

COMMENTARY

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The microbial world in a changing environment

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Abstract

Background: In this article we would like to touch on the key role played by the microbiota in the maintenance of a sustainable environment in the entire planet. For obvious reasons, this article does not intend to review thoroughly this extremely complex topic, but rather to focus on the main threats that this natural scenario is presently facing.

Methods: Recent literature survey.

Results: Despite the relevance of microorganisms have in our planet, the effects of climate change on microbial communities have been scarcely and not systematically addressed in literature. Although the role of microorganisms in emissions of greenhouse gases has received some attention, there are several microbial processes that are affected by climate change with consequences that are presently under assessment. Among them, host-pathogen interactions, the microbiome of built environment, or relations among plants and beneficial microbes.

Conclusions: Further research is required to advance in knowledge of the effect of climate change on microbial communities. One of the main targets should be a complete evaluation of the global microbial functional diversity and the design of new strategies to cope with limitations in methods to grow microorganisms in the laboratory. These efforts should contribute to raise a general public awareness on the major role played by the microbiota on the various Earth ecosystems.

Keywords: Biogeochemical cycles, Climate change, Functional diversity, Microbial biodiversity, Pollution

In the Anthropocene era that we are presently living, human activities are affecting the environment as never before [34]. As a result, scientists are now discussing, among other issues, how much of climate change we observe is due to greenhouse gases emitted by industry and transport. In addition, severe pollution of the oceans, freshwater and soils generates enormous concern from local governments and international organizations [32]. Agricultural and forest activities, in turn, lead to soil degradation and erosion, while changes in land use threaten terrestrial ecosystems.

The uncontrolled use of both renewable and non-renewable natural resources affects biodiversity due to its impact in climate change and environmental pollution [10]. In all fairness, we are concerned about the impact on flora and fauna that have phenomena such as over-exploitation of mine ores, deforestation of the Amazon rainforest or pollution of the oceans with plastics [10]. Understandably, we focus primarily on the species that our naked eyes can see. For example, in the case of the Amazon, trees, shrubs, mammals and birds in danger of extinction [25]. In the oceans, studies focus on the 100 thousand marine creatures and one million sea birds that die every year due to plastic entanglement or consumption [26].

However, little is discussed about the impact of human activities, climate change and pollution on microbial

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communities. This is paradoxical for two reasons: microbial biodiversity is probably orders of magnitude higher than biodiversity of plants and animals (1.75 million described species) [20]. Additionally, microorganisms from the three domains of life, i.e. Bacteria, Archaea, and five out of seven kingdoms of Eukarya [28], play an irreplaceable role in the maintenance of the healthy global ecosystem that supports all life forms. They do so by being part of plant and animal holobionts (including humans), playing roles that are presently far to be completely understood [27]. In addition, they are responsible of the biogeochemical cycling of the main elements required for life and of the metabolism of the greenhouse gases carbon dioxide, methane, nitric oxide and nitrous oxide [5]. In this context, it should be mentioned that 10 out of the 17 sustainable development goals defined by United Nations [32], are directly related with phenomena or processes where microorganisms play a significant role.

A paradigmatic example that illustrates the influence of microorganisms in determining the planet's environmental conditions is represented by oxygenic photosynthesis initiated by cyanobacteria 2.3 billion years ago, an innovation that profoundly altered the course of evolution by allowing aerobic respiration and the appearance of complex multicellular life [31]. Today, marine phytoplankton, despite representing only 1% of the photosynthetic biomass of the entire biosphere, contributes about half of the carbon dioxide fixation that occurs through the Calvin Cycle [11]. Therefore, cyanobacteria, diatoms and dinoflagellates composing the phytoplankton are key players in the food webs of both marine and terrestrial species. In turn, highly specialized microorganisms also support the nitrogen cycle. Exclusively bacteria and archaea conduct biological nitrogen fixation, whereas bacteria, archaea and fungi perform nitrification and denitrification. Marine environments are also important in the turnover of this vital element. Marine nitrogen fixation is 30% higher than terrestrial, whereas denitrification in the oceans more than doubles the terrestrial [5].

Another interesting case to mention regarding the exclusive role played by microorganisms in shaping the environment is that of methane [9]. This simple hydrocarbon is 30 times more potent than carbon dioxide as greenhouse gas. Human activities that produce methane include fossil fuel production, the livestock industry, rice cultivation, biomass burning, and waste management [9]. It is currently estimated that while about 90% of the methane released into the atmosphere by these activities plus other natural processes has a biological origin, its biosynthesis is conducted only by microorganisms [18]. On Earth, methane is degraded by aerobic and anaerobic bacterial and archaeal methanotrophs that metabolize this gas as their only source of carbon and energy,

whereas atmospheric methane is oxidized by hydroxyl radical, giving rise to carbon dioxide and water vapor.

