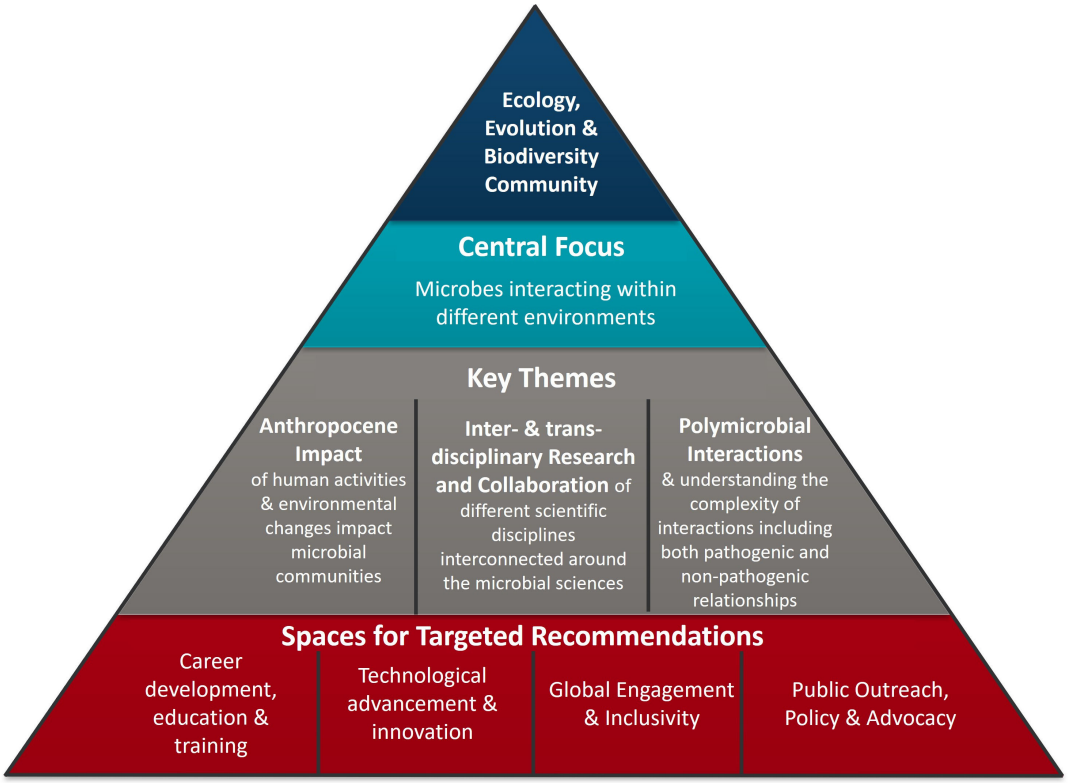

FIG 4 Components for the future of Ecology, Evolution, and Biodiversity (EEB) Community. Visual representation of the foundational elements of the EEB community (top section), focusing on microbial organisms within diverse environments such as the human body, soil, and water (upper center). During the retreat, three major themes were identified as critical for the future of EEB: the impact of the Anthropocene, interdisciplinary and transdisciplinary collaborations (building external connections), and the complexity of polymicrobial interactions in various environments (lower center). The retreat also pinpointed specific areas for targeted recommendations to achieve the highest impact on the EEB community (bottom section).

underrepresented regions aims to broaden the scope of microbial ecology studies and mitigate geographical biases. In addition, the scientific community also engages with the broader public. Building trust and value to scientific discoveries with the public is vital to the continued support of the microbial sciences. Bridging the gap between the scientific community and the public through outreach initiatives and policy advocacy not only can foster understanding but also underscore the critical role of microbiology in addressing global challenges.

