

# *Aspergillus* and *Penicillium* in the Post-genomic Era

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Cover design adapted from image courtesy of Jan Dijksterhuis, Ad Wiebenga and Ronald P. de Vries (*Aspergillus niger* grown on wheat bran).

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# 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.

Ronald P. de Vries  
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Start by marking "Aspergillus and Penicillium in the Post-Genomic Era" as Want to Read: Want to Read savingâ€¦| Want to Read. See a Problem? We'd love your help. Let us know what's wrong with this preview of Aspergillus and Penicillium in the Post-Genomic Era by Ronald P De Vries. Problem: It's the wrong book It's the wrong edition Other. Details (if other): Cancel. Thanks for telling us about the problem. Return to Book Page. Not the book you're looking for? Preview "Aspergillus and Penicillium in the Post-Genomic Era" by Ronald P De Vries. Aspergillus and Penicillium in the Post-Genomic Era. by. Ronald P De Vries (Editor) Aspergillus penicillioides is a species of fungus in the genus Aspergillus, and is among the most xerophilic fungi. Aspergillus penicillioides is typically found in indoor air, house dust, and on substrates with low water activity, such as dried food, papers affected by foxing, and inorganic objects such as binocular lenses. The distribution of the fungus is worldwide; it has been found in bed dust from maritime temperate, Mediterranean, and tropical climates. The abundance of the fungus is influenced Even though species in the Aspergillus and Penicillium genera (family Aspergillaceae, class Eurotiomycetes) are some of the most significant technologically and medically relevant fungi, we still lack a genome-scale phylogeny of the lineage or knowledge of the parts of the phylogeny that exhibit conflict among analyses. Our analyses provide a robust and comprehensive evolutionary genomic roadmap for this important lineage, which will facilitate the examination of the diverse technologically and medically relevant traits of these fungi in an evolutionary context. INTRODUCTION. "This new and well-presented book gives the impression of a vibrant field and the prospect of an increasingly exciting age of understanding in the biology and physiology of species in these two genera" from IMA Fungus. "specialists in the field should definitely take a look at the book" from Biospektrum (2017) 23: 107-108. No customer reviews. 5 star (0%). Database of Genomic Structural Variation (dbVar). Database of Genotypes and Phenotypes (dbGaP). A generic assay for all target species of Aspergillus, Penicillium and Paecilomyces was also developed and tested. Using a previously reported DNA extraction method, estimated conidia detection limits for target species ranged from less than one to several hundred per sample for the different assays. Total quantities of Aspergillus, Penicillium and Paecilomyces conidia in the samples, determined by the generic assay and the summed totals from the specific assays, were in general agreement, suggesting that all of the numerically dominant species in the samples were accounted for by the specific assays.