

Environmental microbiomes



Linda L Blackall

Email: lblackall@swin.edu.au

The March 2015 issue of *Microbiology Australia*¹ was devoted to ‘Mammalian microbiomes’ and this March 2018 issue on ‘Environmental microbiomes’ complements that previous one. Additionally, authors of articles in the current issue were largely chosen from oral presenters at the inaugural ASM-sponsored Australian Microbial Ecology (AUSME2017) conference held a year ago in Melbourne. That 3-day conference in February 2017 celebrated the field of Microbial Ecology.

Like the various compartments of mammals covered in the March 2015 *Microbiology Australia* issue, a complex suite of microbes including prokaryotes (Bacteria and Archaea), microbial eukaryotes, and viruses are found in the majority of niches on Earth. These ‘environmental microbiomes’ are vital to all global nutrient cycles, pollution biodegradation and bioremediation, in host-associations (e.g. of all non-mammals and in plant nutrient provisioning) and in ecosystem health (including in the built environment). The generation of metagenome sequences, of metatranscriptomic, metaproteomic and metametabolomic information and their data analyses and interpretation continue to be major drivers in microbiome application.

In a recent Nature Microbiology consensus statement article², which catalogued global microbiome research, ‘Microbiomes’ were defined as ‘...host-, ecosystem- or habitat-associated communities of microorganisms’, and ‘microbiome research’ was defined as ‘...those studies that emphasise community-level analyses using “omics technologies”’. In the non-human related microbiome field, major national but mostly international collaborative programmes have titles like Microbial Observatories, the International Census of Marine Microbes, the International Soil Metagenome Sequencing Consortium ‘TerraGenome’, and the Earth Microbiome Project. Philanthropic (e.g. Gordon and Betty

Moore and W. M. Keck Foundations) and Governmental agencies (many nations) have come together to co-fund these overarching microbiome research initiatives whose goals are ambitious like understanding causes of climate change in forest, grassland, and permafrost ecosystems and constructing a microbial map of planet Earth. The consensus article concluded that the dominant microbiome research activities were related to human niches and/or they focussed on basic biology research themes. The following were identified as significant future needs: computational biology; biorepositories for data; development of high throughput tools; and longitudinal, functional and interdisciplinary research topics. The practical application of microbiome research to Earth’s sustainability and for improved human livelihood will involve deeper industry and commercial involvement³.

Projections for future microbiome studies have been reported in recent outlook manuscripts. A recent non-peer reviewed perspective piece⁴ proposed that distinct microbiome characteristic types including microbial processes, microbial community properties, and microbial membership should be linked to each other and to higher level system processes that they impact. In another perspective piece, Xu *et al.*⁵, argue that over the next 10 years, microbiome research will be propelled by changes in our thinking and in technology. It ambitiously described how microbiome research will move to determining the state, function and interactions of microbes by developing imaging and visualisation methods, individuals rather than consortia will be probed, and we will move to data science from data analysis. The cardinal feature in many viewpoint papers is the fact that method development has been and will continue to be a major stimulus for studying, comprehending, and manipulating microbiomes. An essential part of this development is standardisation of protocols and use of controls⁶.

Although human-associated ecosystems might dominate the microbiome field², environmental microbiome investigations have revealed staggering microbial biodiversity and unprecedented biochemical transformation scope – a few specific examples are given here. In 2016 Hug *et al.*⁷ dramatically expanded and reformatted the tree of life, and described a whole Candidate Radiation Phylum. Anantharaman *et al.*⁸, reported many new sub-surface sourced microbial genomes and discovered metabolic handoffs in simple consortia. In late 2017, Parkes *et al.*⁹ reported 7903 bacterial genomes from public metagenome data submissions inflating the

bacterial and archaeal phylogenetic diversity by an amazing >30%. Great contributions to environmental microbiomes continue to be provided by several Australian research groups^{9–13}, as well as groups with articles in this *Microbiology Australia* issue.

The articles in this *Microbiology Australia* issue cover a broad range of environmental microbiome studies, largely from Australian-based researchers – demonstrating the vibrancy of the field. The environments covered include marine (water and host-associated), terrestrial (soil), bioremediation (wastewater treatment, bioleaching, mining), and cultural artworks. Papers cover microbial processes (chemotaxis, nitrogen cycling, synergism, life without water), biotechnological advances and opportunities, microdiversity, and microbial and trait-based ecology. Numerous microbial groups including Bacteria, Archaea, Fungi and Viruses are topics from different contributors. It comprises a panorama of subjects within the field of Environmental Microbiomes.

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Biography

Linda I. Blackall is an environmental microbial ecologist. She is a Professor in the Environmental Microbiology Research Initiative in the Faculty of Science at the University of Melbourne and an adjunct Professor at Swinburne University of Technology, Melbourne. She has studied many different complex microbial communities ranging from host associated through to free living in numerous environments. Her research has covered mammalian microbiomes of marsupials, humans, ruminants and horses, and the microbiota of non-mammals including corals and sponges. Environmental microbiomes explored in Linda's research span wastewater treatment (aerobic and anaerobic), solid waste digestion (landfill and composting), bioelectric systems and microbiologically influenced corrosion. The numerous methods she develops and employs in her research allow elucidation of microbial complexity and function in these diverse biomes.



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