



ELSEVIER

GfÖ

GfÖ Ecological Society of Germany,
Austria and Switzerland

Basic and Applied Ecology 00 (2021) 1–3

Basic and
Applied Ecology

www.elsevier.com/locate/baae

EDITORIAL

Special Issue—Causes and consequences of microbiome changes

Stefan Geisen^a, Madhav P. Thakur^b

^aDepartment of Plant Science, Laboratory of Nematology, Wageningen University, 6700 ES Wageningen, the Netherlands

^bInstitute of Ecology and Evolution, University of Bern, 3012 Bern, Switzerland



Current trends of ‘microbiome research’

Microorganisms are the most abundant and diverse organisms in any system on the planet (Bar-On, Phillips & Milo, 2018; Fierer, Strickland, Liptzin, Bradford & Cleveland, 2009). Together with plants, they compose most biotically bound carbon on Earth (Bar-On et al., 2018). Microorganisms are defined as small organisms usually not visible to the naked eye, with the microbiome containing all its members in a given system. The term microbiome has increasingly become an umbrella-term to study microbial diversity. All prokaryotes (bacteria and archaea) and most eukaryotic diversity (fungi and protists) (Fierer, 2017; Geisen et al., 2018) are part of these microbiomes. Viruses as non-living organisms are also often considered part of microbiomes (Fierer, 2017). A century-long history of research on microorganisms starting with microscopic observations, studies of individual microbial (human- or plant-pathogenic) taxa has recently shifted towards diversity-focused community analyses using modern molecular high-throughput sequencing tools. Given these trends, we are now aware that environmental microbial diversity is driving large-scale ecosystem processes, such as the global

carbon cycle (Singh, Bardgett, Smith & Reay, 2010; Torsvik & Ovreas, 2002; Worden et al., 2015) and have begun to appreciate the vast diversity and functional importance of previously unknown microorganisms inside humans (Cho & Blaser, 2012; Clemente, Ursell, Parfrey & Knight, 2012; Gilbert et al., 2018; Gill et al., 2006; Turnbaugh et al., 2007; Yatsunenko et al., 2012), animals and plants (Berendsen, Pieterse & Bakker, 2012; Bulgarelli et al., 2012; Lundberg et al., 2012; Mendes et al., 2011). The microbiome differs profoundly between environments and hosts, but is rarely viewed in an integrated way; by integrative, we mean both its taxonomic entity (different microbial groups) and approaches for studying microbes in different systems.

Those studies that attempted to integrate microbiome work have revealed that community and diversity patterns of microorganisms differ profoundly among systems (Bahram et al., 2018, Bahram et al., 2021; Thompson et al., 2017; Xiong et al., 2021) as microorganisms are essentially structured by the physicochemical surroundings in the environment or inside hosts. Taxon-wide microbiome studies are even more rare but are useful to study questions related to differences in biogeography, community assembly or responsiveness to different land use practices (Luan et al., 2020; Urich et al., 2008; Zhao et al., 2019). Another aspect that urgently needs to find its place in mainstream microbiome research is the inclusion of functional consequences of taxonomic changes in microbial communities. Similar to the sequencing techniques to better map taxonomic microbiome profiles, we now have many tools in our hands to understand microbial functions. For example, molecular qPCR- or sequencing-based techniques allow targeting microbial genes, while protein-, enzyme- or metabolite-based approaches provide direct evidence for the importance of microbiome functioning.

E-mail addresses: stefan.geisen@wur.nl (S. Geisen), madhav.thakur@iee.unibe.ch (M.P. Thakur).

<https://doi.org/10.1016/j.baae.2021.03.010>

1439-1791/© 2021 Gesellschaft für Ökologie. Published by Elsevier GmbH. All rights reserved.

Predictive microbiome research

This special issue covers several of the above-mentioned shortcomings as it is aimed to provide a synopsis of microbiome knowledge by including studies across different systems (flower and leaf, tree and entire forest soils, peat swamp forests and groundwater), various microbial groups (bacterial species, bacterial and entire prokaryotic communities, fungal communities), contemporary methods (cultivation, qPCR, genomics, amplicon sequencing, biomass measures, biochemical analyses, functional gene and functional assays) and further links between the microbiome taxon composition and functioning. We believe that these contributions are an important step to acknowledge microbiomes beyond a singular microbiome view, and towards making microbiome science more predictive using integrative approaches. In this editorial, we highlight the key findings of the papers included in this special issue.

Gaube, Junker and Keller (2021) investigated leaf and flower microbiomes focusing on bacterial communities in two plant species across three biogeographic regions in Germany. Their analyses revealed that bacterial communities did not differ between biogeographic regions but between plant species and plant organs, with interesting insights into the likely origin of the bacteria. Leaf bacterial taxa were predominantly soilborne, while flower bacteria taxa were most likely obtained through pollinators. Another emerging finding from this study is that more intense land use overall reduced bacterial diversity, with even distinct microbial taxa being indicative of land use intensity. This holistic overview of leaf and flower bacteria shows the potential of microbiome analyses even within highly specific habitats.

