

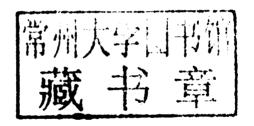
Metabolomics in food and nutrition

Edited by Bart C. Weimer and Carolyn Slupsky



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Introduction

Metabolomics has emerged as a science with the capacity to cause a major paradigm shift in the way we approach all aspects of public health, including nutrition, agriculture, and food production. Metabolomics biochemically describes the total metabolism and metabolic interactions of cells, organisms, and communities of organisms, to provide a framework on which to understand cellular and organism function in a given environment. Incorporating metabolomics into systems biology will allow a comprehensive understanding of the breadth of health and disease by linking genomics, transcriptomics, proteomics and metabolomics at the organism and/or community level. This system-level knowledge will be key to understanding the network and the communication within the metabolic network that leads to overall health or disease. Moreover, clarifying how the genome and transcriptome are ultimately related to the end products of metabolism will enable a better assessment of the impact of environment, pathogens, and genetic modification on the nutritional and sensory qualities of food. The goal of this book is to provide a working knowledge of metabolomics in health and agriculture to researchers, students, and policy makers by first outlining the technology in detail, and how the wealth of information generated is used to gain meaningful information. Secondly, this book provides several chapters on how this type of research is being used in laboratories and industries to solve important problems, and where this research will lead in the future. This book will provide an invaluable reference tool on techniques and methods in metabolomics, allowing the reader a greater understanding of this rapidly expanding field.

Progress in systems biology, and in particular metabolomics, has occurred through breakthroughs in both technology (especially equipment and techniques for mass spectrometry (MS) and nuclear magnetic resonance (NMR)) and our understanding and integration of these -omics sciences through computational methods. For MS, more sophisticated instrumentation, along with the establishment of standard chemical fragmentation libraries and advances in computer hardware and software, means that thousands of chemicals within a single sample can be measured. Similarly, for NMR, increases in magnetic field strength, the