

Preface

The proteome comprises all protein species resulting from gene expression in a cell, organelle, tissue or organism. By definition, proteomics aims to identify and characterize the expression pattern, cellular location, activity, regulation, post-translational modifications (PTMs), molecular interactions, three-dimensional (3D) structures and functions of each protein in a biological system. Due to the highly dynamic nature of the proteome, proteomics studies tend to focus on more specific goals as part of approaches to understand the function and regulation of biological systems. Proteome analysis is applied on different levels: (i) to catalogue the proteins synthesized in an organism, tissue or organelle; (ii) to characterize changes occurring during a developmental process; (iii) to identify proteins differing between biological samples or (iv) to identify proteins on the basis of a functional property (e.g. ligand binding). These types of analysis are all illustrated in the different chapters of this book.

Proteomics techniques are increasingly applied over the entire spectrum of biological sciences. All approaches have in common that they involve the separation, characterization and analysis of many proteins at once. Since 1975, 20 years before the term 'proteome' was first coined, separation of proteins in complex mixtures has been achieved by 2D-gel electrophoresis. Gel-based proteomics studies, despite limitations, are still of great value since 2D-gels can provide a unique overview of the different protein forms in a sample. However, gel-free techniques based solely on chromatographic separations and mass spectrometry are used increasingly frequently and have enabled the identification and characterization of low abundance, hydrophobic, basic or otherwise elusive proteins that are not amenable to 2D-gel analysis. Technological advances in 2D-gel electrophoresis systems and particularly in mass spectrometry have meant that proteome analysis is now financially and technically feasible for many laboratories. A wide spectrum of technical approaches will be found throughout the volume.

In plant science, the number of proteome studies is rapidly expanding after the completion of the *Arabidopsis thaliana* genome sequence, and proteome analyses of other important or emerging model systems and crop plants are in progress or are being initiated. Proteome analysis in plants is subject to the same obstacles and limitations as in other organisms, however the nature of plant tissues, with their rigid cell walls and complex variety of secondary metabolites, means that extra challenges are involved that may not be faced when analysing other organisms.

In several cases, the technologies described in this volume have not yet been applied to plant proteins, but point the way for future plant proteome studies. In Chapter 1, some of the challenges involved are introduced together with an overview of the technical and bioinformatic resources available for plant proteome analysis.

Much of the complexity of the proteome is due to PTMs of proteins. Mass spectrometry has revolutionized analysis of PTMs and new types of modification continue to be identified. Approaches for identification and characterization of PTMs in proteomes are presented in Chapter 2. In Chapter 3 approaches to analyse multi-protein complexes and protein–protein interactions in plants are discussed. Redox regulation of proteins is of major importance for many aspects of plant physiology. Recently there have been an increasing number of functional proteomics approaches taken to identify proteins undergoing cysteine and disulphide oxidation. An overview of this field is given in Chapter 4. High throughput structure determination of proteins can give important and often unexpected insights into the roles of previously uncharacterized proteins. An example of such a structural proteomics approach is described in Chapter 5.

An overview of proteome studies in cereal crop plants and the status for comprehensive analysis of rice proteomes is presented in Chapter 6. Proteomics approaches to identify proteins involved in specific developmental processes in plants, with particular reference to seed development and germination are covered in Chapter 7. Two chapters covering organelle proteomics highlight some of the technical challenges involved in these analyses and the type of data that can be obtained from them. Chapter 8 covers analyses of the plant cell wall and secreted proteins that are notoriously challenging to isolate and study. Plant mitochondria have been the subject of numerous proteomics studies, including analysis of both soluble and membrane proteins, post-translationally modified proteins and spanning expression and functional proteome approaches using a wide range of techniques. Chapter 9 provides a detailed overview of the new information about plant mitochondrial function that has been gained from these studies.

A few common themes emerge from plant proteome analyses, including those presented in this volume: many proteins are typically identified in proteomics studies that are not similar to any protein with known function. In fact, the functions of approximately a third of the annotated genes in the *Arabidopsis thaliana* genome are unknown, suggesting that we still have a great deal to learn about plant biology. Another common outcome of plant proteomics projects is the identification of plant-specific proteins, that is, where the only similar sequences also originate from plants. The functions of many of these are also unknown, but are likely to be crucial for our understanding of plant physiology. Thus, one of the challenges arising from plant proteome research is to understand the functions of the proteins that are identified. Structural proteomics initiatives combined with information obtained from interaction, expression and functional proteomics studies can guide biochemical studies to elucidate protein function. In-depth biochemical characterization at the level of individual proteins or genes is an important requirement to validate and understand the significance of the data produced by proteomics, transcriptomics and metabolomics studies. Currently, few studies combine proteome analysis with genomics, transcriptomics and/or metabolomics, but future integration of these more or less high throughput techniques will bring us closer to a 'systems biology' approach to plant science.

The aim of this volume is to highlight ways in which proteome analysis has been used to probe the complexities of plant biochemistry and physiology. It is aimed at researchers in plant biochemistry, genomics, transcriptomics, proteomics and metabolomics who wish to gain an up-to-date insight into plant proteomes, the information plant proteomics can yield and the directions plant proteome research is taking.

Christine Finnie