

Painting Molecular Pictures of Biological Systems via Mass Spectrometric Imaging

by

Prof Lingjun Li

*School of Pharmacy and Department of Chemistry
University of Wisconsin-Madison, 777 Highland Avenue, Madison,
Wisconsin 53705, USA*

Date : 27 June 2017 (Tuesday)

Time : 3:00 p.m.

Venue: OEE601
Oen Hall Building East Wing
Ho Sin Hang Campus
Hong Kong Baptist University

All Interested are Welcome

Abstract

Mass spectrometric imaging (MSI) provides an attractive opportunity to detect and probe the molecular content of tissues in an anatomical context. This technique creates distribution maps of select compounds without the need for *priori* knowledge of target analytes. In this presentation, I will describe our efforts and recent progress in mapping and imaging of a wide variety of signaling molecules in several biological systems, highlighting the unique challenges and important roles of MSI in the areas of proteomics, peptidomics and metabolomics.

Although high resolution accurate mass (HRAM) MSI platform offers unique advantages for mapping small molecule metabolites due to its high resolution and accuracy measurement, typical MALDI-LTQ-Orbitrap platform suffers from limited utility for large peptide and protein analysis due to its maximum m/z 4000. To overcome this challenge, we employed volatile matrices to produce multiply charged ions in MALDI source via laserspray ionization (LSI) and matrix assisted ionization in vacuum (MAIV) techniques on the MALDI Orbitrap platform. These new ionization techniques enabled substantial expansion of the mass range of the instrument and generated improved fragmentation efficiency compared to traditional MALDI-MS. To further enhance the chemical information extracted from *in situ* MALDI MSI experiments, we report on a multiplex-MSI method, which combines HRAM MSI technology with data dependent acquisition (DDA) tandem MS analysis in a single experiment. To improve the dynamic range and efficiency of *in situ* DDA, we introduced a novel gas-phase fractionation strategy prior to MS/MS scans, to decrease molecular complexity of tissue samples for enhanced peptidome coverage. In addition, the application of HRAM MALDI MSI to lipid analysis in a restenosis rat model will be described. Finally, the utility of a high resolution atmospheric pressure (AP) MALDI-Q-Orbitrap platform for multi-mode ionization and data acquisition will be demonstrated through *in situ* analysis of various biomolecules.