J Biotechnol Biomater 2018, Volume: 8
DOI: 10.4172/2155-952X-C7-107

Application of quantitative post translational modification proteomics and interactomics in plant biology study

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Quantitative and functional post-translational modification (PTM) proteomics and interactomics have emerged as powerful omics approaches in studying cellular events in various model organisms. In this seminar, I intend to show several examples on how to apply in planta metabolic labeling and *in vitro* chemical labeling-based (4C) quantitative PTM proteomic and interactomic workflow (SILIA, SQUA-D and AQUIP) in investigation of cell signaling in the model plant *Arabidopsis* and its potential impact in the plant cell biology research in general. To elucidate the molecular mechanism underlying plant hormone ethylene signaling in *Arabidopsis* on a number of plant responses, several well-known *Arabidopsis* ethylene response loss-of-function mutants (ctr1-1, rcn1-1, ein2-5 and eil3eil1) were selected as target plant materials for both stable isotope metabolic labeling (SILIA) and *in vitro* dimethyl labeling (SQUA-D) for the PTM quantitation. The 4C quantitative proteomics and interactomics results clearly revealed that there exist multiple PTM-mediated signaling pathways in *Arabidopsis*. This quantitative PTM proteomics was able to identify rapidly phosphorylated proteins, such as TREPH1, MAP Kinase Kinases, CPKs, in response to 40 second of touch or 150 seconds of gravity stimulation in *Arabidopsis*. The following reverse genetic and transgenic plant approaches in combination with cell biology studies validated the biological functions of these key candidate phosphoproteins in these internal and external signals-mediated cellular events and dramatic plant responses. These successful research results suggest that our PTM proteomic approach can be quantitative, repeatable, accurate and versatile in addressing many important biological questions in life sciences.

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