Perhaps one of the most outstanding characteristics of microorganisms, especially the prokaryotes, is their enormous capacity of adaptation and resilience when facing environmental disturbances [1]. They do so by altering their physiology as well as by changing their genomes by mutations and gene acquisition by horizontal gene transfer [30]. Adaptive responses of the microbiota, such as changes in the regulation of gene expression, metabolic activity, cell size and growth rate are also observed [4]. Due to their short generation times causing highly abundant populations, microbes have the potential to evolve on time scales of months or years [19]. At an evolutionary scale, this adaptive capacity is evidenced by microbial communities thriving in a wide range of habitats, including those exhibiting anthropocentrically termed extreme conditions, such as high or low temperatures, high or low pH, high pressure, etc. For example, it has been shown that soils in the driest area of the Atacama Desert, which in turn is the driest desert on Earth, are teeming with microorganisms that proliferate under high UV radiation, high temperature, very low organic matter content and with complete absence of liquid water all year long [3].

Most of the difficulties concerning the prediction of the effects that human economic activities, climate change and/or pollution would have on microbial communities arise from the lack of reasonable understanding of the detailed roles microorganisms play at different biological levels. For example, how would alteration or disappearance of natural biocontrol species populations affect phytopathogen fitness and aggressiveness [12]; or what would be the consequences on the microbiome of the built environment (our houses, working places, etc.), potentially leading to implementation of more strict health protecting rules [22]; or still, what would be the changes at the ecosystemic or biome levels arising from the (potential) alteration, or disappearance of microorganisms performing key processes such as methanotrophy, nitrogen or carbon fixation, among others.

For a long time, our lack of understanding about microbial biodiversity, both in terrestrial and aquatic environments, was profoundly underestimated due to the inability of the great majority of microorganisms to grow in either liquid or solid cultures in the laboratory [23]. However, in the last two decades, metagenomics has been offering a powerful tool to unveil the previously hidden components of microbial ecosystems [14]. Currently, shotgun metagenomics and high throughput sequencing, with the necessary support of bioinformatic tools, provide information about which microorganisms are present, what are their main metabolic processes and what are the mutual interactions taking place in the

ecosystem. Using bioinformatic approaches to analyze metagenomic databases from 18 biomes, it has been recently reported that redox microbial reactions, leading energy transfer, are the best functional predictor for the organization of global microbial communities, even superior to taxonomic markers [24].

These plus other modern “omic” techniques allow much more accurate determinations of microbial community structure, dynamics, and functions, including biodiversity losses in the various habitats due to human activities, climate change and environmental pollution. These improvements are most welcome, since these various stresses may have profound consequences in the overall biosphere. Thus, comprehensive studies aimed at determining changes in microbial community structure and dynamics in the time frame of years in communities subjected to disturbances such as elevated levels of carbon dioxide, mineral fertilization, temperature changes, and carbon source amendments, have shown that in the great majority of cases, the microbial component is altered with respect to those of undisturbed communities [16, 17, 33]. The main challenge is to determine in what ways and to what extent, changes in microbial composition affect ecosystem functioning. This is by no means a straightforward task, since microbes live in very diverse communities in which they interact among themselves, other organisms and the environment in complex and not fully understood ways. Also, it is necessary to establish suitable spatial and temporal baselines. An additional challenge is to distinguish between changes that are transitory from those that are permanent, since only the latter will have a long-term impact in the proper functioning of the biogeochemical cycles and the other aforementioned processes.

Despite of the extraordinary capacity of adaptation of microorganisms, we are now well aware that photoautotrophic species, including microbes, algae and plants, are not capable of recycling all the carbon dioxide released by industry and transport, to which should be added the carbon dioxide provided by global respiration, 50% of it being microbial [16]. Something similar occurs with methane, whose concentration increases faster than natural sinks can offset it [18]. It is precisely this adaptive capacity the one that is being affected by human activity and more specifically by climate change and the increasing contamination of natural habitats.

