Thiellement, H., Zivy, M., Damerval, C., Méchin, V.: **Plant Proteomics. Methods and Protocols.** - Humana Press, Totowa 2007. 390 pp. ISBN: 978-1-58829-635-1

Proteomics from plant tissue has a many specifics in comparison to proteomics from another materials. The first papers seeking changes in protein expression in different plant tissue, organs or organelles under influence of internal of external stimuli were published thirty years ago. From that time many scientists around the world working on this topic suggested new methodologies and processes. This book belongs to the series "Methods in Molecular Biology" edited by J.M. Walker. It represents the complex of 29 chapters, which describe up-to-date methods and protocols for plant proteomics, each written by expert researchers from leading laboratories. Experimental methods are explained clearly and in detail.

The basic method for plant proteomics is two-dimensional gel electrophoresis (2D-PAGE), the only analytical technique that can be routinely applied for parallel quantitative expression profiling of large sets of complex protein mixtures, such as total cell or tissue extracts. Standard procedures of 2D-PAGE were described in chapters 1 and 2. Significant progress has been achieved in protein extraction, which is particularly difficult with plant tissue containing proteases and other secondary metabolites that interfere with proteins. Further, the classical procedure has been optimised for peculiar tissues (chapters 3 - 5). The next chapters (7 - 11) suggest solutions for extraction of protein from specific organelles such as nuclei, chloroplasts, *etc*. Chapter 12 sets to the selection and application of appropriate detergents and chaotropes for protein solubilization before 2D-PAGE. Staining of 2D-PAGE gels is a crucial step in comparative proteome analysis with respect to the number of protein analysed, the accuracy of spot quantification, and compatibility with mass spectrometry. Chapter 14 describes staining with several visible and fluorescent dyes.

Two-dimensional differential gel electrophoresis technology (2D-DIGE), discussed in chapter 15, adds an accurate quantitative component to comparative 2D gel analysis. It can be used to compare protein abundance changes across multiple samples with concurrent statistical measurements of confidence. Protein samples are firstly labelled with high sensitive cyanine fluorescent dyes, then mixed together and run on the same 2D gel. This removes any gel-to-gel variability, thus allowing much higher accuracy in relative quantification.

If these chapters deal with the techniques of extraction of proteins or methods improving the process of electrophoresis, the next chapters focus on methods of protein identification and data analyses. In chapter 16 the quantitative analysis of 2D gels and in chapter 17 multivariate data analyses of proteome data are discussed. MALDI-TOF peptide mass fingerprinting (chapter 19) is the fastest and cheapest method of protein identification, when the complete sequence of the organism is available. Tandem Mass Spectrometry (MS/MS) analysis (chapters 20 and 21) is more laborious but can identify individual peptides without databases (*de novo* sequencing). Effective sequence determination of proteins that could not be easily purified by conventional column chromatography is allowed by combination of 2D-PAGE, Western blotting and Edman sequencing (chapter 18).

Following chapters deal with separation and identification of specific membrane proteins (chapter 22), phosphorylated proteins (chapters 24 and 29) or glycosylated proteins (chapter 25). The methods as a blue-native gel electrophoresis or electroelution of intact proteins from SDS-PAGE gels are mentioned in chapters 26 and 27. The last two chapters (28 and 29) present the possibilities of protein microarray technology in plant science.

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