

Preface

In the last decade of the 20th century, biological research has seen a vast accumulation of genomic and transcriptomic information that contributed greatly to the rapid advancement of functional genomics, a field where dynamic aspects resulting from the integration of genomic and transcriptomic knowledge as opposed to the static aspects based on genome information are deemed more substantial and essential. However, this may not be sufficient for the complete elucidation of more complicated quantitative phenotypes. Metabolites, resulting from the interaction of the system's genome with its environment, are not merely the end product of gene expression but also form part of the regulatory system of various biological processes in an integrated manner. Hence, profiling of metabolites is a promising tool for addressing this limitation.

Metabolomics, the global quantitative assessment of metabolites in a biological system, is considered the answer to the problem of analyzing complicated quantitative phenotypes. In addition, integration of metabolomics information into the upstream "omics" such as genomics, transcriptomics, and proteomics would be very important albeit more difficult than expected. Metabolomics involves three different technical elements, namely biology, analytical chemistry, and informatics. Several analytical methods have been utilized for metabolomics and among them, mass spectrometry is one of the most important techniques due to its high sensitivity and quantitative capability. Mass spectrometry-based metabolomics can be a very demanding technique for biologists without special experience in quantitative mass spectrometry, thus the purpose of this book is to explain the complicated know-how of metabolomics. A number of case studies are also introduced for easy understanding of the metabolomics workflow and its practical applications in various research fields. Based on our extensive experience in mass spectrometry-based metabolomics, I decided to summarize our past achievements in the establishment of robust and reproducible protocols from sample

preparation to data analysis. This book lays out the fundamental concepts and principles in metabolomics research (Chapter 1) and can act as a good practical guide to start metabolomics research. The whole workflow is also extensively covered in this book that includes experimental design (Chapter 2), preparation of biological samples (Chapter 3), analysis using various instruments (Chapter 4 and Chapter 5), and data processing and data analysis (Chapter 6). In addition, case studies are illustrated in Chapter 7.

Finally, I would like to express my special gratitude to our editors and publisher for providing us with the opportunity of writing this book. I hope that this book will be useful for academicians and researchers of all disciplines in their metabolomics pursuits.

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