Preface

Béatrice CLOUET-D'ORVAL[1], Bruno FRANZETTI[2] and Philippe OGER[3]

[1] *MCD-CBI, CNRS, Université de Toulouse, France*

[2] *IBS, CNRS, Université Grenoble Alpes, France*

[3] *MAP, CNRS, INSA Lyon, Villeurbanne, France*

More than 40 years ago, *archaea* were proposed as a new domain of life alongside bacteria and eukaryotes. It is now accepted that these organisms constitute a distinct group, unique in many cellular and molecular aspects. The discovery of these universally important organisms represents one of the greatest advances in modern biology. Archaea have evolutionary links with early eukaryotic cells and are now used to elucidate fundamental biological questions. As champions of extremophilia, archaea have also shed light on the limits of life on Earth. Over the years, our understanding of archaeal microorganisms has evolved considerably. Far from being exotic forms of microbial life, archaea are found to be omnipresent in all terrestrial sites (>20% of marine microbial biomass) and are notably present in the human microbiota. As new genomes are sequenced, it becomes evident that archaea represent a complex, extremely diverse world and also possess a largely unexplored virosphere. In soils and oceans, archaea play a key role in the planet's major geochemical cycles. In particular, methanogens, exclusively represented by archaea, are central to issues of climate change and energy challenges. To understand their impact on the environment and human health, it is imperative to decode their unique features at a molecular level. The molecular machinery deciphered in archaea will provide key paradigms for understanding fundamental biological processes conserved across life forms. Notably, the molecular bases of genetic information processing in archaea are often very similar to their counterparts in eukaryotes (translation, transcription, replication, recombination and DNA repair), even though archaea have a cellular structure similar to bacteria. Moreover, the regulatory

Biology of Archaea 2,
coordinated by Béatrice CLOUET-D'ORVAL, Bruno FRANZETTI and Philippe OGER.
© ISTE Ltd 2025.

systems for gene expression through post-transcriptional mechanisms remain poorly understood.

Our knowledge of archaea is rapidly evolving thanks to the advent of high-throughput sequencing of entire genomes. It is time to introduce a wide audience to the advances that illuminate our understanding of biology and reveal the originality of this domain of life.

The 14 chapters, divided into two volumes, review the discovery and evolution of the domain of archaea and summarize our current knowledge of cellular and molecular processes to better integrate this domain into the broader understanding of life.

January 2025