



Microbes in Earth's aqueous environments

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Earth is called the “water” planet since such a large fraction of the Earth's surface is covered by water. However, the majority of this water is saline and the few percentage points of water that exist in freshwater forms is in ice, or small reservoirs at or below the Earth's surface. Aquatic habitats are teeming with microscopic life that control the habitability of the planet through their roles in biogeochemical cycles and food webs. Freshwater resources are in danger from a multitude of environmental problems, including salination, contamination and overuse. The oceans are also sensitive to long-term environmental changes including those of anthropogenic origin (Hoegh-Guldberg and Bruno, 2010). Microbial activities are integral to how these ecosystem changes are reflected in biogeochemical cycles and food webs, and how microorganisms will respond will partially, if not primarily, determine the fate of freshwater and marine resources and the Earth's climate. The social, political and economic aspects of global climate change effects on freshwater resources and ocean-atmosphere dynamics challenge our knowledge of microbial biology at global scales. One of the most critical current challenges of the aquatic microbiology discipline is to provide information and guidance for the use and sustainability of Earth's aquatic resources.

The study of microorganisms in aqueous environments, aquatic microbiology, is an inter-disciplinary science with multi-disciplinary approaches that spans diverse habitat types, spatial and temporal scales, and perspectives that range from biological organization of cells and nucleic acids to the biogeochemical transformations of inorganic and organic materials. Aquatic microbiology ranges from the Earth's deep subsurface to distant galaxies, as our understanding of life on Earth provides the basis

for examining the possibility of life on other planets (exobiology/astrobiology), and determining how and where to find it.

Aquatic microbiology research needs to cross large scales, from the structure, assembly and function of intracellular bodies and organelles to the biogeochemical budgets of lakes, rivers and estuaries and the global ocean. Current techniques can provide information over even global scales using remote sensing by satellites, or between and within cells using electron microscopy, scanning confocal microscopy or atomic force microscopy, for example. Knowledge across this range of scales is necessary to understand the patterns and activities of microbes in aquatic environments and be able to use this knowledge to predict the future response and function of microbes in our changing planet. Integrating across such large scales is challenging, but scaling of complex systems is fundamental to the systems biology perspective (Raes and Bork, 2008) which ultimately should help to see the cross-scale patterns of organisms and ecosystems and to a degree simplify our understanding at multiple scales. “The New Biology” integrates evolution and genomics into biological research and is currently changing the way many biologists approach biological research (Rose and Oakley, 2007). Conceptually the New Biology was described as the “the integration of many sub-disciplines of biology, and the integration into biology of physicists, chemists, computer scientists, engineers, and mathematicians to create a research community with the capacity to tackle a broad range of scientific and societal problems” (National Research Council, 2009). In this sense, aquatic microbial ecology has and always will be central to the New Biology, as it has always been necessary to integrate across physics, chemistry and engineering to understand and manage water resources. The

challenge of aquatic microbiology is to continue to cross, merge and extend traditional disciplines and sub-disciplines to be able to develop a predictive level understanding of how the activities at the very small scale control the global environment.

The recognition of the extent of microbial diversity and how severely limited our microbial cultivated isolates are in representing natural populations in the environment (Pace et al., 1986) have been particularly important in focusing research on the diversity of uncultured microorganisms in the environment. We have learned much of the diversity of these organisms, but there is much yet to learn, as we still struggle with the concepts of describing microbial taxa from kingdoms and domains to “species” and “ecotypes”. Accelerated and cheaper DNA sequencing has provided much new information on microbial genomes¹, including marine microorganisms and communities of microorganisms², but metagenomic and metatranscriptomic sequencing (DeLong, 2005; Rusch et al., 2007; Frias-Lopez et al., 2008) continue to suggest that we have a long way to go to understand the diversity of taxa in the environment. Some methods, which target DNA sequences rather than genomes, suggest that there is even greater diversity in natural populations, although the significance of this diversity with respect to microbial community function and evolution remains an open question. Our ignorance of microbial taxa is superseded by our ignorance of genes and gene products- a large fraction of proteins in sequenced genomes and metagenomes are “hypothetical proteins”. Furthermore, the discovery of roles of small RNA molecules in regulation (Nahvi et al., 2002) require not only a redesign of our concept of biological function, but requires new approaches and tools in order to study.

¹<http://www.microbesonline.org/>

²<http://camera.calit2.net/node/3091>

Clearly we will not understand microorganisms and their ecological functions very well, if we do not understand the underlying mechanisms that define microbial diversity. We need a new level of understanding that integrates sequence diversity, with genome differences, “species” function and adaptability. Environmental microbiology needs to develop practical definitions of organismal diversity that reflects the “operational taxonomic unit” (OTU) definition so commonly used in gene sequence diversity studies.

Isotope technologies and transcriptomics have provided information on the functions of microorganisms and microbial communities, but improved understanding of how the composition of microbial communities, and the organisms themselves, relate to ecosystem function is needed. It was previously argued (Finlay et al., 1997), and there is a general understanding (Allison and Martiny, 2008) that ecosystem function is not sensitive to changes in microbial community composition. The explosion of information on microbial genomic and physiological diversity suggests otherwise, but there is still relatively little data linking microbial diversity and genetic redundancy to specific ecosystem functions or services (Allison and Martiny, 2008). Most genetic or genomic information has yet to be directly coupled to an understanding of the control of microbial activities, such as biogeochemical transformations. There are good examples of where these links have been made, but the relationship of this information to the underlying microbial diversity, and the plasticity or resilience of microorganisms to environmental change is not well understood (Allison and Martiny, 2008). In other words there is a disconnect between our understanding of microbial evolution and adaptation and the roles of microbes in aquatic ecosystems. How and where will bottlenecks caused by environmental change occur, or will they?

Perhaps there is not a “grand challenge” in aquatic microbiology, but many. An important challenge is scaling our understanding of the biology of microorganisms, Bacteria, Archaea and Eukarya, to the function of ecosystems. An important challenge in this regard is understanding the interactions among microorganisms, the very features that make a “community” rather than a random assemblage. I suggest this is probably the most poorly understood aspect of microbial biology in aquatic ecosystems and the world in general. Studying these interactions will require new approaches and new perspectives that have yet to be developed, but are crucial for our ability to scale from microorganisms to ecosystems. Undoubtedly, enhanced resolution of microbial distributions and activities in space and time will help to scale from microbe biology to ecosystem function, and methods including mathematical modeling are needed to bridge this gap.

Aquatic microbiology has always been a diverse forward-looking discipline, and bridges basic and applied sciences. The challenge now is to integrate new approaches and develop a “New Microbiology” that can link microbes to global ecosystems: this will require acceleration in inter-disciplinary training and research and will, and already is, yielding fundamental exciting new information on the roles of aquatic microbes on Earth.

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