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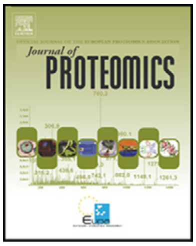

Review

Plant proteomics update (2007–2008): Second-generation proteomic techniques, an appropriate experimental design, and data analysis to fulfill MIAPE standards, increase plant proteome coverage and expand biological knowledge

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ABSTRACT

This review is the continuation of three previously published articles [Jorrin JV, Maldonado AM, Castillejo MA. Plant proteome analysis: a 2006 update. Proteomics 2007; 7: 2947–2962; Rossignol M, Peltier JB, Mock HP, Matros A, Maldonado AM, Jorrin JV. Plant proteome analysis: a 2004–2006 update. Proteomics 2006; 6: 5529–5548; Canovas FM, Dumas-Gaudot E, Recorbet G, Jorrin J, Mock HP, Rossignol M. Plant proteome analysis. Proteomics 2004; 4: 285–298] and aims to update the contribution of Proteomics to plant research between 2007 and September 2008 by reviewing most of the papers, which number approximately 250, that appeared in the Plant Proteomics field during that period. Most of the papers published deal with the proteome of *Arabidopsis thaliana* and rice (*Oryza sativa*), and focus on profiling organs, tissues, cells or subcellular proteomes, and studying developmental processes and responses to biotic and abiotic stresses using a differential expression strategy. Although the platform based on 2-DE is still the most commonly used, the use of gel-free and second-generation Quantitative Proteomic techniques has increased. Proteomic data are beginning to be validated using complementary -omics or classical biochemical or cellular biology techniques. In addition, appropriate experimental design and statistical analysis are being carried out in accordance with the required Minimal Information about a Proteomic Experiment (MIAPE) standards. As a result, the coverage of the plant cell proteome and the plant biology knowledge is increasing. Compared to human and yeast systems, however, plant biology research has yet to exploit fully the potential of proteomics, in particular its applications to PTMs and Interactomics.

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Contents

1. Introduction

1.1. *Where is (Plant) Proteomics and where should it be?*

"How", "where", "when", and "what for" are the several hundred thousand of individual protein species produced in a living organism? How do they interact with one another and with other molecules to construct the cellular building? How do they work in order to fit in with programmed growth and development, and to interact with their biotic and abiotic environment? To answer all of these questions is the objective, first, of Proteomics, and ultimately of Systems Biology [4].

In order to approach the above questions experimentally, continuous improvements in techniques and protocols for High-throughput Proteomics are being made at all workflow stages, starting from the laboratory (tissue and cell fractionation, protein extraction, depletion, purification, separation, MS analysis) and ending at the computer (algorithms for protein identification and bioinformatics tools for data analysis, databases and repositories). Since no single approach can fully unravel the complexity of living organisms, and experimental results need to be validated, Proteomics, like any methodology, should be considered as part of a multidisciplinary integrative analysis at different levels, extending from the gene to the phenotype through proteins. This analysis should involve -omics (Genomics, Transcriptomics, Proteomics, Metabolomics) as well as classical biochemical and cellular biology techniques [5–7]. Integrative transcriptomic and proteomic studies, and depending on the biological system, may or may not show good correlationship between the level of protein and mRNA. Biological or methodological explanations are normally forwarded to explain such discrepancies [8–11].

Despite the technological achievements in Proteomics, only a tiny fraction of the cell proteome has been characterized so far, and only for a few biological systems (human, fruit fly, *Arabidopsis*, rice). Even for these organisms, the function of quite a number of proteins remains to be investigated [12]. Proteomic techniques have a number of limitations, such as sensitivity, resolution and speed of data capture. They also face a number of