
PREFACE

The beginning of the twenty-first century is certainly a great time to be involved in plant proteomics. This new millennium has placed an ever growing amount of sophisticated technology (i.e., the ever growing list of annotated genes and genome sequence databases from *Arabidopsis*, rice and other plant species) at the disposal of the modern scientist to the benefit of all. The research performed with this technology has the potential to bring the answers to important and complex biological questions and problems (especially those relating to crop plants and the human food supply) within reach.

Proteomics in plants began in 1990s, but has accelerated with an unexpected pace and momentum since 1999 when many economical techniques (which are standard today) were developed to characterize proteins on a proteome-wide scale. The proteomics burst seen in the literature in recent years has made a significant impact on plant biology mainly by answering many of the questions associated with the genome annotation and the number of functional proteins expressed in a given organism. Indeed, when one looks at the progress achieved to-date in the field of plant proteomics and its overall impact on biological research, it is clear just how essential proteomics is to our understanding of the physiology of any organism. For example, proteomics is perhaps the only means that enables one to fully understand post-translational modifications of proteins. Thus, it would not be far from the truth to say that the "power of proteomics" (and indeed the omic sciences as a whole) is one of the driving forces of twenty-first century biological science.

A current (early 2008) literature survey in PubMed indicates that the number of publications containing the term "plant proteomics" is 100-fold higher today, compared to same period in 1999. Not surprisingly, this survey also indicates that proteomic studies have primarily been conducted in the two widely accepted flowering model plants, the weed *Arabidopsis thaliana* and the cereal crop rice (*Oryza sativa* L.). The publication of the genome sequences of these two plants represents a significant landmark in the history of plant biology. However, one must ask: Are we fully aware of the true potential of plant proteomics and if so, are we using this knowledge to its full effect? The principles of good science are as true in this age of omics still hold true today and the disciplined scientist must keep these principles in mind to avoid rushing blindly into the field (intentionally or unintentionally) without first obtaining a thorough understanding of its fundamental principles.

When one looks at the impressive progress of proteomics in plant science, as well as its immense importance in biological sciences as a whole, it is clear that a need for

a textbook, exists to translate/disseminate the knowledge acquired by leading experts in the field to the wider scientific community. This was the impetus for the book you are currently reading. Though we knew that such a project would be a daunting challenge, we also knew that it would bring the opportunity to work closely with the leading experts of the field. What we did not fully appreciate when we started was how much of a truly unparalleled experience it would be to work with each and every one of the contributors of this book, whom we genuinely thank for being part of this ambitious endeavor.

This book is composed of 9 sections in the following order: overview of proteomics in plant biology, technologies, computational/expression/organelle/modification proteomics, multiprotein complex, plant defense and stress, structural proteomics, systems biology, and proteomics in developing countries. The 47 chapters provide excellent coverage of almost all the studies conducted to-date on plant growth and development at the proteomics level. Each chapter also contains a five-year viewpoint which discusses the scope for investigating proteomes and innovative improvements in proteomic technologies over the next decade. We hope this book will be beneficial in scope and practical knowledge to readers, whose response will be the final judge of the validity of the work.

As a final point, it is fitting that we acknowledge the people who gave their unconditional and inspiring support, without which this book would not have reached completion. First and foremost we would like to thank Professor Dominic M. Desiderio (Department of Neurology, University of Tennessee, Memphis, Tennessee, USA) for being our mentor in this endeavor and enabling completion of this tremendous milestone in our lives.

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