Lipidomics of Eicosanoids Highlights Infection and Inflammation Progression

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The largest numbers of distinct molecular species in cellular metabolism are the lipids where tens of thousands of distinct molecular species exist in cells/tissues. We have developed novel liquid chromatographic-mass spectrometric based lipidomics techniques termed "CLASS" [1] to solve lipidomics problems, often in the context of an overall omics analysis of immunologically-activated macrophages integrating transcriptomics, proteomics, and metabolomics of lipid metabolites [2]. As part of the LIPID MAPS Consortium [www.lipidmaps.org], our laboratory has developed a robust and comprehensive approach to the lipidomics analysis of hundreds of fatty acids, acylethanolamines and inflammatory eicosanoids [3]. We have built on our previous application of lipidomic analysis to characterize "synergistic" cellular lipid signaling of Toll-like (TLR) and purinergic receptors in stimulated macrophages as models of bacterial infection and inflammation. This has recently led to an elucidation of the dual role of aspirin in enhancing lipoxin formation during inflammasome formation [4] and the dual role cytosolic PLA_2 [5] plays in lipoxin synthesis. To elucidate viral infection and inflammation, we have explored the effect of influenza infection by lipidomic profiling of bioactive lipid species in a mouse influenza model using virus strains of both low and high pathogenicity [6]. Human plasma has also been profiled [7]. We have recently developed and optimized protocols for separating phospholipid and sphingolipid classes from a phospholipid mixture and human serum using Hydrophilic Interaction Liquid Chromatography (HILIC), Reversed Phase (RP) Chromatography, and Differential Ion Mobility Spectrometry (DMS). Besides optimizing each approach separately, we also explored advantages of combining HILIC-UPLC with DMS as well as RP-UPLC with DMS [8] [Supported by LIPID MAPS Glue Grant U54 GM069338, R01 GM020501, R01 GM064611]

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