In a growth chamber experiment by Macdonald et al. (2021), eucalyptus tree seedlings were grown under ambient and increased CO₂ and temperature to decipher links to seedling performance and the associated rhizosphere microbiome. The tree biomass was strongly enhanced by increasing CO₂ with resulting effects on plant and soil microbial C:N ratio, but further abiotic changes did not affect the soil microbiome. In this multi-methodological study that measured a wide range of plant, microbial and physicochemical properties, the authors conclude that in low-nutrient soils planted with fast-growing plant species, there is rather one unidirectional importance with plants essentially determining the soil microbiome.

Netherway, Bengtsson, Krab and Bahram (2021) review the potential importance of mycorrhiza as nutrient providers in forests and their role on the forest microbiome. They differentiate between the two key mycorrhizal types, ectomycorrhiza and arbuscular mycorrhizal, to show their fundamentally different impacts on the surrounding soil physicochemical and biotic properties. In particular, many ectomycorrhizal symbioses seem to reduce biodiversity by inducing harsh environmental conditions to support little tree species, while arbuscular mycorrhiza generally promoting biodiversity both in soils

and in tree species. This conceptual piece provides an interesting view on the importance of mycorrhizal-tree symbiosis as determinant of the soil microbiome and the surrounding vegetation.

Too, Ong, Yule, & Keller, 2020 looked into the functioning of single bacterial isolates obtained from tropical peat swamp forests. By whole-genome sequencing of four bacterial taxa they could show that the phylogenetically diverse bacteria from three different genera (*Dyella*, *Klebsiella* and *Paraburkholderia*) all share a wide reservoir of genetic pathways involved in carbon and nitrogen cycling in peat swamp forests. They confirmed the genomic functional potential with bioassays. Together, their study reveals that diverse bacteria do not only survive in the often anaerobic conditions in the peat swamps but even contribute to elemental cycling including those that retain C and N in these systems.

Marxsen, Rütz and Schmidt (2021) decipher the entire biodiversity including prokaryotic microbes and metazoans in floodplain aquifers using a long term data. They found that differences in groundwater zones determined the biodiversity but revealed partly contrasting patterns of microbial and metazoan communities, often explained by external nutrient input and oxygen availability. Therefore, this study shows the importance of linking multiple biodiversity components in ecosystem studies to get a comprehensive picture of the resident biodiversity, revealing that microbiome interpretations could be biased when only looking at individual biodiversity fractions.

These five studies show the enormous potential for making the microbiome field a more predictive science by utilizing a diversity of microbiome work. However, the studies only cover a tiny fraction of all microbiome work in hosts and the environment as major host and environmental systems (animal and human hosts, diverse non-forest soils, freshwater waterbodies, marine systems etc.), microbial groups (protists, viruses) and methods (metatranscriptomics, metaproteomics, metabolomics, functional assays etc.) are together encompassing the microbiome field. Yet, the compilation of microbiome papers in this special issue should make readers and microbiome researchers aware of the immense diversity of the microbiome field, which, without any doubt, will continue to rapidly advance in the near future.

References

- Bahram, M., Hildebrand, F., Forslund, S. K., Anderson, J. L., Soudzilovskaia, N. A., Bodegom, P. M., et al. (2018). Structure and function of the global topsoil microbiome. *Nature*, *560*, 233–237.
- Bahram, M., Netherway, T., Frioux, C., Ferretti, P., Coelho, L. P., Geisen, S., et al. (2021). Metagenomic assessment of the global distribution of bacteria and fungi. *Environmental Microbiology*, *23*, 316–326 n/a.

