MALDI MASS SPECTROMETRY IMAGING APPLIED TO SMALL MOLECULES LOCALIZATION

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Overview

Purpose: We present here the MALDI mass spectrometry imaging technique applied to plant and animal metabolomic studies.

MALDI Mass Spectrometry Imaging (MALDI-MSI) is a two-dimensional MALDI mass spectrometric technique used to visualize the spatial distribution of a large variety of biological molecules (from small metabolites to large proteins) without extraction, purification, separation or labelling of biological samples. Since its introduction by Caprioli et al in 1997, it has become one of the most important molecular histology methods for biomarker hunting and for understanding the spatial distribution of biomolecules in various tissues. MALDI-MSI is thus ideal for complementing the expanding field of metabolomics. Despite the fact that MALDI-MSI have been very successfully applied in diverse studies (even in clinical applications) its use remains far from routine, and there is still a need to adapt protocols to suit specific tissues or metabolites. Here we describe the methodology of MALDI-MSI with examples taken from applications in plant (Chichorium intybus) and in seaweeds (Mytilus edulis).

MALDI Imaging: Molecular localization directly on tissue section

MALDI-MSI combine the advantages of mass spectrometry (MS) and microscopy in a single experiment and allow detection of hundreds molecules in one analysis. Analysis can be achieved in a relatively short time scale (hours) and possibility to detect various compounds.

MALDI – MSI Images from two ongoing studies

MALDI – MSI Images from Chichorium intybus

MALDI imaging mass spectrometry enables the visualization of the distribution of a range of biomolecules that have varied structures in the cells and tissue sections. This emerging imaging technology was initially developed as a tool for protein imaging, but recently it is increasingly being used for the imaging of small organic molecules. For reviews see Kaspar et al 2011 Proteomics 11-9, p1845-50

MALDI – MSI Images from Mytilus edulis

For data treatment several software are available and other are on the way. A common data exchange format (imzML) have been developed. Specific algorithm are developed (Intensity correlation analysis and Statistical analysis like ClinProTools (Bruker) and other software see www.maldi-msi.org).

Conclusions

Comparaison of toxins levels in digestive glands of Mytilus edulis after feeding with Proorocentrum lima during (0, 4 or 11 Days, from left )

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