Collaboration between the EEB Community and other ASM Communities is pivotal in leading microbial sciences into the future. Promoting diverse model microorganisms and leveraging innovations in tools and technologies can revolutionize the understanding of microbial interactions and their impact on the environment, human health, and the Anthropocene. The recommendations proposed during the EEB retreat call for a new era of collaboration, innovation, and societal relevance for microbiology (46). Embracing the proposed directives, the ASM and EEB Community stand poised to chart a course toward a more comprehensive understanding of microbial ecosystems, impact on microbial sciences, and the application for the benefit of all.

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ChatGPT3 aided in combining the retreat notes and transcripts from the Zoom recording. The transcripts from each speaker's talk, including the questions/comments from the Zoom chat, were submitted to ChatGPT3. Then the ChatGPT3 program was asked to identify major themes from the materials provided. Authors then reviewed the ChatGPT3 output to verify accuracy compared to the retreat notes and recordings. The ChatGPT3 output, along with the retreat notes, were then adapted into the narrative components of this paper.

D.M.A.: Conceptualized the project, organized the retreat, wrote the original paper, edited the paper, and supervised. A.E.O.: Conceptualized the project, organized the retreat, wrote the original paper, and edited the paper. P.R.G.: Conceptualized the project, organized the retreat, wrote the original paper, and edited the paper, B.D.B.: Edited the paper and supervised. V.S.C.: Conceptualized the project, organized the retreat. R.S.P.: Edited the paper and supervised. B.T.T.: Edited and reviewed. E.L.: Conceptualized content for the retreat. R.J.W.: Conceptualized content for the retreat. K.L.W.: Conceptualized content for the retreat. C.J.E.M.: Conceptualized content for the retreat.

AUTHOR AFFILIATIONS

[1]U.S. Geological Survey, Geology, Energy & Minerals Science Center, Reston, Virginia, USA
[2]American Society for Microbiology, Washington, DC, USA
[3]Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, Massachusetts, USA
[4]School of Plant and Environmental Sciences, Virginia Tech, Blacksburg, Virginia, USA
[5]Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania, USA
[6]Center for Evolutionary Biology and Medicine, University of Pittsburgh School of Medicine, Pittsburgh, Pennsylvania, USA
[7]Department of Biological Sciences, University of Illinois Chicago, Chicago, Illinois, USA

[8]Physiology and Biophysics—Institute for Computational Biomedicine, Weil Cornell Medicine, New York, New York, USA
[9]Department of Global Ecology, Carnegie Institution for Science, Stanford, California, USA
[10]Department of Microbiology, University of Illinois at Urbana-Champaign, Urbana, Illinois, USA
[11]Department of Molecular Biology and Biochemistry, University of California Irvine, Irvine, California, USA
[12]Department of Ecology and Evolutionary Biology, Princeton University, Princeton, New Jersey, USA

AUTHOR ORCIDs

Denise M. Akob http://orcid.org/0000-0003-1534-3025
A. Elizabeth Oates http://orcid.org/0009-0007-8744-7938
Peter R. Girguis http://orcid.org/0000-0002-3599-8160
Brian D. Badgley http://orcid.org/0000-0001-8269-1586
Vaughn S. Cooper http://orcid.org/0000-0001-7726-0765
Rachel S. Poretsky http://orcid.org/0000-0001-5401-449X
Elena Litchman http://orcid.org/0000-0001-7736-6332
Rachel J. Whitaker http://orcid.org/0000-0003-2263-5798
Katrine L. Whiteson http://orcid.org/0000-0002-5423-6014
C. Jessica E. Metcalf http://orcid.org/0000-0003-3166-7521