- Bar-On, Y. M., Phillips, R., & Milo, R. (2018). The biomass distribution on Earth. *Proceedings of the National Academy of Sciences*, *115*, 6506–6511.
- Berendsen, R. L., Pieterse, C. M. J., & Bakker, P. A. H. M. (2012). The rhizosphere microbiome and plant health. *Trends in Plant Science*, *17*, 478–486.
- Bulgarelli, D., Rott, M., Schlaeppli, K., Ver Loren van Themaat, E., Ahmadinejad, N., Assenza, F., et al. (2012). Revealing structure and assembly cues for *Arabidopsis* root-inhabiting bacterial microbiota. *Nature*, *488*, 91–95.
- Cho, I., & Blaser, M. J. (2012). The human microbiome: At the interface of health and disease. *Nature Reviews Genetics*, *13*, 260.
- Clemente, J. C., Ursell, L. K., Parfrey, L. W., & Knight, R. (2012). The impact of the gut microbiota on human health: An integrative view. *Cell*, *148*, 1258–1270.
- Fierer, N. (2017). Embracing the unknown: Disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology*, *15*, 579–590.
- Fierer, N., Strickland, M. S., Liptzin, D., Bradford, M. A., & Cleveland, C. C. (2009). Global patterns in belowground communities. *Ecology Letters*, *12*, 1238–1249.
- Gaube, P., Junker, R. R., & Keller, A. (2021). Changes amid constancy: Flower and leaf microbiomes along land use gradients and between bioregions. *Basic and Applied Ecology*, *50*, 1–15.
- Geisen, S., Mitchell, E. A. D., Adl, S., Bonkowski, M., Dunthorn, M., Ekelund, F., et al. (2018). Soil protists: A fertile frontier in soil biology research. *FEMS Microbiology Reviews*, *42*, 293–323 in press, fuy006-fuy006.
- Gilbert, J. A., Blaser, M. J., Caporaso, J. G., Jansson, J. K., Lynch, S. V., & Knight, R. (2018). Current understanding of the human microbiome. *Nature Medicine*, *24*, 392.
- Gill, S. R., Pop, M., DeBoy, R. T., Eckburg, P. B., Turnbaugh, P. J., Samuel, B. S., et al. (2006). Metagenomic analysis of the human distal gut microbiome. *Science*, *312*, 1355–1359.
- Luan, L., Jiang, Y., Cheng, M., Dini-Andreote, F., Sui, Y., Xu, Q., et al. (2020). Organism body size structures the soil microbial and nematode community assembly at a continental and global scale. *Nature Communications*, *11*, 6406.
- Lundberg, D. S., Lebeis, S. L., Paredes, S. H., Yourstone, S., Gehring, J., Malfatti, S., et al. (2012). Defining the core *Arabidopsis thaliana* root microbiome. *Nature*, *488*, 86–90.
- Macdonald, C. A., Anderson, I. C., Khachane, A., Singh, B. P., Barton, C. V. M., Duursma, R. A., et al. (2021). Plant productivity is a key driver of soil respiration response to climate change in a nutrient-limited soil. *Basic and Applied Ecology*, *50*, 155–168.
- Marxsen, J., Rütz, N. K., & Schmidt, S. I. (2021). Organic carbon and nutrients drive prokaryote and metazoan communities in a floodplain aquifer. *Basic and Applied Ecology*, *51*, 43–58.
- Mendes, R., Kruijt, M., de Bruijn, I., Dekkers, E., van der Voort, M., Schneider, J. H., et al. (2011). Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science*, *332*, 1097–1100.
- Netherway, T., Bengtsson, J., Krab, E. J., & Bahram, M. (2021). Biotic interactions with mycorrhizal systems as extended nutrient acquisition strategies shaping forest soil communities and functions. *Basic and Applied Ecology*, *50*, 25–42.
- Singh, B. K., Bardgett, R. D., Smith, P., & Reay, D. S. (2010). Microorganisms and climate change: Terrestrial feedbacks and mitigation options. *Nature Reviews Microbiology*, *8*, 779–790.
- Thompson, L. R., Sanders, J. G., McDonald, D., Amir, A., Ladau, J., Locey, K. J., & Knight, R. (2017). A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, *551*, 457–463.
- Too, C. C., Ong, K. S., Yule, C. M., & Keller, A. (2020). Putative roles of bacteria in the carbon and nitrogen cycles in a tropical peat swamp forest. *Basic and Applied Ecology*. doi:10.1016/j.baae.2020.10.004.
- Torsvik, V., & Ovreas, L. (2002). Microbial diversity and function in soil: From genes to ecosystems. *Current Opinion in Microbiology*, *5*, 240–245.
- Turnbaugh, P. J., Ley, R. E., Hamady, M., Fraser-Liggett, C. M., Knight, R., & Gordon, J. I. (2007). The human microbiome project. *Nature*, *449*, 804.
- Urich, T., Lanzén, A., Qi, J., Huson, D. H., Schleper, C., & Schuster, S. C. (2008). Simultaneous assessment of soil microbial community structure and function through analysis of the meta-transcriptome. *PLoS One*, *3*, e2527.
- Worden, A. Z., Follows, M. J., Giovannoni, S. J., Wilken, S., Zimmerman, A. E., & Keeling, P. J. (2015). Environmental science. Rethinking the marine carbon cycle: Factoring in the multifarious lifestyles of microbes. *Science*, *347*, 1257594.
- Xiong, W., Jousset, A., Li, R., Delgado-Baquerizo, M., Bahram, M., Logares, R., et al. (2021). A global overview of the trophic structure within microbiomes across ecosystems. *Environment International*, *151*, 106438.
- Yatsunenko, T., Rey, F. E., Manary, M. J., Trehan, I., Dominguez-Bello, M. G., Contreras, M., et al. (2012). Human gut microbiome viewed across age and geography. *Nature*, *486*, 222.
- Zhao, Z.-B., He, J.-Z., Geisen, S., Han, L.-L., Wang, J.-T., Shen, J.-P., et al. (2019). Protist communities are more sensitive to nitrogen fertilization than other microorganisms in diverse agricultural soils. *Microbiome*, *7*, 33.

Available online at www.sciencedirect.com

ScienceDirect