Presentation title

Lipidomics Workflows – From discovery Experiments to Quantitative Analysis

Presentation description

Lipids are essential constituents of the cell and play a major role in physiological functions. The lipidome is complex because of the diversity of lipids both within a lipid class and at a global level. The amount of work needed to determine the lipid targets and to ensure that the ID of each lipid target is validated is daunting.

We have used a validated, well tested, rugged targeted lipidomics method that covers 44 lipid classes as a starting point to develop a workflow for targeted lipidomics[1]. We call the targeted lipidomics method the "Backbone" method. Our workflow allows the flexibility of adding panels of lipids to the original, validated "Backbone" method. This gives us the ability to expand the initial set of lipid classes. Lipid classes can be added based on discovery experiments or from theoretical predictions.

1. High-Throughput Plasma Lipidomics: Detailed Mapping of the Associations with Cardiometabolic Risk Factor, Kevin Huynh, Christopher K. Barlow, Kaushala S. Jayawardana, Jonathan E. Shaw, Brian G. Drew, Peter J. Meikle, Cell Chemical Biology, Volume 26, 71-84, 2019.

Speaker

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Sheher Mohsin is a senior applications scientist at Agilent Technologies. She received her Ph. D in physical chemistry from the University of Illinois and an MBA from Rockhurst University. She started her career at the US Environmental Protection Agency working on dioxin analysis with high resolution mass spectrometers. She later joined Bayer and worked in the special analysis lab using mass spectrometry to solve problems in synthesis, impurity determination and submission of final product impurity profile to regulatory agencies. Sheher's current focus is on lipidomics using GC, LC and SFC separations and mass spectrometry. Sheher collaborates with academic and government researchers working on complex problems to come up with innovative, simplified workflows using the latest tools in separation and mass spectrometry.