THE CHINESE UNIVERSITY OF HONG KONG

SCHOOL OF LIFE SCIENCES

LIFE SCIENCES SEMINAR SERIES
2015 – 2016

Food & Plant Sciences Focus Group

Functional and quantitative phosphoproteomics in study of plant cell signaling

by

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on

24 September 2015
(Thursday)

at

12:30 – 1:15 pm

at

Room 103
Y.C. Liang Hall
The Chinese University of Hong Kong

ALL ARE WELCOME

Functional and quantitative phosphoproteomics in study of plant cell signaling

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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 ***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 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.