

# Preface

The introduction of penicillin in the 1940s not only revolutionized medicine but also triggered the screening of microbes for the production of bioactive secondary metabolites. Since then, respective attempts led to the discovery of tens of thousands of substances and revealed filamentous fungi as invaluable resources that produce a large number and diversity of chemical structures. Not only Ascomycetes like the well-studied *Aspergillus*, *Penicillium*, and *Fusarium* species but also Basidiomycetes are among the currently known highly prolific producers of secondary metabolites. During recent years, the potential of underexplored fungi, such as the plant-inhabiting endophytes or marine fungi, as a reservoir of novel biologically active substances has been recognized and the role of secondary metabolites in the interaction of fungi with their biotic environment came into focus.

The increasing availability of “omics” technologies opened up new avenues in fungal research. These approaches allow comprehensive system-level analyses and hence the identification of the complete genomic inventory of secondary metabolic gene clusters in a given fungus, the detailed study of their activation, and the global profiling of the resulting metabolites. Taking into account that fungi harbor large numbers of secondary metabolism-associated cryptic gene clusters, “omics”-guided approaches together with genetic engineering allow the exploitation of fungi for novel products. Furthermore, recent developments such as metagenomics and metatranscriptomics currently have found their way into research on fungal secondary metabolism. These techniques bear great potential by enabling to screen even unculturable fungi in their natural microbial communities and habitats for genes involved in the production of novel compounds and hence will contribute to natural product discovery from the large pool of the untapped fungal biodiversity.

In appreciation of the tremendous progress in the research on fungal secondary metabolism during recent years, we are pleased to present this book, the second volume on the *Biosynthesis and Molecular Genetics of Fungal Secondary Metabolites* within the Springer book series on Fungal Biology. This book aims to continue the compilation of the best-studied fungal secondary metabolites contained in the first volume by adding aspects on regulatory key players and epigenetic control of their biosynthesis, genomics- and metabolomics-guided approaches for a further unearthing of the potential of fungi as resources of novel biologically active

substances, the use of secondary metabolite profiles in fungal chemotaxonomy, less-exploited substances and their producers, and the biological roles of secondary metabolites in organismic interactions.

Fungal secondary metabolites significantly impact mankind as they comprise substances contributing to human well-being such as antibiotics, antivirals, immunosuppressives, antitumor, and anticholesterolemic agents, as well also toxins that act as virulence factors in their respective hosts and that may cause health problems by contaminating our food and indoor environment. For both, the use of beneficial substances in medicine and pharmaceutical industry and the risk reduction of fungal metabolites with adverse health effects, a detailed knowledge and understanding of fungal secondary metabolism are fundamental. The recent emergence of high-throughput “omics” techniques constitutes an important step in this regard and will further significantly contribute to the discovery of novel fungal metabolites.

We are grateful to all the authors who contributed to this book and we hope that this book will help the reader to obtain novel insights into the current status and future directions of this fascinating field.

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