
Preface

Aspergillus has more than 200 highly diverged species. It includes economically important species widely used for fermentation, mostly in the Orient, such as *Aspergillus oryzae*, *Aspergillus sojae*, *Aspergillus niger*, and *Aspergillus awamori*. They produce various useful enzymes and organic acids. A long history of these species in the food industries has resulted in their inclusion in the Generally Recognized As Safe (GRAS) list of the United States Food and Drug Administration. Conversely, aspergilli are known to produce various secondary metabolites, some of which are harmful to humans, or are thought to be important for pathogenicity in animals or plants. *Aspergillus flavus*, *Aspergillus parasiticus* and *A. niger* are known to produce mycotoxins of strong carcinogenic activity: aflatoxin and ochratoxin, the former of which is one of the most potent natural compounds. Interestingly, *A. oryzae* and *A. flavus* genomes have a high sequence similarity (99% or greater), and furthermore, *A. niger* has, in addition to the strains used industrially, strains with opposite characteristics in terms of safety to the human body. The phenotypic diversity of species or strains with a very close genetic background may have been attributed to a local difference in a corresponding chromosome, or a deletion or mutation of the gene responsible for a particular phenotype. Recent advances in molecular biology have revealed global regulation of secondary metabolic genes at a transcriptional level as well. This could significantly enhance the safety of industrial species allowing greater reliability in their use in fermentation.

Even apart from industrial applications, *Aspergillus* includes a species extremely important for basic research, *Aspergillus nidulans*. Its ability in sexual development, which is a critical feature for classical genetics, has made this species a model microorganism for filamentous fungi as well as for the aspergilli. *Aspergillus fumigatus* is an opportunistic pathogen to humans and is known to cause the fatal infectious disease aspergillosis. Because of the industrial and medical importance of the aspergilli, whole-genome sequencing including publication of four species has been accomplished, and genome sequences of a further ten species are also nearly in completion. Comparative genomics could be the key to elucidate the developmental molecular mechanisms for the huge diversity, acquisition of pathogenicity and domestication of the aspergilli. Recent analyses of genome structures of the aspergilli strongly proposed horizontal gene transfer as one of the potential mechanisms for acquiring high gene diversity. Gene duplication followed by extensive mutagenesis could be another possible mechanism, not only for diversity but also for novel gene generation.

This book includes fine reviews written by leading researchers in *Aspergillus*, which summarize the most important aspects of *Aspergillus* molecular biology and genomics. Chapter 1 presents an overview of the genus *Aspergillus* covering from its nomenclature to recently developed genomics. The genus *Aspergillus* is one of the better studied taxonomies among the filamentous fungi, and *Aspergillus* can be divided into eight subgen-

era based on the recent phylogenetic analysis of multilocus sequence data (Chapter 2). Several chapters deal with comparative genomics (mainly among the eight *Aspergillus* species whose genome analyses have been completed), systems biology studies and bioinformatics in *Aspergillus* (Chapters 3, 4, and 9). Genome analyses of several aspergilli revealed that a large number of genes for transcription factors with zinc finger motifs were present in their genomes, which are summarised in Chapter 5. The following three chapters deal with the genomic aspects of sexual

development in *A. nidulans*, secondary metabolism in *Aspergillus*, and aflatoxin biosynthesis in *A. flavus*. Finally, novel industrial approaches using genome information and DNA microarrays of *A. oryzae* that have been used in the traditional Japanese fermentation industry are described in Chapter 10.

In closing, we editors sincerely thank all the authors for their excellent contributions to this book. We are also grateful to Annette Griffin and the staff of Horizon Scientific Press for their patience and assistance in publishing this book.

Masayuki Machida

Katsuya Gomi