It could be expected that an adaptive response to rising carbon dioxide levels in marine environments would be an increase in phytoplankton primary production, although this may occur only when sufficient nutrients are available. On the other hand, rising temperatures result in warming of surface waters and sea and freshwater ice melting, leading to an increase in stratification that affects microbial dispersal and nutrient transport in the

water column. Together with a slight acidification (0.1 pH unit) of the oceans due to climbing carbon dioxide levels and the expansion of oxygen minimum zones, they represent disturbances that, with regional variability, have measurable consequences in various processes. The latter include carbon dioxide fixation, nitrification, denitrification, methane turnover, marine food webs and carbon export to the seabed [33]. For example, ocean acidification inhibits nitrification, whereas deoxygenation favors denitrification [17]. The most straightforward effect is a change in microbial composition and structure, a phenomenon that results particularly critical for the microbiota associated to coral [15].

In terrestrial environments, one of the relevant roles of the microbiota is to recycle nutrients and organic carbon stored in soils. Several studies have shown that although responses may vary according to the conditions of the soils, both higher temperatures and elevated levels of carbon dioxide increase the decomposition of organic matter, the higher release of carbon dioxide to the atmosphere resulting in a vicious cycle in favor of climate change [13, 21]. Eventually, microbial activity slows down upon carbon depletion. The ways by which organic contaminants modify carbon decomposing microbial communities is presently poorly understood. In turn, thawing of permafrost within Arctic and sub-Arctic regions, in addition to allowing microbial decay of organic matter, promotes anaerobic methanogenesis in water-saturated soils [29]. Changes in the environmental conditions also affect the multiple beneficial interactions between microbes and plants, some of which result in better plant growth and increased resistance to disease and abiotic stresses [7]. As expected, the response depends on the type of plant, soil and microbiota. However, the majority of studies show that elevated CO₂ levels favor root colonization by mycorrhizal fungi and symbiotic interaction between legumes and rhizobia is enhanced [8]. The response to warming appears to be more variable, with both positive and negative effects in the composition of the microbiota associated to the plant roots, some of them driven by changes in the plant exudates [2].

Another area of active research is the effect of changes in the environmental conditions on pathogens causing diseases in humans, animals and plants. It has already been demonstrated that climate change may affect the survival, reproduction, life cycle, host-pathogen interaction and dispersal of pathogens, although with net health effects that are still not conclusive [35]. Knowledge collected in this field will be essential for the adoption of the proper measures to succeed in the prevention and control of infectious diseases, with the potential to become epidemic or pandemic phenomena. In this context, a rather less explored topic is the role of climate

change and other disturbances on the microbial communities of the built environment, which have the potential to both, protect us from pathogens or be a source of them [22].

Several research needs should be addressed, of which we want to highlight a complete assessment of the global microbial functional diversity, which is key for predicting the effects of microbial diversity losses and the resilience/recovery potential of microbial communities. The latter point is crucial to foresee the actual, effective and permanent effects of human economic activities, climate change, and/or pollution on composition and structure of microbial communities. In this context, a counterintuitive scenario is that such perturbations do not necessarily produce significant changes in microbial communities' performance, as they have been thriving in our planet for near 4000 million years, being able to overcome changes on Earth even more dramatic than those posed by the Anthropocene era.

The scientific community has shown many signs of its concern about the deep impact that these disturbances may have on microbial biodiversity, and thus on the proper functioning of the biogeochemical cycles, spread of infectious diseases and other microbial driven processes. Two manifestations of this concern are the colloquium "Microbes and Climate Change", jointly convened by the American Academy of Microbiology and the American Geophysical Union (<https://www.asmscience.org/content/99>). At this meeting held in Washington, DC, in March 2016, experts discussed about microbial contributions and responses to climate change across global settings and proposed priority areas for future studies. Likewise, there is the consensus statement released last year entitled "Scientists' warning to humanity: microorganisms and climate change" [6]. This document, signed by a large number of microbiologists, emphasizes the crucial role and global importance of microorganisms in climate change biology and puts forward ten recommendations of which we would like to highlight the need to reach greater recognition that the microbial life is the support of the entire biosphere, including humans, and the need to incorporate microbial processes into ecosystem models to improve predictions under climate change scenarios. Let us hope that public policy makers and academic institutions join forces to address this issue that challenges the whole biosphere.

Conclusions

There is no question that the significant role microorganisms play in the maintenance of a sustainable environment on Earth is interrelated to climate change. A present challenge in this respect is to assess the effect of climate change on various microbial communities. For this purpose, several research needs have to be also

fulfilled. These include a complete evaluation of microbial functional diversity at a global scale, consideration of microbial functions and processes in ecosystems modeling and new strategies to cope with limitations in methods to grow microorganisms in the laboratory. These efforts should contribute to support the task of policy makers as well as to raise a general public awareness on the major role played by the microbiota on the various Earth ecosystems.

