
Preface

The kingdom Fungi constitutes an independent group equal in rank to that of plants and animals. It is a diverse clade of heterotrophic eukaryotic organisms that shares some characteristics with animals and includes mushrooms, molds, yeasts as well as many other types of less well known organisms. Approximately 100,000 species have been described, which comprise less than 10% of the estimated number of fungal species in nature. Fungi can be found in every place wherever adequate moisture, temperature, and organic substrates are available; however, they also occupy extreme habitats, from hot volcanoes to arctic zones, arid deserts, and deep oceans.

The importance of fungi as a group is tremendous; most species are saprobes and play prime roles in decomposition and the recycling of organic matter and nutrients, and many of them produce enzymes and metabolites with important applications in pharmacology, biotechnology, and other industries. Alongside the positive aspects, fungi also cause huge damage, primarily as plant pathogens. Fungi are highly amenable to molecular work, and a few fungal species serve as model systems to study basic processes with results that are applicable to many organisms, including humans.

Fungal research has made enormous progress in the past two decades. Two main stages can be identified: (1) the development of fungal transformation systems in the 1980s, which represents the shift of fungal research to the molecular era, and (2) sequencing of the *Saccharomyces cerevisiae* genome in the late 1990s, which represents the entrance of fungal research to the genomic era. Currently over 70 fungal genomes have been published and numerous others are being sequenced. This wealth of genomic information along with high throughput methods has revolutionized fungal research. The combination of the genomic approaches with the more traditional molecular and cell biology methods, particularly the readily available transformation and gene knockout procedures, open new horizons in fungal research, and we may expect that the coming years will bring exciting discoveries and developments.

Lessons from advanced model systems, particularly the yeast *S. cerevisiae*, show that the increased use of high throughput methods will be paralleled by increased research of single genes and proteins, products of such high throughput analyzes. Indeed, molecular, biochemical, and cellular-type work is now practiced in many fungal research laboratories to investigate the function of newly identified genes/proteins/metabolic pathways/signal cascades, etc.

The primary purpose of *Molecular and Cell Biology Methods for Fungi* is to provide readers with an up-to-date set of practical protocols that cover the range of frequently used methods to study molecular and cellular aspects of fungal biology. The set of protocols described in this book includes classical protocols such as transformation systems and traditional protein analysis methods, which have been widely used for many years, alongside the most advanced techniques such as genome amplification, whole genome knockout methods, sophisticated in vivo imaging techniques, etc.

The methods in each chapter describe protocols for specific fungal species. However, the described methods should be useful in a wide range of species; detailed *Notes* are provided in each protocol, which should allow easy adaptation of the protocol to various other species. It is my hope that this book will be helpful to both experienced fungal research laboratories as well as to those that are interested in using fungi as hosts to study their favorite genes.

Finally, I would like to take this opportunity to thank all authors for their commitment, cooperation, and contributions. I am also thankful to John Walker, the series editor, for his professional guidance during all stages and for making this process an enjoyable and educating experience.

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