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香港浸會大學
HONG KONG BAPTIST UNIVERSITY
FACULTY OF SCIENCE

ICTS Institute of Computational and Theoretical Studies 計算及理論研究所

Department of Biology & ICTS Joint Seminar

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Quantitative Phosphoproteomics and Its Application in the Study of Plant Signaling

Being sessile organisms, plants must regulate their growth and development to respond to a variety of internal and external stimuli during their life cycles. The transduction of these signals is mainly mediated by protein post-translational modifications (PTMs), among which protein phosphorylation is one of the essential PTMs. Proteomics was demonstrated as a useful tool in the study of life sciences over the past decades. We have developed a quantitative phosphoproteomics approach based on *in planta* stable isotope labeling and applied it to the various studies of plant signaling. Ethylene is a vital plant hormone that participates in the regulation of numerous biological processes and cellular events. To address how ethylene is signaled through phosphorylation relay in plant cells, this quantitative phosphoproteomics approach was performed to the wild type and distinct ethylene-related loss-of-function mutants of Arabidopsis, including *ctr1* (constitutive triple response 1) mutant, *eer1* (enhanced ethylene response 1) mutant and *ein3/eil1* (ethylene insensitive 3 and ethylene insensitive 3-like 1) double mutant. Our quantitative phosphoproteomics results proposed the existence of signal transduction pathways bypassing the well-documented linear signaling pathway. One of our major findings is that ethylene increases water transport rate in Arabidopsis cells via phosphorylating S280 and/or S283 residues at C-terminus of aquaporin protein PIP2, which may regulate water loss during leaf and flower petal wilting. Immunoblotting analysis and single cell assays further verified it. This proteomics strategy was also applied to the study of mechanosignaling. The external mechanosimulation was applied to Arabidopsis seedlings through the touch treatment. Thousands of phosphosites were identified and dramatic alterations (up to 13 fold) in protein phosphorylation, which occurred within 40 seconds, were discovered in our study. Among the dozens of mechano-regulated phosphoproteins, our following experiments illustrated that phosphorylation of S625 site near the C-terminus of TREPH1 (Touch-regulated phosphoprotein1) protein underlies the delay-bolting, a major component of thigomomorphogenetic response of Arabidopsis to external mechanostimulation. These successes demonstrated that our quantitative phosphoproteomics approach based on *in planta* stable isotope labeling is an effectively strategy to discover the key players in cell signaling of plants.

Date : Friday, 17th August 2018
Time : 11:00 am to 12:00 noon
Venue : FSC703, HSH Campus, HKBU

ALL ARE WELCOME