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Authors' contributions

RV and BG conceive the idea, survey literature and prepare and revise the manuscript. The author(s) read and approved the final manuscript.

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References

- Allison SD, Martiny JBH. Resistance, resilience and redundancy in microbial communities. *Proc Natl Acad Sci U S A*. 2008;105:11512–9. <https://doi.org/10.1073/pnas.0801925105>.
- Alshaal T, El-Ramady H, Al-Saeedi AH, Shalaby T, Elsakhawy T, Omara AE-DGADA, Hamad E, El-Ghamry A, Mosa A, Amer M, Abdalla N. The rhizosphere and plant nutrition under climate change. In: Naeem M, et al, editors. *Essential plant nutrients*: Springer International Publishing AG; 2017. https://doi.org/10.1007/978-3-319-58841-4_11.
- Azúa-Bustos A, Caro L, Vicuña R. Discovery and microbial content of the driest site of the hyperarid Atacama Desert, Chile. *Environ Microbiol Rep*. 2015;7:388–94. <https://doi.org/10.1111/1758-2229.12261>.
- Bleuven C, Landry CR. Molecular and cellular bases of adaptation to a changing environment in microorganisms. *Biol Sci*. 2016;283:20161458. <https://doi.org/10.1098/rspb.2016.1458>.

5. Canfield DE, Glazer AN, Falkowski PG. The evolution and future of Earth's nitrogen cycle. *Science*. 2010;330:192–6. <https://doi.org/10.1126/science.1186120>.
6. Cavicchioli R, Ripple WJ, Timmis KN, Azam F, Bakken LR, Baylis M, Behrenfeld MJ, Boetius A, Boyd PW, Classen AT, Crowther TW, Danovaro R, Foreman CM, Huisman J, Hutchins DA, Jansson JK, Karl DM, Koskella B, Mark Welch DB, Martiny JBH, Moran MA, Orphan VJ, Reay DS, Remais JV, Rich VI, Singh BK, Stein LY, Stewart FJ, Sullivan MB, van Oppen MJH, Weaver SC, Webb EA, Webster NS. Scientists warning to humanity: microorganisms and climate change. *Nat Rev Microbiol*. 2019;17:569–86. <https://doi.org/10.1038/s41579-019-0222-5>.
7. Cheng YT, Zhang L, He SY. Plant-microbe interactions facing environmental challenge. *Cell Host Microbe*. 2019;26:183–92. <https://doi.org/10.1016/j.chom.2019.07.009>.
8. Compant S, van der Heijden MGA, Sessitsch A. Climate change effects on beneficial plant-microorganism interaction. *FEMS Microbiol Ecol*. 2010;73:197–214. <https://doi.org/10.1111/j.1574-6941.2010.00900.x>.
9. Conrad R. The global methane cycle: recent advances in understanding the microbial processes involved. *Environ Microbiol Rep*. 2009;1:285–92. <https://doi.org/10.1111/j.1758-2229.2009.00038.x>.
10. Crist E, Mora C, Engelman R. The interaction of human population, food production, and biodiversity protection. *Science*. 2017;356:260–4. <https://doi.org/10.1126/science.aal2011>.
11. Falkowski P. The power of plankton. *Nature*. 2012;483:S17–20. <https://doi.org/10.1038/483S17a>.
12. Fira D, Dimkić I, Berić T, Lozo J, Stanković S. Biological control of plant pathogens by *Bacillus* species. *J Biotechnol*. 2018;285:44–55. <https://doi.org/10.1016/j.jbiotec.2018.07.044>.
13. Hicks Pries CE, Castanha C, Porras RC, Torn MS. The whole-soil carbon flux in response to warming. *Science*. 2017;355:1420–3. <https://doi.org/10.1126/science.aal1319>.
14. Hiraoka S, Yang CC, Iwasaki W. Metagenomics and bioinformatics in Microbial Ecology: Current status and beyond. *Microbes Environ*. 2016;31:204–16. <https://doi.org/10.1264/jsme2.ME16024>.
15. Hughes TP, Barnes ML, Bellwood DR, Cinner JE, Cumming GS, Jackson JBC, Kleypas J, van de Lempert IA, Lough JM, Morrison TH, Palumbi SR, van Nes EJJ, Scheffer M. Coral reefs in the Anthropocene. *Nature*. 2017;546:82–90. <https://doi.org/10.1038/nature22901>.
16. Hutchins DA, Fu F. Microorganisms and ocean global change. *Nat Microbiol*. 2017;2:17058. <https://doi.org/10.1038/nmicrobiol.2017.58>.
