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Selected Publication

Hu Q, Guo G, Yang Z, Li Y and Li N (2014) Stable isotope metabolic labeling-based quantitative thiol redox proteomic analysis of hydrogen peroxide-treated Arabidopsis plant. *IJ Proteomics Bioinform* 7:5

Research Aims and Interests

Quantitative and functional proteomics and post-translational modification (PTM) proteomics have emerged as powerful Omics approaches in studying cellular events in various model organisms. In this presentation, I intend to show several examples on how to apply quantitative PTM proteomics (*SILIA and AQUIP, OxNSIL*) in study of cell signaling in the model plant Arabidopsis and on the potential impact of this approach in the cell biology research in general. To elucidate the molecular mechanism underlying the time-dependent and dual-and-opposing (DOE) effect of a plant hormone ethylene on a number of plant responses, several well-known Arabidopsis ethylene constitutive and insensitive mutants, such as *ctr1, rcn1, ein2-5* and *eil3eil1* and octuple *acs* deletion mutant, were selected as target plant materials for the stable isotope metabolic labeling (*SIML*)-based quantitative phosphoproteomics research. Our quantitative PTM proteomics results clearly revealed that there are multiple ethylene signaling pathways in Arabidopsis, which are *EIN2*- and *EIN3EIL1*-independent. This *SIML*-based quantitative PTM proteomics was able to identify rapidly phosphorylated proteins in response to 1-minute of ethylene treatment from Arabidopsis plants. Reverse genetic and transgenic plant approaches in combination with cell biology studies validated the important biological functions of these candidate phosphoproteins in ethylene-mediated cellular events. These successful research results suggest that the functional PTM proteomic approach is quantitative, repeatable, accurate and versatile in addressing the important biological questions in life sciences.