REFERENCES

1. Leeuwenhoek A. 1677. Observations, communicated to the publisher by Mr. Antony van Leewenhoeck, in a dutch letter of the 9th Octob. 1676. here English'd: concerning little animals by him observed in rain-well-sea- and snow water; as also in water wherein pepper had lain infused. Philos Trans R Soc London 12:821–831. https://doi.org/10.1098/rstl.1677.0003
2. Banerjee S, van der Heijden MGA. 2023. Soil microbiomes and one health. Nat Rev Microbiol 21:6–20. https://doi.org/10.1038/s41579-022-00779-w
3. Berg G, Dorador C, Egamberdieva D, Kostka JE, Ryu CM, Wassermann B. 2024. Shared governance in the plant holobiont and implications for one health. FEMS Microbiol Ecol 100:fiae004. https://doi.org/10.1093/femsec/fiae004
4. Whiticar MJ. 2020. The biogeochemical methane cycle, p 1–78. In Wilkes H (ed), Hydrocarbons, oils and lipids: diversity, origin, chemistry and fate. Springer International Publishing, Cham.
5. Friedlingstein P, O'Sullivan M, Jones MW, Andrew RM, Bakker DCE, Hauck J, Landschützer P, Le Quéré C, Luijkx IT, Peters GP, et al. 2023. Global carbon budget 2023. Earth Syst Sci Data 15:5301–5369. https://doi.org/10.5194/essd-15-5301-2023
6. Geider RJ, Delucia EH, Falkowski PG, Finzi AC, Grime JP, Grace J, Kana TM, La Roche J, Long SP, Osborne BA, Platt T, Prentice IC, Raven JA, Schlesinger WH, Smetacek V, Stuart V, Sathyendranath S, Thomas RB, Vogelmann TC, Williams P, Woodward FI. 2001. Primary productivity of planet earth: biological determinants and physical constraints in terrestrial and aquatic habitats. Glob Chang Biol 7:849–882. https://doi.org/10.1046/j.1365-2486.2001.00448.x
7. Peixoto RS, Harkins DM, Nelson KE. 2021. Advances in microbiome research for animal health. Annu Rev Anim Biosci 9:289–311. https://doi.org/10.1146/annurev-animal-091020-075907
8. Zehr JP, Capone DG. 2020. Changing perspectives in marine nitrogen fixation. Science 368:eaay9514. https://doi.org/10.1126/science.aay9514
9. Locey KJ, Lennon JT. 2016. Scaling laws predict global microbial diversity. Proc Natl Acad Sci U S A 113:5970–5975. https://doi.org/10.1073/pnas.1521291113
10. Garcias-Bonet N, Roik A, Tierney B, García FC, Villela HDM, Dungan AM, Quigley KM, Sweet M, Berg G, Gram L, Bourne DG, Ushijima B, Sogin M, Hoj L, Duarte G, Hirt H, Smalla K, Rosado AS, Carvalho S, Thurber RV, Ziegler M, Mason CE, van Oppen MJH, Voolstra CR, Peixoto RS. 2024. Horizon scanning the application of probiotics for wildlife. Trends Microbiol 32:252–269. https://doi.org/10.1016/j.tim.2023.08.012
11. Hellal J, Lise B, Annette B, Aurélie C, Giulia C, Simon C, Cristiana C-L, Caroline DC, Nicolas G, Marina H, Fabrice M-L, Jean M, Soizic M, Carmen P, Stéphane P, Agnès R, Stéphane V. 2023. Unlocking secrets of microbial ecotoxicology: recent achievements and future challenges. FEMS Microbiol Ecol 99:fiad102. https://doi.org/10.1093/femsec/fiad102
12. McNichol J, Dyksma S, Mußmann M, Seewald JS, Sylva SP, Sievert SM. 2022. Genus-specific carbon fixation activity measurements reveal distinct responses to oxygen among hydrothermal vent *Campylobacteria*. Appl Environ Microbiol 88:e0208321. https://doi.org/10.1128/AEM.02083-21
13. Overholt WA, Trumbore S, Xu X, Bornemann TLV, Probst AJ, Krüger M, Herrmann M, Thamdrup B, Bristow LA, Taubert M, Schwab VF, Hölzer M, Marz M, Küsel K. 2022. Carbon fixation rates in groundwater similar to those in oligotrophic marine systems. Nat Geosci 15:561–567. https://doi.org/10.1038/s41561-022-00968-5
14. Hwang Y, Roux S, Coclet C, Krause SJE, Girguis PR. 2023. Viruses interact with hosts that span distantly related microbial domains in dense hydrothermal mats. Nat Microbiol 8:946–957. https://doi.org/10.1038/s41564-023-01347-5
15. Tokunou Y, Toyofuku M, Nomura N. 2022. Physiological benefits of oxygen-terminating extracellular electron transfer. mBio 13:e0195722. https://doi.org/10.1128/mbio.01957-22
16. Abed J, Emgård JEM, Zamir G, Faroja M, Almogy G, Grenov A, Sol A, Naor R, Pikarsky E, Atlan KA, Mellul A, Chaushu S, Manson AL, Earl AM, Ou N, Brennan CA, Garrett WS, Bachrach G. 2016. Fap2 mediates *Fusobacterium nucleatum* colorectal adenocarcinoma enrichment by binding to tumor-expressed Gal-GalNAc. Cell Host Microbe 20:215–225. https://doi.org/10.1016/j.chom.2016.07.006
17. Armour CR, Nayfach S, Pollard KS, Sharpton TJ. 2019. A metagenomic meta-analysis reveals functional signatures of health and disease in the human gut microbiome. mSystems 4:e00332-18. https://doi.org/10.1128/mSystems.00332-18
18. Kiousi DE, Kouroutzidou AZ, Neanidis K, Karavanis E, Matthaios D, Pappa A, Galanis A. 2023. The role of the gut microbiome in cancer immunotherapy: current knowledge and future directions. Cancers (Basel) 15:2101. https://doi.org/10.3390/cancers15072101

