
Preface

Fungal genomics has experienced unprecedented growth since the turn of the millennium. Starting with the completion of the first fungal genomes nearly 10 years ago, the genomes of over 60 species spanning major taxonomic groups and ecological niches have been sequenced. The rate at which fungal genomes are being sequenced has increased dramatically with the refinement of next-generation sequencing technologies, making genomics-based approaches feasible for a broad range of fungi. This dramatic expansion of resources and techniques is poised to fundamentally redefine the study of fungal biology.

In upcoming years, fungal genomics is likely to advance on three fronts. First, more and more genomes will be sequenced. To assist readers in this ongoing process, we present chapters describing techniques for genome sequencing and assembly, including a discussion of next-generation sequencing technologies. Second, sequenced genomes will be mined extensively for useful information. To this end, we have included chapters that describe protocols and programs to identify and analyze telomeres and repetitive sequences in the fungal genomes. Third, genomic sequences will provide a foundation for powerful techniques to explain biological processes, and much of this book is dedicated to explaining established and emerging genomics-based technologies in filamentous fungi. Four chapters describe gene expression profiling techniques, including expressed sequence tags (ESTs) and microarrays. Three chapters describe techniques for fungal proteomics, including how to identify proteins in a given biological sample, affinity purification of proteins based on protein–protein interaction, and how ChIP-chip can be used to study promoter elements and other functions at the chromatin or DNA–protein interaction levels. Other chapters provide case studies that could be adapted to a wide range of fungi, including procedures to generate, characterize, and manage a large number of knockout mutants in *Neurospora crassa*, the study of mycoviruses and hypovirulence in the chestnut blight fungus, metabolic fingerprinting in *Fusarium verticillioides* to determine gene function, and large-scale insertional mutagenesis in *Magnaporthe oryzae* to identify novel virulence or pathogenicity factors.

Contributors to this book were urged to emphasize unpublished tips, potential pitfalls, common mistakes, and special considerations based on their unique experiences. Our goal was to provide fungal biologists at any stage of their careers a user-friendly resource for fungal genomics, especially as readers branch out into unfamiliar but exciting new areas of study.

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