

PREFACE

Advances in sequencing, bioinformatics, and genome editing now enable us to access the rich chemistry encoded within the metabolic pathways of plants and microbes. A major focus in metabolism is the secondary, or specialized, pathways that produce small, biologically active molecules with applications in pharmaceutical, agrochemical, or other biotechnological sectors. In recent years, metabolic engineering/synthetic biology approaches have shown remarkable promise for the exploitation of these pathways for human use. In these two volumes, we highlight some of the most important approaches that have been used to harness microbial and plant metabolic pathways.

In Volume 1, we focus on advances that have been made in microbial-based systems. The discovery some three decades ago that bacterial specialized metabolic pathways are clustered on the genome has greatly facilitated the identification and characterization of these pathway genes. Coupled with the fact that bacterial genomes can now be sequenced rapidly and inexpensively, the last decade has seen a staggering increase in our knowledge of bacterial specialized metabolism. Additionally, it is now known that fungal specialized pathways also cluster on the genome. While fungal genomes are larger than those from bacteria, these genomes can still can be easily sequenced, and substantial advances in elucidating fungal metabolism have been made. Consequently, a wealth of new opportunities in metabolic engineering have been opened. In this volume, we highlight how better production of these compounds can be achieved, and how these biosynthetic enzymes can be engineered to generate new biocatalysts and new products. We also discuss how microbial species can be manipulated to serve as a host for reconstitution of plant pathways. The volume concludes with several representative examples of new tools that allow us to rapidly manipulate the genetic material of the microbial host.

Volume 2 focuses on the metabolism of plants. Historically, elucidating plant metabolism has been challenging due to the lack of tightly genome-clustered pathways that are observed in microbial systems, along with the large size of plant genomes and transcriptomes. The first set of articles in this volume describe a variety of strategies to elucidate plant-specialized metabolism. Notably, the specialized metabolism of plants is controlled by complex regulatory processes. Furthermore, plant biosynthetic processes are also complicated by the fact that the metabolic reactions occur in a

variety of different cell types and subcellular compartments. Therefore, several articles in this volume also describe efforts to control the regulatory networks that maintain the levels of metabolism production in plants, along with methods to understand the mechanisms of transport and localization of specialized metabolic intermediates. Finally, we highlight emerging tools to harness plant metabolism: new plant-based expression platforms and expression tools for production of metabolites are discussed.

Metabolic engineering has progressed rapidly in the last several years. The advent of genome editing, the ability to sequence complex genomes quickly and inexpensively, and the successful manipulation of plant and microbial hosts for more effective pathway reconstitution have collectively demonstrated that metabolic engineering holds substantial promise for improving our access to the end products of specialized metabolism. I note that these two volumes scratch the surface of this field, providing only a survey of some of the efforts being made in this area. I am deeply indebted to all of the contributors to this volume who graciously provided their time and effort to make a contribution to this work.

S.E. O'CONNOR

The John Innes Centre

Department of Biological Chemistry