19. Singh K, Ghoshal UC. 2006. Causal role of *Helicobacter pylori* infection in gastric cancer: an Asian enigma. World J Gastroenterol 12:1346–1351. https://doi.org/10.3748/wjg.v12.i9.1346
20. Zhang S, Wang R, Li D, Zhao L, Zhu L. 2021. Role of gut microbiota in functional constipation. Gastroenterol Rep (Oxf) 9:392–401. https://doi.org/10.1093/gastro/goab035
21. Brock TD. 1985. Life at high temperatures. Science 230:132–138. https://doi.org/10.1126/science.230.4722.132
22. Brock TD. 1997. The value of basic research: discovery of *Thermus aquaticus* and other extreme thermophiles. Genetics 146:1207–1210. https://doi.org/10.1093/genetics/146.4.1207
23. Graumann P, Marahiel MA. 1996. Some like it cold: response of microorganisms to cold shock. Arch Microbiol 166:293–300. https://doi.org/10.1007/s002030050386
24. Roncarati D, Scarlato V. 2017. Regulation of heat-shock genes in bacteria: from signal sensing to gene expression output. FEMS Microbiol Rev 41:549–574. https://doi.org/10.1093/femsre/fux015
25. Zhang Y, Gross CA. 2021. Cold shock response in bacteria. Annu Rev Genet 55:377–400. https://doi.org/10.1146/annurev-genet-071819-031654
26. Air GM, Harris JI. 1974. DNA-dependent RNA polymerase from the thermophilic bacterium *Thermus aquaticus*. FEBS Lett 38:277–281. https://doi.org/10.1016/0014-5793(74)80072-4
27. Chien A, Edgar DB, Trela JM. 1976. Deoxyribonucleic acid polymerase from the extreme thermophile *Thermus aquaticus*. J Bacteriol 127:1550–1557. https://doi.org/10.1128/jb.127.3.1550-1557.1976
28. Guyer RL, Koshland Jr DE. 1989. The molecule of the year. Science 246:1543–1546. https://doi.org/10.1126/science.2688087
29. Saiki RK, Gelfand DH, Stoffel S, Scharf SJ, Higuchi R, Horn GT, Mullis KB, Erlich HA. 1988. Primer-directed enzymatic amplification of DNA with a thermostable DNA polymerase. Science 239:487–491. https://doi.org/10.1126/science.2448875
30. Hutchinson GE, Wollack A. 1940. Chemical analyses of a core from Lindley Pond, North Branford, part 2 of studies on Connecticut lake sediments. Am J Sci 238:493–517. https://doi.org/10.2475/ajs.238.7.493
31. Pireddu PL. 2023. The relationship between George Evelyn Hutchinson and Vladimir Ivanovic Vernadsky: roots and consequences of a biogeochemical approach. J Hist Biol 56:339–363. https://doi.org/10.1007/s10739-023-09717-9
32. Ronfeldt D, Arquilla J. 2020. Whose story wins rise of the noosphere, noopolitik, and information-age statecraft. RAND Corporation, Santa Monica, CA.
33. Vidal C. 2024. What is the noosphere? Planetary superorganism, major evolutionary transition and emergence. Syst Res Behav Sci 41:614–622. https://doi.org/10.1002/sres.2997
34. Perrakis A, Sixma TK. 2021. AI revolutions in biology: the joys and perils of AlphaFold. EMBO Rep 22:e54046. https://doi.org/10.15252/embr.202154046
