



Introductory Remarks

Hee-Moon Park

Department of Microbiology, Chungnam National University, Daejeon 305-764

In a universal phylogenetic tree conducted by nucleotide sequence analysis and comparative biochemistry, we can see that fungi represent one of the ultimate branches of the eukarya domain, evolutionary closest to present-day plants animals, but distinct from them. Today, the relevance of fungi as model organisms is evident, however, mycology, the study of fungi, was a descriptive discipline and largely neglected as an experimental science until 1904, in which the evidence for heterothallism was provided by Blakeslee. Soon to follow was the demonstration that sexually reproducing fungi exhibit Mendelian inheritance and that it was possible to conduct formal genetic analysis with fungi.

The discovery of penicillin by Fleming, who shared a Nobel Prize in 1945, provided further impetus for experimental research with fungi. Thus began a period of interest in mutation induction and analysis of mutants for biochemical traits. Such fundamental research, conducted largely with *Neurospora crassa*, led to the one gene: one enzyme hypothesis and to a second Nobel Prize for fungal research awarded to Beadle and Tatum in 1958. Fundamental research in biochemical genetics was extended to other fungi, especially to *Saccharomyces cerevisiae*, and fungal systems were much favored for studies in eukaryotic molecular biology. In fact Hartwell and Nurse, who shared the 2001 Nobel Prize, have been performed various experiments with yeasts *S. cerevisiae* and *Schizosaccharomyces pombe* to understand the eukaryotic cell cycle control at molecular level.

The experimental achievements in research on the genetics and molecular biology of fungi have benefited more generally studies in the related fields of fungal biochemistry, plant pathology, medical mycology, and systematics. Today, there is much interest in the genetic manipulation of fungi for applied research. The study of fungal biology has changed dramatically in recent years as the techniques for isolating and characterizing genes have become easier and more information has steadily accumulated regarding fundamental process such as cell cycle control, hyphal growth, septation and cell wall development, and fungal pathogenicity. The advent of genome-level analysis, following the completion of the genome sequence of yeasts *S. cerevisiae*, *S. pombe*, and *Candida albicans* has also changed the research landscape enormously. Recent availability of several filamentous fungal genomes from *Magnaporthe oryzae*, *Aspergillus nidulans*, and *N. crassa* in public databases is also an exciting prospect. There is the real prospect of studying the integrated action of many genes during developmental and physiological process and producing a far greater understanding of fungal biology than has hitherto been possible.

My hope in assembling this variety of fungal research systems in a single session is that anyone studying or willing to study a fungal organism can get the ideas for starting a new venue of investigation.