

# Preface

The ascomycete genera *Aspergillus* and *Penicillium* are among the most widely studied filamentous fungi. They have had a profound impact on human society and continue to do so. The antibiotic penicillin, produced by *Penicillium rubens*, has been instrumental in treating patients with infections during and after World War II and *Penicillium* species are still actively mined for novel antibiotics. *Aspergillus* species are better known for the industrial production of enzymes and metabolites (e.g. organic acids) that have found applications in various industrial sectors, such as food & feed, paper & pulp, textiles, beverages, wine, beer, pharmaceuticals, and biofuels & biochemicals. Several *Aspergillus* species also have a darker side, being able to cause invasive infections in immune-compromised patients, leading still to a high mortality rate.

Genome sequencing has affected studies into the biology of all classes of organisms and this is certainly true for filamentous fungi. The level with which biological systems can be studied since the availability of genomes and postgenomic technologies is beyond what most people could have imagined previously. *Aspergillus* and *Penicillium* are at the forefront of fungal genomics with many genome sequences available and a whole genus genome sequencing project in progress for *Aspergillus*. Genomic and post-genomic analysis has both broadened and changed our understanding of fungal biology, in particular with respect to the complexity of fungal biology and the high diversity amongst fungal species.

In this book we showcase the impact of genomics on studies in *Aspergillus* and *Penicillium*. The book starts with an overview of the taxonomy these two genera and its sister genus *Talaromyces*, which has recently been re-visited and updated. It then continues with three chapters on techniques currently used in relation to genomics.

Next several chapters present a genomic look on a variety of biological processes in these fungi: pathogenicity, carbon starvation, sulfur metabolism, feruloyl esterases, secondary metabolism and pH modulation. The final chapter presents a novel approach to generating targeted mutants that in combination with genomics can help to gain more insights into the mechanism underlying enzyme production.

While this book only provides a small selection of the broad range of topics that are actively studied in these fungi by many scientists around the world, its contents provide a clear picture of the influence of genomics on fungal biology. It also demonstrates the areas that require further development and as such can be a reference not only for scientists working with these genera but for fungal biology as a whole.

We are very grateful for the many authors who contributed to the book and provided us with high quality chapters sharing their considerable expertise. It is those contributions that provide the quality to this book and we enjoyed our interaction with them very much.

Finally, we would also like to thank Annette Griffin and the other staff at Caister Academic Press, who have made this a smooth and efficient process and were also available for any queries we have had.

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