35. Makhalanyane TP, Bezuidt OKI, Pierneef RE, Mizrachi E, Zeze A, Fossou RK, Kouadjo CG, Duodu S, Chikere CB, Babalola OO, Klein A, Keyster M, du Plessis M, Yorou NS, Hijri M, Rossouw T, Kamutando CN, Venter S, Moleleki LN, Murrell C. 2023. African microbiomes matter. Nat Rev Microbiol 21:479–481. https://doi.org/10.1038/s41579-023-00925-y
36. Guerra CA, Heintz-Buschart A, Sikorski J, Chatzinotas A, Guerrero-Ramírez N, Cesarz S, Beaumelle L, Rillig MC, Maestre FT, Delgado-Baquerizo M, et al. 2020. Blind spots in global soil biodiversity and ecosystem function research. Nat Commun 11:3870. https://doi.org/10.1038/s41467-020-17688-2
37. Lennon JT, Frost SDW, Nguyen NK, Peralta AL, Place AR, Treseder KK. 2023. Microbiology and climate change: a transdisciplinary imperative. mBio 14:e0333522. https://doi.org/10.1128/mbio.03335-22
38. Carvalho GS, Lima N. 2022. Public perception of microorganisms and microbiology education: a need for enhancing society's microbiology literacy, p 31–45. In Importance of microbiology teaching and microbial resource management for sustainable futures. Elsevier.
39. Lloyd ML, Berry JA. 2022. Improving public understanding of microorganisms by integrating microbiology concepts into science teaching throughout the education system, p 107–133. In Importance of microbiology teaching and microbial resource management for sustainable futures. Vol. Elsevier.
40. Hutchins DA, Jansson JK, Remais JV, Rich VI, Singh BK, Trivedi P. 2019. Climate change microbiology — problems and perspectives. Nat Rev Microbiol 17:391–396. https://doi.org/10.1038/s41579-019-0178-5
41. Smith DFQ, Casadevall A. 2022. Disaster microbiology-a new field of study. mBio 13:e0168022. https://doi.org/10.1128/mbio.01680-22
42. Timmis K, Cavicchioli R, Garcia JL, Nogales B, Chavarría M, Stein L, McGenity TJ, Webster N, Singh BK, Handelsman J, et al. 2019. The urgent need for microbiology literacy in society. Environ Microbiol 21:1513–1528. https://doi.org/10.1111/1462-2920.14611
43. Capozzi V, Fragasso M, Russo P. 2020. Microbiological safety and the management of microbial resources in artisanal foods and beverages: the need for a transdisciplinary assessment to conciliate actual trends and risks avoidance. Microorganisms 8:306. https://doi.org/10.3390/microorganisms8020306
44. Kamenshchikova A, Wolffs PFG, Hoebe C, Horstman K. 2020. Transdisciplinary work against antimicrobial resistance. Lancet Infect Dis 20:526–527. https://doi.org/10.1016/S1473-3099(20)30137-7
45. Sharma P, Dahiya S, Kaur P, Kapil A. 2023. Computational biology: role and scope in taming antimicrobial resistance. Indian J Med Microbiol 41:33–38. https://doi.org/10.1016/j.ijmmb.2022.12.005
46. Girguis P, Oates EA. 2023. The origins and evolution of the environmental microbiology field. Available from: https://www.youtube.com/watch?v=ofZOMAphLc4&t=23s. Retrieved 03 Mar 2024.

