SCHOOL OF
BIOLOGICAL SCIENCES
THE UNIVERSITY OF HONG KONG

Application of stable isotope labeling-based quantitative PTM proteomics in study of plant cell signaling

Date: July 6ᵗʰ, 2022

Time: 11 am

Venue: KBSB 6N-11

About the speaker:

Professor Ning Li is a professor in the Division of Life Science at the Hong Kong University of Science and Technology. His current research areas include mass spectrometry-based quantitative and functional PTM proteomics and interactomics, post-translational modification (PTM) and protein-protein interaction networks in eukaryotic cell signaling and cycling.

Abstract:

Terrestrial plants, as sessile organisms, have evolved sophisticated sensing systems and flexible adaptive abilities to respond to both internal and external signals. In the present studies, we have applied *in vitro* dimethyl-labelling-based quantitative phosphoproteomics to study drought-triggered phosphorylation changes in soybean cultivars. At the same time, another *in vitro* dimethyl-labelling-based quantitative acetylproteomics was developed to investigate the changes of acetylproteome in an ethylene-insensitive mutant *ein3eil1* under ethylene treatment. In total, we have identified 9457 and 6733 repeatable phosphopeptide and acetylpeptide groups (or called unique PTM peptide arrays, UPAs), respectively, from soybean and *ein3eil1*. The isotope labeling-based quantitative phosphoproteomics and acetylproteomics contributed 54% and 135% novel PTM peptides to its repository, respectively. Further performing of *in vivo* metabolic SILIA-based 4C quantitative phosphoproteomics on the touch-induced Arabidopsis revealed 24 touch-regulated phosphoproteins out of 4895 phosphopeptide groups. Functional studies found that TREPH1 protein is a cytoskeleton protein, which plays a role in regulating the bolting of Arabidopsis. The 4C quantitative PTM proteomics is evidently a powerful approach in identifying cell signaling components mediating the plant responses to both hormone and environmental signals.

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4. Liu, SC, Yu, FC, Yang, Z, Wang, TL, Xiong, HR, Chang, C, Yu, WC* and Li, Ning* (2018) Establishment of Dimethyl labeling-based quantitative acetylomics in Arabidopsis. *Mol Cell Proteomics*. 17:1010-1027.