J Chromatogr Sep Tech 2016, 7:7 (Suppl)
http://dx.doi.org/10.4172/2157-7064.C1.023

Molecular imaging of proteins in biological samples using ambient ionization mass spectrometry

Cheng-Chih Hsu[1, 2] and **Richard N Zare**[2]
[1]National Taiwan University, Taiwan
[2]Stanford University, USA

Molecular imaging of lipids and metabolites in tissues under ambient conditions is readily achieved using desorption electrospray ionization (DESI), but DESI is essentially blind to the presence of proteins. In 2013, we demonstrated that the use of nanospray desorption electrospray ionization (nanoDESI) in combination with an inverted microscope overcomes this problem and allows us to visualize proteins in tissue samples in a label-free manner at atmospheric pressure with only minimum sample preparation. However, this microscopy-guided approach is not efficient especially while imaging larger tissue sections. To improve the utility of this technique, we interfaced a 2D stage with nanoDESI to direct and for continuous mass spectrometry scannings on tissue sections. Multiple charged proteins with masses up to 15 kDa were successfully measured by nanoDESI using an LTQ Orbitrap mass spectrometers. In a mice brain section, expression of proteins was previously found by matrix-assisted laser desorption ionization (MALDI) mass spectrometry imaging, including ubiquitin, β-thymosin, and myelin basic protein, were spatially-mapped, and the identified via top-down approaches. We also determined the location of methylation on myelin basic protein. This imaging modality was further implemented to MYC-induced lymphomas. We observed an array of truncated proteins in the region where normal thymus cells were infiltrated by tumor cells, in contrast to healthy tissue. The detection limits for cytochrome c and insulin are 10-50 picomoles per mg of tissue, at which level many endogenous proteins are expressed in cells. It is expected that this new tool will provide important biological insight into cellular processes.

ccrhsu@ntu.edu.tw

When mass spectrometry meets nanoparticles; weighing, manipulating and fragmenting single nanoparticles in the gas phase

Rodolphe Antoine
University of Lyon, France

Within the past two decades, electrospray ionization mass spectrometry (ESI-MS) has become a cornerstone technique for analyzing large intact biomolecules of all types, and is ideally suitable for compounds with molecular weight (MW) below 100 kDa. Analysis of large molecules (i.e. megadalton compounds for which MW>1 MDa) is difficult, in part due to the low efficiency of ion detectors of mass spectrometers in this range of size. Notable improvements were obtained with the development of the charge-sensitive technique for macroion detection. Charge detection mass spectrometry (CD-MS) can quantify the charge on an individual ion and its mass-to-charge (m/z) ratio. In this work, we used the charge detection mass spectrometry combined to ESI technique for weighing large DNAs, nanoparticles and biopolymer self-assemblies in the megadalton to gigadalton range of molecular weight. This work also presents the implementation of tandem mass spectrometry for experiments on single electrosprayed ions from compounds of megadalton (MDa) molecular weight, using two charge detection devices. Single MDa ions can be stored for several dozen milliseconds. During the trapping time, single ions can be irradiated by a continuous wavelength CO_2 laser. Illustration of infrared multiphoton dissociation tandem mass spectrometry are given for single megadalton ions of poly(ethylene oxide)s and DNAs. Finally, I will present the recent results on the coupling between charge detection mass spectrometry and size exclusion chromatography for the characterization of polymers of ultra-high molecular weight.

rodolphe.antoine@univ-lyon1.fr