AUTHOR BIOS

Denise M. Akob, PhD, is a microbial ecologist and biogeochemist at the U.S. Geological Survey (USGS) and the head of the Reston Microbiology Laboratory in Reston, VA. She obtained her PhD in biogeochemical oceanography from Florida State University and then was a Marie-Curie postdoctoral research fellow at the Friedrich Schiller University Jena in Germany. Dr. Akob's research aims to understand the interactions between microbes and their environment in order to solve anthropogenic issues. She has published over 60 papers on uranium bioremediation, microbe-metal interactions, subsurface biodiversity, acetylenotrophy, environmental effects of oil and gas development, and PFAS biotransformations. From 2023–2024, Dr. Akob serves as the chair of the American Society of Microbiology's Council on Microbial Sciences. In addition, she serves on the editorial boards of *Applied and Environmental Microbiology*, *FEMS Microbiology Ecology*, and *ISME Communications*. Dr. Akob received a USGS Early Career Leadership Award in 2017 for her outstanding service and scientific achievements in representing the agency. Dr. Akob co-leads the USGS Environmental Health Energy Integrated Science Team Project, which aims to understand the environmental health impacts associated with the life cycle of energy resource development.

A. Elizabeth Oates, PhD, is a microbiologist specializing in biomedical microbiology and molecular genetics, with a focus on polymicrobial interactions. She holds a B.S. in molecular and cellular biology from Illinois State University and earned her Ph.D. from the Department of Microbiology, Immunology, and Molecular Genetics at the University of Kentucky's College of Medicine. Over the course of her career, Dr. Oates has concentrated on promoting the advancement of biology through science communication, advocacy, and policy, with a deep commitment to fostering diversity and equity across the scientific field. Dr. Oates has published widely, contributing scholarly articles, policy recommendations, science communication pieces, and organizational briefs. She has also served in leadership roles at the community and national levels, where she has been instrumental in shaping scientific discourse and advancing initiatives in microbiology. Currently, she serves as a senior specialist in governance at the American Society for Microbiology (ASM). In this role, she leads and manages the ASM Council on Microbial Sciences, an advisory body of over 90 volunteer microbiology experts, providing strategic guidance to ASM leadership and the broader microbiology community. Dr. Oates is motivated by the challenges of leadership, combining her skills in program development, management, and a proactive approach to foster productivity and drive innovation.

Peter Girguis, PhD, is a professor of organismic and evolutionary biology at Harvard University. His research focuses on understanding the physiological and biochemical adaptation of microbes and animals to "extreme environments." He is renowned for building novel instruments and sensors, such as underwater mass spectrometers and microscale microbial samplers. Dr. Girguis received his B.S. from the University of California, Los Angeles; received his Ph.D. from the University of California, Santa Barbara; and completed postdoctoral research at the Monterey Bay Aquarium Research Institute prior to joining Harvard University. He was a distinguished lecturer for the National Science Foundation, a Merck Co. Innovative Research Awardee, and a Department of Energy E.C.-U.S. Biotechnology Fellow. Dr. Girguis has authored or co-authored over 95 publications, served as chair of the National Deep Submergence Science Committee (2010–2016), and serves as a member of several notable ocean advisory boards, including the Ocean Exploration Trust. Girguis's honors include the 2007 and 2011 Lindbergh Foundation Award for Science & Sustainability, the 2018 Lowell Thomas Award for groundbreaking advances in Marine Science and Technology, and the 2020 Petra Shattuck Award for Distinguished Teaching. He was named a Gordon and Betty Moore Foundation Investigator for his research on marine symbioses.