Functional and quantitative phosphoproteomics in study of plant cell signaling

by

Professor Li Ning  
Professor  
Division of Life Science  
The Hong Kong University of Science and Technology

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ALL ARE WELCOME
Functional and quantitative phosphoproteomics in study of plant cell signaling

Ning Li, PhD
Professor
Division of Life Science,
The Hong Kong University of Science and Technology,
Clear water bay
Hong Kong SAR, China

Abstract

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 seminar, I intend to show several examples on how to apply quantitative and functional PTM proteomics (SILIA 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 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 response mutants, such as ctrl, 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 exist multiple phosphor-relay-mediated 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.