Quantization of Lipids in High Throughput; the shotgun lipidomics profiling of NAFLD & steatohepatitis by ion mobility-MS data acquisition techniques.

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Abstract

This presentation will address technologies that directly address clinical research experimentation of lipids in tissue extracts, keeping sampling and data processing throughput in mind. The human lipidome contains >100,000 different molecular species found within a small mass range; consequently, isobaric overlap makes unambiguous identification and quantization of lipid species difficult. Herein, methods that utilize high sensitivity MS/MS techniques using a high sensitivity triple quadruple linked LIT mass spectrometer to isolate lipid classes for identification of molecular composition and quantization have been investigated. Furthermore, QqQ platforms can now be coupled to differential ion mobility (DMS) devices and have shown to resolve phospholipids sub-classes, triglycerides, and strikingly, the sphingomyelins (SM) were resolved from PC molecular species. The latter observation is significant considering these two classes cannot be resolved using triple quadruple strategies alone, and their masses overlap significantly. The instances of a T-pattern may be seen as repeated statistical pseudo-fractal objects characterized by statistically significant translation symmetry. THEME tm (by M.S. Magnusson, ©Pattern Vision Ltd) is special purpose T-pattern detection and analysis PC software using a special CI detection algorithm combined with an evolution algorithm, presented here together with results from the analysis of behavior and interactions. From the relatively slow time scale of human and animal interactions to the much faster interactions within populations of neurons in living rat brains. Analogies are discussed between T-pattern structure and functions in the cities of proteins (cell city) and human cities, especially regarding specialization and the particular case of religious behavior.

Biography:

Brigitte Simons is a market development specialist at SCIEX, specializing in metabolomics using accurate mass time-of-flight mass spectrometry solutions. Prior to working at SCIEX, Brigitte received her Ph.D. in Chemical Biology at the University of Ottawa. She then completed two research post-doctoral fellowships at the Centre for Biologics Research at Health Canada and the National Institute of Heart Lung and Blood in Bethesda MD. Brigitte also spearheads an academic partnerships program for our North American business – which listeners can browse sciex.com for more information or contact Brigitte for more information.

Speaker Publications:

1. "Similarity of hierarchical structured clustering in human and neuronal interactions and on DNA: Structural and functional analogies"; Journal of R&D. / 2020 / 8(8) /pp 2311-3278

9th Global Summit on Mass Spectrometry October 16-17, 2020 webinar

<u>Abstract Citation:</u>

Brigitte Simons, Quantization of Lipids in High Throughput; the shotgun lipidomics profiling of NAFLD and steatohepatitis by ion mobility-MS data acquisition techniques, Mass Spectrometry 2020, 9th Global Summit on Mass Spectrometry October 16-17, 2020; Webinar

(https://massspectra.com/speaker/2020/brigitte-simons-university-sciex-canada)