

Quantifying human impact on Earth's microbiome

Stephen B. Pointing, Noah Fierer, Gavin J. D. Smith, Peter D. Steinberg and Martin Wiedmann

The global effect of human activities on Earth's microbiota has not yet been considered. Here, we identify potential trajectories of microbial change, and highlight knowledge gaps that need to be addressed to better understand how microbial communities across the globe will change in the future.

Human impact on natural and managed environments has arisen through displacement and transformation of Earth's abiotic and biotic resources. The scale of such impact varies from the organismal level, to ecosystems and globally. Identifying how these changes affect microbial communities has seldom been considered beyond the microhabitat scale, and microbiologists are only just beginning to identify global patterns in microbial diversity¹. The effect of an increasingly managed environment on microbial communities and their ecosystem services therefore remains unclear for most biomes. Given that microorganisms comprise approximately one third of Earth's standing biomass and they perform the majority of biogeochemical transformations, we argue these issues should motivate research in microbial ecology.

Current understanding of trajectories for microbial groups as a result of human population growth is patchy at best (Fig. 1a). The most direct and readily quantifiable impact surrounds the human microbiome. Each individual harbours 3.9×10^{13} bacteria² and so the global human microbiome currently comprises $>3.8 \times 10^8$ kg of bacteria, a several fold increase since the industrial revolution. This has been accompanied by shifts in microbial diversity due to advances in hygiene and medicine, emerging and re-emerging pathogens³, and changes in diet⁴. Increasing urbanization and other changes in land-use can alter the amounts and types of microorganisms found in the near-surface atmosphere⁵, and as humans spend more of their time indoors we are undoubtedly altering our microbial exposures⁶. This may influence pathogen transmission, the assembly of our gut and skin microbiomes and the prevalence of allergies, asthma, and other immunological disorders.

Human population growth has also been accompanied by large increases in livestock and arable agriculture at the

expense of natural terrestrial habitats, such that agriculture utilizes approximately half of all terrestrial ice-free land globally. Although estimating microbial biomass and diversity at a global scale is problematic⁷, land clearance for agriculture results in greater evenness and loss of endemic taxa in soil microbial communities⁸, and can increase human exposure to reservoirs of emerging pathogens³. Anthropogenic inputs of agricultural nitrogen can also alter microbial diversity in soil and aquatic environments⁹. Livestock animals make up the majority of mammalian biomass on Earth and specifically the 1.4 billion cattle represent a massive cellulolytic rumen microbiome. Additionally endophytic and rhizosphere microorganisms associated with major crops have undoubtedly increased in abundance¹⁰. The oceans display significant latitudinal patterns in the distribution of microbial taxa¹¹, and these may shift as oceans warm due to climate change and ocean acidification. In coastal systems multiple sources of change to microbial communities arise from coliforms in human waste, harmful algal blooms, eutrophication, benthic anoxia and hypoxia, heavy metal and hydrocarbon contamination¹². Climate change is also leading to increased disease prevalence as well as negatively affecting key microbial symbionts of hosts, particularly corals¹³.

Overall, we estimate that human population growth has resulted in both positive and negative impacts on the global diversity and abundance of microorganisms. The biggest quantifiable increases have undoubtedly been microorganisms associated with the human body and livestock, whilst the greatest losses are likely from the increasing conversion of natural to managed environments. Given predictions of human population growth to a global maximum of 11 billion, future trajectories are likely to include further increases from human-associated microorganisms. Increasing human impact on environmental microorganisms is also

likely, particularly for marine taxa as warming and oxygen depletion exert major impact on the oceans. We identify three areas where increased research attention will probably have a profound influence on understanding.

Major advances will arise when microbiologists begin to address the ecology of microorganisms across all domains of microbial life with similar effort (Fig. 1b). Since the advent of high throughput sequencing, which provides the most accurate estimates to date for global microbial diversity, the majority of studies have focused on the bacterial domain. Efforts to resolve environmental diversity of archaeal and eukaryal microorganisms lag significantly behind. Part of the reason for this lies in the reliance on PCR amplification of environmental marker genes. These are well established for Bacteria but there is less confidence in the ability of 'universal' primers for Archaea and Eukarya to capture a representative level of diversity for these domains. The holy grail of microbial ecology remains direct (PCR-independent) diversity assessment, but in the meantime rRNA gene databases are gaining more value as they become better curated, and metagenomes and other multi-omic studies are beginning to resolve evolutionary and functional relationships¹⁴. Perhaps the greatest insight will arise from metagenomic sequencing efforts to understand the complexity of the virome in different habitats since viruses may outnumber all other microbial domains by several orders of magnitude.

