OMICS International
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J Chromatogr Sep Tech 2015, 6:4
http://dx.doi.org/10.4172/2157-7064.S1.008

International Summit on Current Trends in Mass Spectrometry

July 13-15, 2015 New Orleans, USA

Quantitative imaging of lipids and metabolites using nanospray desorption electrospray ionization mass spectrometry

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Mass spectrometry (MS) is ideally suited for the analysis of complex biological samples with high sensitivity, speed and unprecedented chemical specificity. When operated in the imaging mode, it provides detailed chemical information on the identity and the distribution of biomolecules in the sample. Ambient pressure (AP) surface ionization MS is particularly attractive for imaging of biological samples without special sample preparation. We have developed nanospray desorption electrospray ionization (nano-DESI) -- A novel AP surface ionization method that relies on localized liquid extraction of molecules from ambient surfaces and efficient transfer of the desorbed analyte molecules to a mass spectrometer inlet. Nano-DESI has been used for imaging of fully hydrated biological samples and living microbial communities with high sensitivity and spatial resolution without sample preparation. In nano-DESI imaging, quantification is performed by doping the nano-DESI solvent with appropriate standards and normalization of the ion image to the ion image of the standard compensates for matrix effects Nano-DESI imaging enables online quantification and identification of the observed metabolites and lipids in biological tissue sections.

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Bioinformatics for mass spectrometry imaging in augmented systems histology

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Over 800 million pathology tests are performed in the UK alone each year, and over 95% of all clinical patient pathways rely on access to effective pathology services. The "gold standard" for diagnostics is tissue biopsy and histo-pathological assessment. There is an increasing demand for cancer diagnostics with improved quality, safety, efficiency and lower costs. Mass spectrometry Imaging (MSI) has the potential to deliver a paradigm shift in digital pathology services and cancer diagnostics because it augments cellular morphological analysis with highly accurate and robust data on cellular metabolic and proteomic molecular content. Effective clinical translation of histology-driven MSI in systems oncology requires precise co-localization of morphological and biochemical features as well as advanced methods for data treatment and interrogation. This presentation outlines current roadblocks in translational MSI and introduces a comprehensive workflow designed to address current methodological limitations. I show that this strategy offers unique insights into tumour micro-environmental biochemistry; tumour induced heterogeneity of molecular phenotypes and should facilitate the compilation of a large-scale tissue morphology-specific MSI spectral database to pursue next-generation, fully automated histological approaches.

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