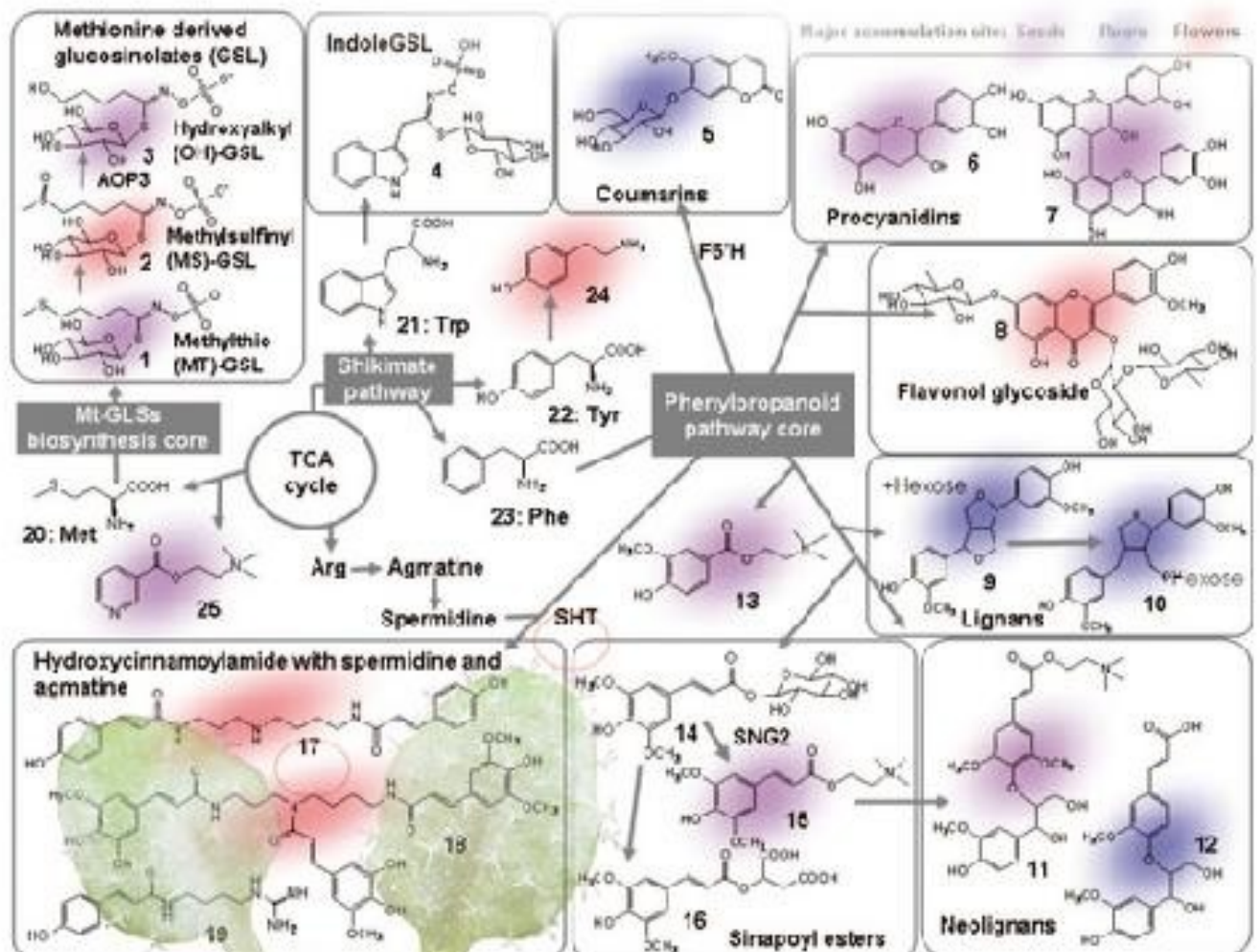


The Handbook of Plant Metabolomics

Edited by Wolfram Weckwerth
and Günter Kahl



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Dedicated to

*Ulrich and Hannelore Weckwerth
for their endless sympathy, patience and guidance*

Preface

Whereas the most modern topics of plant research, grouped into the term “omics,” such as genomics, transcriptomics, and proteomics, are comparatively new, the strategies to isolate, purify, identify, and quantify a multitude of low molecular weight cellular compounds (called metabolites) look back on a long history. While initially only metabolites present in comparatively high concentrations could be isolated and quantified (sometimes only semiquantified), the advent of enzymatic detection techniques in the 1970s brought a breakthrough in precise metabolite analysis. Unfortunately, these techniques required the coupling of a metabolite's detection to the reduction/oxidation of NAD^+ to NADP^+ , and therefore excluded the majority of metabolites, especially secondary metabolites. More recent developments in mass spectrometry (MS), matrix-assisted laser desorption/ionization (MALDI)–MS for metabolite imaging, gas chromatography coupled to mass spectrometry (GC–MS), liquid chromatography coupled to mass spectrometry (LC–MS), and NMR technology for medium- to high-throughput identification and quantification of low molecular weight compounds pushed metabolite analysis to today's advanced level, where various physico-chemical separation techniques are combined to analyze metabolite profiles in considerable detail and accuracy. The present state of technology for metabolite analysis has been denoted “metabolomics.”

Metabolomics reflects the physiological state of an organism or its organs, tissues, or cells, and therefore allows a hitherto not possible comprehensive understanding of the biology of an organism and its response to intrinsic or environmental changes or influences. The various techniques of metabolomics allow the comprehensive profiling of cellular metabolites at the systems level, thereby providing a direct readout of biochemical activity that can be correlated with phenotype and used to identify therapeutic targets. This omics discipline then bridges the gap between genotype and phenotype. The present *Handbook of Plant Metabolomics* not only witnesses the present state-of-the-art metabolomics and its widespread applications, but also portrays up-to-date technical advances in metabolite fingerprinting and the *in silico* analysis of the resulting, mostly very complex, metabolite patterns.

The Handbook of Plant Metabolomics (Metabolite Profiling and Networking) is the fourth volume of the successful Wiley-VCH series of *Handbooks of Plant Genome Analysis*, and follows the warmly welcomed *The Handbook of Plant Genome Mapping (Genetic and Physical Mapping)*, *The Handbook of Plant Functional Genomics (Concepts and Protocols)*, and *The Handbook of Plant Mutation Screening (Mining of Natural and Induced Alleles)*. It provides informative introductions to each chapter, detailed descriptions of techniques for metabolite profiling, and robust and ready-to-go laboratory protocols, in addition to some applications, all written by internationally renowned experts in their research fields. Although this volume focuses on *plant* metabolomics, the techniques presented are broadly applicable to other biological systems exemplifying the pioneering and original character of metabolomics in plant biology. This rapid development of metabolomics to a mature technology is catalyzing the application of metabolomics in other fields of research also, such as biomedicine.

The Editors very much appreciate the excellent chapters contributed by all the authors, and expect that *The Handbook of Plant Metabolomics* will reproduce the worldwide success of its three progenitors.

Vienna (Austria)
Frankfurt am Main (Germany)
August 2012

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