A second major goal should be to improve estimates for the true extent of microbial colonization on Earth (Fig. 1c). A major focus of most microbial studies has been in resolving relative taxon abundances without estimating biomass, although the latter is highly relevant to understanding microbial contributions to ecosystem function. The problem is that reliable techniques for directly estimating biomass from environmental samples are

often lacking. Whilst in marine systems direct counts are relatively common, estimates for microbial biomass in other environments is often overlooked or inferred indirectly from structural compounds, genetic or metabolite data. There are currently few options for phylum-specific biomass estimation, and the development of methodology for estimating viral abundance in environmental samples should be a priority given growing awareness of their importance. Greater emphasis on quantifying environmental microbial biomass *in situ* will add new insight to their role in biogeochemical transformations and biotic interactions.

Arguably the greatest insight into human impacts on the Earth's microbiome will arise from efforts to identify the differences between the microbiota found in natural systems with those in built and managed environments (Fig. 1d). Improved resolution of the microbial ecology of natural systems is required to gain greater understanding of ecosystem function and how disturbance will impact this, as well as identify microorganisms for potential exploitation. Any robust attempt at ecological restoration from a microbial perspective will also require this information. The level of threat to historically undisturbed microbial niches

such as those found in the deep subsurface and higher latitude ecosystems are also poorly understood. Managed environments such as urban and intensive agricultural systems support a unique microbiome and these should be more fully characterized in order to better understand how human exposure to microorganisms will change in response to the increasing urbanization of populations¹⁵.

We have highlighted likely trajectories for the Earth's microbiota as a result of human population growth and identified where major advances can be made in future research. We conclude that humans are a major determinant of the global microbiome, and by better resolving multi-domain diversity, quantitative estimates of microbial abundance and the changes that occur between natural and managed microbiomes, a more informed response to environmental impacts of future human population growth will be possible. □

Stephen B. Pointing^{1,2*}, Noah Fierer^{3,4},
Gavin J. D. Smith^{5,6,7}, Peter D. Steinberg^{8,9}
and Martin Wiedmann¹⁰.

¹Institute for Applied Ecology New Zealand, Auckland University of Technology, Auckland 1010, New Zealand. ²Institute of Nature and Environmental Technology, Kanazawa University, Kanazawa 920-1192, Japan. ³Cooperative Institute for Research in Environmental Sciences, University of Colorado, Boulder, Colorado 80309, USA. ⁴Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, Colorado 80309, USA. ⁵Program in Emerging Infectious Diseases, Duke-NUS Graduate Medical School, Singapore 169857, Singapore. ⁶WHO Collaborating Centre for Reference and Research on Influenza, Melbourne, Victoria 3000, Australia. ⁷Duke Global Health Institute, Duke University, Durham, North Carolina 27708, USA. ⁸Sydney Institute of Marine Science, Sydney, New South Wales 2088, Australia. ⁹University of New South Wales, Sydney, New South Wales 2052, Australia. ¹⁰Department of Food Science, Cornell University, Ithaca, New York 14853, USA. e-mail: steve.pointing@aut.ac.nz

References

- Fierer, N. *et al. Proc. Natl Acad. Sci. USA* **109**, 21390–21395 (2012).
- Sender, R., Fuchs, S. & Milo, R. Preprint at <http://dx.doi.org/10.1101/036103> (2016).
- Ostfeld, R. S. *Clin. Microbiol. Infect.* **15**, 40–43 (2009).
- Lozupone, C. A., Stombaugh, J. I., Gordon, J. I., Jansson, J. K. & Knight, R. *Nature* **489**, 220–230 (2012).
- Bowers, R., McLetchie, S., Knight, R. & Fierer, N. *ISME J.* **5**, 601–612 (2011).
- Lax, S. *et al. Science* **345**, 1048–1052 (2014).
- Locey, K. J. & Lennon, J. T. *Proc. Natl Acad. Sci. USA* **113**, 5970–5975 (2016).
- Rodrigues, J. L. M. *et al. Proc. Natl Acad. Sci. USA* **110**, 988–993 (2013).
- Leff, J. W. *et al. Proc. Natl Acad. Sci. USA* **112**, 10967–10972 (2015).
- Chuansheng, M. & Flinn, B. *Recent Pat. Biotechnol.* **4**, 81–95 (2010).
- Brown, M. V., Ostrowski, M., Grzymalski, J. J. & Lauro, F. M. *Mar. Genomics* **15**, 17–28 (2014).
- Halpern, B. S. *et al. Nature Commun.* **6**, 7615 (2015).
- Harvell, D. *et al. Oceanography* **20**, 172–195 (2007).
- Jansson, J. K. & Baker, E. S. *Nature Microbiol.* **1**, 16049 (2016).
- Kembel, S. W. *et al. ISME J.* **6**, 1469–1479 (2012).

