Published in final edited form as:

J Chromatogr B Analyt Technol Biomed Life Sci. 2009 September 15; 877(26): 2663. doi:10.1016/j.jchromb.2009.07.007.

Lipidomics: Developments and applications

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Lipidomics, defined as the large-scale study of cellular lipids (i.e., the lipidome), has recently emerged as a rapidly expanding research field under the umbrella of systems biology [1–4]. Investigators in lipidomics examine the structures, functions, interactions, and dynamics of cellular lipids, identify their cellular localization (i.e. subcellular membrane compartments and domains), and determine the dynamic changes that occur during physiological and pathophysiological perturbations.

The emergence of this new discipline is built on the foundation established by numerous pioneering studies with multiplexed catalysts. These include (1) recent advances in systems biology in both conception and instrumentation; (2) increasing appreciation among investigators that the metabolism of an individual lipid species or individual lipid classes is interwoven and investigation of individual metabolic pathways requires analysis of multiple lipid classes, lipid molecular species, and/or lipid metabolic networks through a systems biology approach; and (3) increasing recognition of the roles of lipids in many epidemic metabolic diseases such as obesity, atherosclerosis, stroke, hypertension, and diabetes (collectively designated the “metabolic syndrome”).

Many modern technologies (including mass spectrometry (MS), NMR, fluorescence spectroscopy, and microfluidic devices) have been developed to identify, quantify, and understand the structure and function of key metabolic nodes in lipidomics. In the development of lipidomic platforms, it is clear that MS techniques occupy a leading position in the characterization, identification, and quantitation of lipids. The developed MS techniques can be mainly categorized into three groups. The first group involves “global” lipidomic analyses which identify and quantify hundreds to thousands of cellular lipid species via a high throughput basis. To this end, different shotgun lipidomics-based platforms have been developed and extensively used to analyze diverse pathways and networks associated with lipid metabolism, trafficking, and homeostasis. Newly emerging mapping techniques play major roles in studying the spatial and temporal relationships of lipids. The second group of MS techniques focuses on the “targeted” lipidomic analysis of one or a few lipid classes of interest. LC-MS and LC-MS/MS based methods have been extensively utilized for this purpose. The third group of MS approaches is directed toward the discovery of novel lipid classes and molecular species. Methodology using LC coupled with MS plays an essential role in this area through different enrichment technologies.

In lipidomic research, large amounts of data are generated in the analysis of lipids which can provide mechanistic insights into changes in cellular function. However, processing these data is extremely challenging despite the development of multiple bioinformatic tools. We should

recognize that in comparison to instrument and technique development in lipidomic research, bioinformatic tools and models in the areas of statistical analysis of datasets, pathway and network analysis, and biophysical lipid modeling are still lagging. Therefore, additional effort is clearly needed in this area of lipidomics.

Considering the growing importance of lipidomics and the development of technologies in the field which rely heavily on chromatography, the editors of the *Journal of Chromatography B* have devoted a special issue to this topic. As a guest editor, I have attempted to cover the majority of recent developments in techniques and the application of lipidomic analysis in biological research in the issue. Unfortunately, this special issue could not include all researches and advances in the field due to the limits of space. It is my sincere hope that through viewing the developments and applications in lipidomics exemplified herein, the readers can appreciate the rapid progress of this nascent field and its future potential.

Finally, I wish to especially thank the editors of the *Journal of Chromatography B* for providing me the opportunity to edit this special issue; the authors and reviewers for their outstanding contributions; and the editorial office (particularly Mr. Eduard Hovens) for their help and assistance. Finally, I would like to extend my sincere appreciation to Dr. Dimitrios Tsikas for all his advice and support during the progress of this project.

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