17. Hutchins DA, Jansson JK, Remais JV, Rich VI, Singh BK, Trivedi P. Climate change microbiology – problems and perspectives. *Nat Rev Microbiol*. 2019;17:391–6. <https://doi.org/10.1038/s41579-019-0178-5>.
18. Knief C. Diversity of methane cycling microorganisms in soils and their relation to oxygen. *Curr Issues Mol Biol*. 2019;33:23–56. <https://doi.org/10.21775/cimb.033.023>.
19. Lensky RE. What is adaptation by natural selection? Perspectives of an experimental microbiologist. *PLoS Genet*. 2017;13:e1006668. <https://doi.org/10.1371/journal.pgen.1006668>.
20. Locey KJ, Lennon JT. Scaling laws predict global microbial diversity. *Proc Natl Acad Sci U S A*. 2016;113:5970–5. <https://doi.org/10.1073/pnas.1521291113>.
21. Melillo J, Feey SD, Deangelis KM, Werner WJ, Bernard MJ, Bowles FP, Pold G, Knorr MA, Grandy AS. Long-term pattern and magnitude of soil carbon feedback to the climate system in a warming world. *Science*. 2017;358:101–5. <https://doi.org/10.1126/science.aan2874>.
22. National Academies of Sciences, Engineering & Medicine. *Microbiomes of the built environment: a research agenda for indoor microbiology, human health, and buildings*. Washington, DC: The National Academies Press; 2017. <https://doi.org/10.17226/23647>.
23. Overmann J, Abt B, Sikorski J. Present and future of culturing bacteria. *Annu Rev Microbiol*. 2017;71:711–30. <https://doi.org/10.1146/annurev-micro-090816-093449>.
24. Ramírez-Flandes S, González B, Ulloa O. Redox traits characterize the organization of global microbial communities. *Proc Natl Acad Sci U S A*. 2019;116:3630–5. <https://doi.org/10.1073/pnas.1817554116>.
25. Rangel TF. Amazonian extinction debts. *Science*. 2012;337:162–3. <https://doi.org/10.1126/science.1224819>.
26. Rochman CM, Browne MA, Underwood AJ, van Franeker JA, Thompson RC, Amaral-Zettler LA. The ecological impacts of marine debris: unraveling the demonstrated evidence from what is perceived. *Ecology*. 2016;97:302–12. <https://doi.org/10.1890/14-2070.1>.
27. Rosenberg E, Xilber-Rosenberg I. The hologenome concept: human, animal and plant microbiota (Springer); 2013. <https://doi.org/10.1007/978-3-319-04241-1>.
28. Ruggiero MA, Gordon DP, Orrell TM, Bailly N, Bourgoin T, Brusca RC, Cavalier-Smith T, Guiry MD, Kirk PM. A higher level classification of all living organisms. *PLoS One*. 2015;10:e0119248. <https://doi.org/10.1371/journal.pone.0119248>.
29. Schuur EAG, McGuire AD, Schadel C, Grosse G. Climate change and the permafrost carbon feedback. *Nature*. 2015;520:171–9. <https://doi.org/10.1038/nature14338>.
30. Sitaraman R. Prokaryotic horizontal gene transfer within the human holobiont: ecological-evolutionary inferences, implications and possibilities. *Microbiome*. 2018;6:163. <https://doi.org/10.1186/s40168-018-0551-z>.
31. Soo RM, Hemp J, Parks DH, Fischer WW, Hugenholtz P. On the origin of oxygenic photosynthesis and aerobic respiration in cyanobacteria. *Science*. 2017;355:1436–40. <https://doi.org/10.1126/science.aal3794>.
32. United Nations. Transforming our world: The 2030 Agenda for Sustainable Development. 2015. <https://sustainabledevelopment.un.org/post2015/transformingourworld>.
33. Verspagen JM, van de Waal DB, Finke JF, Visser PM, Huisman J. Contrasting effects of rising CO₂ on primary production and ecological stoichiometry at different nutrient levels. *Ecol Lett*. 2014;17:951–60. <https://doi.org/10.1111/ele.12298>.
34. Webster NS, Wagner M, Negri AP. Microbial conservation in the Anthropocene. *Environ Microbiol*. 2018;20:1925–8. <https://doi.org/10.1111/1462-2920.14124>.
35. Wu X, Lu Y, Zhou S, Chen L, Xu B. Impact of climate change on human infectious diseases: empirical evidence and human adaptation. *Environ Int*. 2016;86:14–23. <https://doi.org/10.1016/j.envint.2015.09.007>.

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