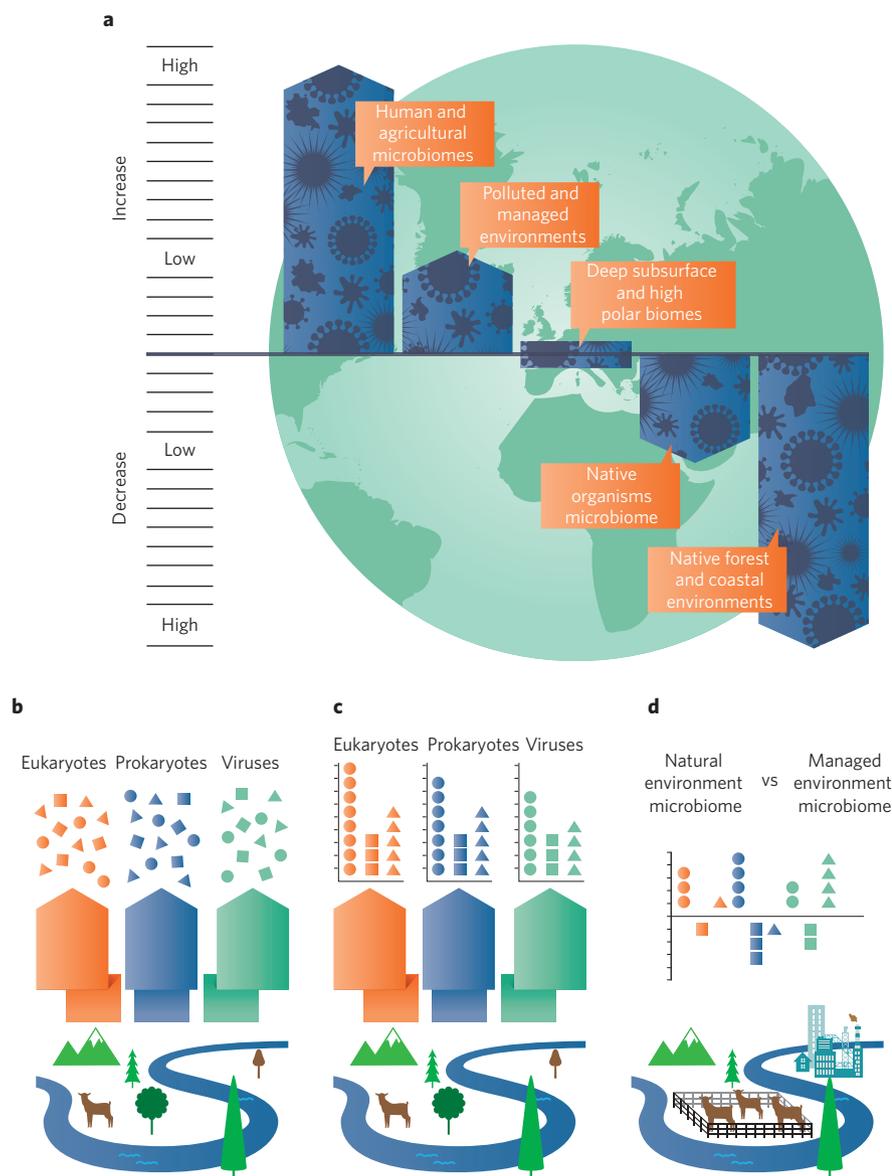


Figure 1 | Global microbial change and knowledge gaps. **a**, Predicted trajectories for abundance of microbial taxa in response to growing human population. **b–d**, Critical knowledge gaps impeding understanding of human impact on Earth's microbiome: similar effort to assess diversity across all domains of microbial life (**b**), reliable quantitative methodology for estimating biomass of microbial taxa (**c**), comparison of microbiota in natural and managed environments (**d**).