

Plant Proteomics

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Plant Proteomics

Methods and Protocols

Edited by

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Preface

The aim of *Plant Proteomics: Methods and Protocols* is to present up-to-date methods and protocols used by recognized scientists in the world of plant proteomics. If this world was a very small one twenty-five years ago when the first papers were published, it has since experienced exponential growth, and in most countries around the world there are laboratories working on plant proteomics.

Two-dimensional gel electrophoresis is still the basic method used, but it has been improved greatly with IPG in the first dimension (Chapter 13) and with new detection methods with fluorochromes (Chapters 14 and 15). Significant progress has been achieved in protein extraction, which is particularly difficult with plant tissues containing phenols, proteases, and other secondary metabolites that interfere with proteins. Standard procedures have been optimized (Chapters 1 and 2) for peculiar tissues (Chapters 3, 4, and 5) and cellular compartments (Chapters 6 to 10). These methods rely on improvements made in the solubilization of proteins from membranes (Chapters 11 and 12). Mass spectrometry was a revolution that permitted the high throughput identification of proteins separated by 2D gels (Chapters 19 and 20) but also from blue native 1D gels (Chapters 27 and 28) despite the fact that Edman sequencing can still be useful (Chapter 18). Associated with other techniques such as 2DLC or LC of intact proteins, mass spectrometry also permits the identification of polypeptides from complexes (Chapters 21 and 22). A rapidly expanding area of plant proteomics concerns the analysis of post translational modifications and protein–protein relationships (Chapters 24 to 29). Finally, proteomics produces different kinds of data (qualitative and quantitative data, spectrometric data) that must be organized in databases to be shared by the community (Chapter 23) and statistic tools are necessary to analyze the abundance of data efficiently (Chapters 16,17)

The authors contribute by explaining in full detail their experimental methodology, either in the wet or in the dry lab, allowing a novice to successfully undertake the described method. Experts in proteomics will also appreciate the chapters dealing with approaches with which they are not familiar.

Hervé Thiellement
Michel Zivy
Catherine Damerval
Valérie Méchin

Contents

| | |
|--|-----|
| Preface | v |
| Contributors | xi |
| 1 Total Protein Extraction with TCA-Acetone <i>Valérie Méchin, Catherine Damerval, and Michel Zivy</i> | 1 |
| 2 Phenol Extraction of Proteins for Proteomic Studies of Recalcitrant Plant Tissues <i>Mireille Faurobert, Esther Pelpoir, and Jamila Chaïb</i> | 9 |
| 3 Protein Extraction from Cereal Seeds <i>Gérard Branlard and Emmanuelle Bancel</i> | 15 |
| 4 Protein Extraction from Xylem and Phloem Sap <i>Julia Kehr and Martijn Rep</i> | 27 |
| 5 Protein Extraction from Woody Plants <i>Christophe Plomion and Céline Lalanne</i> | 37 |
| 6 Isolation of Chloroplast Proteins from <i>Arabidopsis thaliana</i> for Proteome Analysis <i>Klaas J. van Wijk, Jean-Benoît Peltier, and Lisa Giacomelli</i> | 43 |
| 7 Isolation and Subfractionation of Plant Mitochondria for Proteomic Analysis <i>Holger Eubel, Joshua L. Heazlewood, and A. Harvey Millar</i> | 49 |
| 8 Extraction of Nuclear Proteins from Root Meristematic Cells <i>Fernando González-Camacho and Francisco Javier Medina</i> | 63 |
| 9 Isolation of Nuclear Proteins <i>Setsuko Komatsu</i> | 73 |
| 10 Isolation of Cell Wall Proteins from <i>Medicago sativa</i> Stems <i>Bonnie S. Watson and Lloyd W. Sumner</i> | 79 |
| 11 Plant Plasma Membrane Protein Extraction and Solubilization for Proteomic Analysis <i>Véronique Santoni</i> | 93 |
| 12 Detergents and Chaotropes for Protein Solubilization before Two-Dimensional Electrophoresis <i>Thierry Rabilloud, Sylvie Luche, Véronique Santoni, and Mireille Chevallet</i> | 111 |

| | | |
|----|---|-----|
| 13 | Two-Dimensional Electrophoresis for Plant Proteomics Walter Weiss and Angelika Görg | 121 |
| 14 | Visible and Fluorescent Staining of Two-Dimensional Gels François Chevalier, Valérie Rofidal, and Michel Rossignol | 145 |
| 15 | Two-Dimensional Differential In-Gel Electrophoresis (DIGE) of Leaf and Roots of <i>Lycopersicon esculentum</i> Matthew Keeler, Jessica Letarte, Emily Hatstrup, Fatimah Hickman and Paul A. Haynes | 157 |
| 16 | Quantitative Analysis of 2D Gels Michel Zivy | 175 |
| 17 | Multivariate Data Analysis of Proteome Data Kåre Engkilde, Susanne Jacobsen, and Ib Søndergaard | 195 |
| 18 | Edman Sequencing of Plant Proteins from 2D Gels Setsuko Komatsu | 211 |
| 19 | Peptide Mass Fingerprinting: <i>Identification of Proteins by MALDI-TOF</i> Nicolas Sommerer, Delphine Centeno, and Michel Rossignol | 219 |
| 20 | Protein Identification using Nano Liquid Chromatography–Tandem Mass Spectrometry Luc Negroni | 235 |
| 21 | Two-Dimensional Nanoflow Liquid Chromatography–Tandem Mass Spectrometry of Proteins Extracted from Rice Leaves and Roots Linda Breci and Paul A. Haynes | 249 |
| 22 | Separation, Identification, and Profiling of Membrane Proteins by GFC/IEC/SDS-PAGE and MALDI TOF MS Wojciech Szponarski, Frédéric Delom, Nicolas Sommerer, Michel Rossignol, and Rémy Gibrat | 267 |
| 23 | The PROTiCdb Database for 2-DE Proteomics Olivier Langella, Michel Zivy, and Johann Joets | 279 |
| 24 | Identification of Phosphorylated Proteins Maria V. Turkina and Alexander V. Vener | 305 |
| 25 | Plant Proteomics and Glycosylation Anne-Catherine Fitchette, Olivia Tran Dinh, Loïc Faye, and Muriel Bardor | 317 |
| 26 | Blue-Native Gel Electrophoresis for the Characterization of Protein Complexes in Plants Jesco Heinemeyer, Dagmar Lewejohann, and Hans-Peter Braun | 343 |

| | | |
|-------|---|------------|
| 27 | Electroelution of Intact Proteins from SDS-PAGE Gels and Their Subsequent MALDI-TOF MS Analysis Zhentian Lei, Ajith Anand, Kirankumar S. Mysore, and Lloyd W. Sumner | 353 |
| 28 | Generation of Plant Protein Microarrays and Investigation of Antigen–Antibody Interactions Birgit Kersten and Tanja Feilner | 365 |
| 29 | Phosphorylation Studies Using Plant Protein Microarrays Tanja Feilner and Birgit Kersten | 379 |
| Index | | 391 |

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