

Chapter 1

Introduction to prokaryotic metabolism and physiology

The biosphere has been shaped both by physical events and by interactions with the organisms that occupy it. Among living organisms, prokaryotes are much more metabolically diverse than eukaryotes and can also thrive under a variety of extreme conditions where eukaryotes cannot. This is possible because of the wealth of genes, metabolic pathways and molecular processes that are unique to prokaryotic cells. For this reason, prokaryotes are very important in the cycling of elements, including carbon, nitrogen, sulfur and phosphorus, as well as metals and metalloids such as copper, mercury, selenium, arsenic and chromium. Prokaryotes are important not only for shaping the biosphere, but are also involved in the health of plants and animals including humans. Disease-causing bacteria have been a major concern in microbiology from the dawn of the science, while recent developments in ‘microbiome’ research reveal paramount roles in the well-being of higher plants and animals. A full understanding of the complex biological phenomena that occur in the biosphere therefore requires a deep knowledge of the unique biological processes that occur in this vast prokaryotic world.

After publication in 1995 of the first full DNA sequence of a free-living bacterium, *Haemophilus influenzae*, whole genome sequences of thousands of prokaryotes have now been determined and many others are currently being sequenced (see <https://gold.jgi.doe.gov/> and <https://www.ncbi.nlm.nih.gov/guide/gen>

omes-maps/). Our knowledge of the whole genome profoundly influences all aspects of microbiology. Determination of entire genome sequences, however, is only a first step in fully understanding the properties of an organism and its interactions with the environment in which it lives. The functions encoded by these sequences need to be elucidated to give biochemical, physiological and ecological meaning to the information. Furthermore, sequence analysis indicates that the biological functions of substantial portions of complete genomes are so far unknown. Defining the role of each gene in the complex cellular metabolic network is a formidable task. In addition, genomes contain hundreds to thousands of genes, many of which encode multiple proteins that interact and function together as multicomponent systems for accomplishing specific cellular processes. The products of many genes are often co-regulated in complex signal transduction networks, and understanding how the genome functions as a whole presents an even greater challenge. It is also known that for a significant proportion of metabolic activities, no representative genes have been identified across all organisms, such activities being termed as ‘orphan’ to indicate they are not currently assigned to any gene. This also represents a major future challenge and will require both computational and experimental approaches.

It is widely accepted that less than 1 per cent of prokaryotes have been cultivated in pure culture under laboratory conditions. This is also

true of the majority of species associated with higher organisms, including humans, which have not been isolated in pure culture but play important roles in the well-being of the host. Development of new sequencing techniques has allowed us to obtain genomic information from the multitudes of unculturable prokaryotic species and complex microbial populations that exist in nature. Such information might provide a basis for the development of new cultivation techniques. Elucidation of the function of unknown genes through a better understanding of biochemistry and physiology could ultimately result in a fuller understanding of the complex biological phenomena occurring in the biosphere.

Unlike multicellular eukaryotes, individual cells of unicellular prokaryotes are more exposed to the continuously changing environment, and have evolved unique structures and metabolic processes to survive under such conditions. Chapter 2 describes the main aspects of the composition and structure of prokaryotic cells.

Life can be defined as a reproduction process using materials available from the environment according to the genetic information possessed by the organism. Utilization of the materials available in the environment necessitates transport into cells that are separated from the environment by a membrane. Chapter 3 outlines transport mechanisms, not only for intracellular entry of nutrients, but also for excretion of materials including extracellular enzymes and materials that form cell surface structures.

Many prokaryotes, including *Escherichia coli*, can grow in a simple mineral salts medium containing glucose as the sole organic compound. Glucose is metabolized through glycolytic pathways and the tricarboxylic acid (TCA) cycle, supplying all carbon skeletons, energy in the form of ATP and reducing equivalents in the form of NADPH for growth and reproduction. Glycolysis is described in Chapter 4 with emphasis on the reverse reactions of the EMP pathway and on prokaryote-specific metabolic pathways. When substrates other than glucose are used, parts of the metabolic pathways are employed in either forward or reverse directions. Chapter 5 describes the TCA cycle and related metabolic

pathways, and energy transduction mechanisms. Chapter 6 describes the biosynthetic metabolic processes that utilize carbon skeletons, ATP and NADPH, the production of which is discussed in the previous chapters. These chapters summarize the biochemistry of central metabolism that is employed by prokaryotes to enable growth on a glucose–mineral salts medium.

The next five chapters describe metabolism in some of the various trophic variations found in prokaryotes. These are the use of organic compounds other than glucose as carbon and energy sources (Chapter 7), anaerobic fermentation (Chapter 8), anaerobic respiratory processes (Chapter 9), chemolithotrophy (Chapter 10) and photosynthesis (Chapter 11). Some of these metabolic processes are prokaryote specific, while others are found in both prokaryotes and eukaryotes.

Prokaryotes only express a proportion of their genes at any given time, just like eukaryotes. This enables them to grow in the most efficient way under any given conditions. Metabolism is regulated not only through control of gene expression but also by controlling the activity of enzymes. These regulatory mechanisms are discussed in Chapter 12. Finally, the survival of prokaryotic organisms under starvation conditions is discussed in terms of storage materials, resting cell structures and population survival in Chapter 13.

This book has been written as a text for senior students at undergraduate level and postgraduates in microbiology and related subjects. A major proportion of the book has been based on review papers published in various scientific journals including those listed below:

Annual Review of Microbiology
Annual Review of Biochemistry
Current Opinion in Microbiology
FEMS Microbiology Reviews
Journal of Bacteriology
Microbiology and Molecular Biology Reviews (formerly *Microbiology Reviews*)
Nature Reviews Microbiology
Trends in Microbiology

The authors would also like to acknowledge the authors of the books listed below that have been consulted during the preparation of this book.

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Further Reading

Note this section contains key references only. Additional recommended references are available at www.cambridge.org/ProkaryoticMetabolism.

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