Preface

Microorganisms are the most diverse and ubiquitous biological entities, which have successfully colonized diverse ecological niches of the planet. Clear fossil evidence of microbial life was found to exist in ancient stromatolites, such as the fossilized filamentous prokaryote of 3.5 billion years of age in Western Australia. Although Archaea have remained close to the characteristics of the universal ancestor and still occupy extreme habitats with similar characteristics to the ones in existence in the early days of the Earth, bacteria continued to evolve into impressive morphological diversity and occupy a broad range of habitats. They also provided the forerunners of today's mitochondria and chloroplast, leading to the establishment and evolution of Eukaryotic organisms about 1.7 billion years ago. Bacteria, Archaea, and Eukarya throughout the evolution of the Earth established their diverse ecological niches and specialized in diverse functions to maintain ecosystem health, thanks to their metabolic diversity and genetic adaptabilities. Through the application of molecular techniques, it has become clear that microbial diversity is greater than that which their cultured representatives displayed. Metagenomics combined with improved sampling techniques is now taking our understanding further and revealing the existence of novel microorganisms in marine, extreme environments, as well as in the previously explored environments, such as the terrigenous ones. Most importantly, these novel molecular tools are now revealing the functional existence of microorganisms in different niches, providing support for the sustainable existence of higher organisms in these ecosystems.

Biodiscovery and microbial biotechnology are based on the search for exploitable and diverse biological resources. In this search, the screening of microbial natural products still continues to represent an important route to the discovery of novel chemicals for the development of new therapeutic agents. The evaluation of the biosynthetic potential of lesser known and/or new microbial taxa is thus of increasing interest. However, selection of novel bioactive compounds producing microorganisms from nature requires a sound microbial taxonomical knowledge and a better understanding of microbial ecology, physiology, and metabolism. Therefore, taxonomic expertise combined with effective preservation of microbial genetic resources will provide a stronger platform for novel discoveries. Furthermore, emerging new technologies associated with bioinformatics and biogeography are fundamentally changing our capability of applying target-based approaches to selectively culture industrially important microorganisms.

Microbial Resources: From Functional Existence in Nature to Industrial Applications will provide the reader with an exciting interdisciplinary journey covering sequential aspects of microbiology, ranging from functional existence of microorganisms in nature to the transformation of this knowledge at industrial and application levels. The book covers and provides:

- the aspects of foundational information related to the microbial ecology, taxonomy, and preservation of diversity, as well as providing information on microbial genetics, genomics, and cryptic genes with importance to industry;
- information on the sustainable utilization of microbial resources for biodiscovery and biotechnology with significant added value due to the inclusion of comprehensive coverage of the culture collections and biological resource centers;
- legislative issues related to the Convention on Biological Diversity (CBD) and its Nagoya Protocol that identify benefit-sharing deriving from the use of microbial resources; and
- information on the IP, biosafety, and transport of microbiological material.

I thank all authors for their valuable contributions. This book brings pioneers of the field and early career scientists together, which is no doubt an indication of the commitment toward the advancement of microbial biotechnology and biodiscovery, to be continued across the generations to come.

We will embrace emerging molecular advancements, while treasuring the traditions and passions passed to us by the earlier generations, when working with talented microorganisms that will continue to contribute to the benefit of mankind.

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