前　言

在接受为《分子生物学方法》系列丛书编写一卷有关代谢轮廓分析的任务后，我开始揣摩它的涵义所在。Fiehn将其定义为“对某一完整代谢途径或其交叉通路中特定数目代谢物的定性和定量分析”[1]。与之密切相关的概念还包括代谢靶标分析、代谢指纹分析和代谢组学分析，其中代谢组学分析是指对某一生物系统内代谢物波动的定量检测[2]。上述四种概念常常相互通用。回顾近40年的文献资料显而易见，涉及代谢物分析的各概念之间由于分析方法和技术的进步而得以相互关联。譬如，代谢组学的出现不过10年而已，但其赖以存在的诸多流程和仪器基础都源于为先天性代谢缺陷诊断和药物代谢分析而建立的各种策略。因此编撰本书时，我试着囊括能直观地展示从单一化合物分子分析向全面的代谢组学分析发展的各种策略。鉴于此，本书将立足于概括性的描述而不是面面俱到，但是我仍希望本书所述方法能够成为代谢轮廓分析领域内的新老同仁的有益资源。

Thomas O. Metz

参考文献：

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2. Nicholson, J. K., Lindon, J. C., Holmes, E. (1999) 'Metabonomics': understanding the metabolic responses of living systems to pathophysiological stimuli via multivariate statistical analysis of biological NMR spectroscopic data. *Xenobiotica* 29, 1181-1189.

（高鹏　译）

Preface

After accepting the task to edit a volume of *Methods in Molecular Biology* devoted to metabolic profiling, I began to contemplate the definition of the term. Fiehn referred to "metabolic profiling" as the identification and quantification of a select number of metabolites in an entire metabolic pathway or intersecting pathways (1). Closely related disciplines were targeted metabolite analysis, metabolic fingerprinting, and metabolomics, the latter of which was defined as the quantitative measurement of perturbations in the metabolite complement of a biological system (2). These four terms are often used interchangeably; indeed, in reviewing the literature over the past 40 years, it is evident that these various disciplines of metabolite analysis are related via an evolution of methods and technology. For example, while the field of metabolomics is now 10 years old, the protocols and instrumentation that form the foundation for the myriad approaches of this discipline are based on those originally established for the diagnosis of inborn errors of metabolism and drug metabolite analysis. Thus, in compiling this volume, I have made an attempt to incorporate protocols that are illustrative of the evolution of metabolic profiling from single molecule analysis to global metabolome profiling. The constraints of this volume necessitate that its contents will be perspective based, rather than comprehensive. However, it is my hope that the methods contained herein will be a resource for both established and new investigators in the field of metabolic profiling.

Thomas O. Metz

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