

Role of Proteomics in Plant Growth and Development

Reiko Komatsu*

Department of Biotechnology, Fukui University of Technology, Fukui, Japan

DESCRIPTION

Plants durability and adaptation to various environmental circumstances are largely dependent on proteins encoded by genomes. Proteomics provides the additional benefit of taking into consideration post-translational changes, which reveal the functional consequences of protein modifications on plants. Proteome analysis has gained prominence in plant research over the last two decades. When compared to humans and other animals, Protein output from plant samples is limited in other organisms due to the presence of interfering biological pollutants such as nucleic acid. Polyphenols, lipids, carbs, and other pigments are all found in plants. Plant proteomics has developed from the identification of a few proteins to large-scale proteome profiling. This was made possible by the development of a number of unique sample preparation techniques to overcome the challenges posed by the high-dynamic range of protein concentrations. Each type of biological sample is different, and sample processing may need small or substantial changes from established techniques. When planning and performing a proteomics experiment, the first step is to prepare the sample at the protein extraction stage, taking into account protein and peptide fractionations that are compatible with downstream mass spectrometry analysis. Plant tissues have a lesser protein concentration than tissues from other organisms, but they are often rich in proteases, lipids, and phenolic compounds, demanding the breaking down of cell walls to access cellular content. Steps for protein analysis in plants includes; 1) Sample harvesting; 2) Tissue homogenization and sample integrity; 3) Protein extraction in denaturing conditions; 4) Removal of biological contaminants and re-solubilization of proteins. Shotgun proteomics demands the digestion of proteins into peptides, which may be easily charged and identified by nESI-MS/MS. Trypsin is the most often utilized protease in proteomics because it cleaves at the C-terminal following lysine

and arginine efficiently and specifically. Due to basic residues in the C-term end and an ammonia group in the N-term, it forms peptides of MS-compatible size that ionize better for MS/MS analysis, boosting the amount of double charged peptides generated under the acidic conditions of the RP gradients. Several reports where multiprotease digestion was performed demonstrate the limitations in protein identification and sequence coverage imposed by mere use of trypsin. Chymotrypsin, glutamyl peptidase I (Glu-C), Lys-N, and LysargiNase are all serine proteases utilized in protein digestion. In comparison to trypsin alone, the simultaneous use of Lys-N, Lys-C, and trypsin resulted in a 72 percent increase in the amount of detectable phosphopeptides, whereas a trypsin repeated experiment only resulted in a 25 percent increase. Lys-N is remarkable in that it possesses enzymatic selectivity for lysine's N-terminal side, is highly thermo stable, and is resistant to denaturing chemicals like urea. It's a great way to boost your digestion. Membrane proteins, for example, are insoluble proteins. The way a proteome changes in response to stress is challenging since it is dependent on a number of factors, including stress level, plant growth stage, type of plant tissue, species, and genotype. The field of proteomics continues to push the limits of analysis to the biological dynamic range's lower end. Instrument sensitivity advancements and more suitable sample preparation procedures are required advancements for targeting low-abundant proteins while achieving robust and reproducible analysis. Adopting the optimal image preparation strategy based on the sample type will vastly improve proteome coverage and assist in resolving important biological issues. To increase crop output and growth, stress-tolerant or resilient crops must be developed. The field of proteomics may expand on the solid basis that has already been created, and the limits of plant proteomics can be pushed even farther with some innovation and innovative methodologies.

Correspondence to: Reiko Komatsu, Department of Environment and Information Sciences, Fukui University of Technology, Fukui, Japan, E-mail: rkomatsu@fukui-ut.ac.jp

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