

Editorial

Erhard Bremer*

Masters of change

<https://doi.org/10.1515/hsz-2020-0229>

Published online October 1, 2020

Microorganisms are omnipresent in the biosphere and provide the greatest diversity of life on our planet. They successfully colonize every conceivable ecological niche, regardless of its welcoming or hostile condition, either as highly specialized individual cells, as microbial communities, by forming complex multi-cellular structures, or through interactions with eukaryotic cells. Amazingly, some microorganisms can even live inside other microbes or have developed complex symbiotic relationships with their companion bacterial or eukaryotic cells. From a human perspective, microorganisms are not always friendly: they cause diseases and can damage our food-supply. But without them, there would be no life on Earth as we know it as microorganisms drive global carbon, nitrogen, and sulfur cycles. Through their catabolic activities, they even affect the Earth climate. Microorganisms were the first inhabitants of our planet and they will be the last when other life-forms cease to exist.

A key factor of the success of microorganisms in colonizing habitats with varying and often rapidly changing physico-chemical or biological characteristics is their enormous biochemical, physiological, cellular, and genomic adaptation potential. This sets the stage for the ability of microorganisms to adjust to new conditions in their pre-existing habitat, to explore new opportunities in novel environmental settings, and to overcome constraints in cellular metabolism when the nutrient supply fluctuates or even changes entirely. The central outcome of ever changing environmental and cellular constraints, and the accompanying evolutionary forces, generate an enormous microbial diversity and leads to the development of species with unique signal transduction and signal perception abilities, metabolic profiles and cellular traits, best suited for the new tasks.

Even in *Escherichia coli* and *Bacillus subtilis*, model organisms that have been studied for decades and bacteria with moderately sized genomes, approximately one third of all genes have no recognizable function thus far. We have seen nothing yet! Large-scale metagenome studies of marine and terrestrial ecosystems, and of our own microbiome, uncovered the existence of a microbial gene pool comprising millions of genes of so far unknown functions. This is also true for the myriads of bacteriophages that prey on microorganisms or have befriended bacteria as prophages. To understand the function of genes with novel functions is an enormous challenge, while simultaneously providing humans with the unique opportunity to discover new biocatalysts for a bio-based economy and finding new natural products that will allow us to weather the perfect storm of the looming antibiotic crisis. It is obvious that microbiologists cannot simply rely in their studies on a few well-chosen model systems. They must fully embrace microbial diversity.

For most microorganisms, there is only one certainty: change! As a consequence, microorganisms have developed an array of either specialized or generally acting mechanisms that enable both individual cells and cellular communities to recognize environmental changes with high sensitivity and specificity, thereby allowing them to mount adaptive responses in a timely fashion. In this sense, microorganisms are ‘cognitive systems’ because they can interpret and integrate the information gleaned from their very sophisticated array of signal detection devices. This enables microorganisms to react to arising challenges by repairing already occurred damage, alleviating stress, re-adjusting metabolism, and changing the behavior of individual cells or entire microbial consortia.

Research groups located in several departments at the Philipps-University Marburg have a long tradition in studying physiology, ecology, biochemistry and cellular biology of bacteria and archaea, fungi, and algae. Along with those working at the Center for Synthetic Microbiology (SYNMIKRO) of the Philipps-University and at the Max Planck Institute for Terrestrial Microbiology, they strive for excellence in teaching and research. Collectively, research activities of these groups build the solid foundation for comprehensively teaching undergraduate and graduate students in the field of general microbiology. A main

*Corresponding author: Erhard Bremer, Faculty of Biology, Laboratory for Microbiology, Philipps-University Marburg, Karl-von-Frisch-Str. 8, D-35043 Marburg, Germany; and Center for Synthetic Microbiology (SYNMIKRO), Philipps-University Marburg, Hans-Meerwein Str. 6, D-35043 Marburg, Germany, E-mail: bremer@staff.uni-marburg.de, <https://orcid.org/0000-0002-2225-7005>

objective of the microbiologist working in Marburg is also to train the next generation of microbiologist and microbial geneticists through the teaching of advanced courses, seminars, and research-focused projects, thereby enabling young scientists to take up leading positions in academia, industry and society.

An important instrument to achieve these overarching goals in science and education is the formation of theme-focused research consortia. In the last eight years (2012–2020), the German Research Foundation (Deutsche Forschungsgemeinschaft; DFG) funded such a Collaborative Research Consortium (CRC 987) in Marburg that focused on ‘Microbial Diversity in Environmental Signal Response’. The CRC 987 strived to significantly advance the current knowledge about the ability of microorganisms – either as individual cells, as consortia, or in contact with eukaryotic cells – to interrogate and interpret environmental and cellular conditions and to react to the gleaned information with situation-conform adaptive responses. Grasping the mechanisms of such diverse responses to signal perception is crucial for the understanding of the functioning of individual microbial cells and microbial consortia from the

perspective of the long-term evolution of microbial species. These responses are expected to be as varied as the microorganisms that elicit them.

The contributions in this Highlight Issue of *Biological Chemistry* provide insights into the projects conducted under the unifying umbrella of the CRC 987 by current members of this research consortium in Marburg. As the speaker of the CRC 987, I would like to profoundly thank the DFG for their long-term funding of our studies on Microbial Diversity in Environmental Signal Response.



Author contribution: The author has accepted responsibility for the entire content of this submitted manuscript and approved submission.

Research funding: None declared.

Conflict of interest statement: The author declares no conflicts of interest regarding this article.