University of Louisville Department of Chemistry

Fang Yuan Research Seminar

When: August 27, 2020 Time: 2:30 PM Location: Microsoft TEAMS

Mass Spectrometry Based Metabolomics and Lipidomics

Abstract

Strategies for metabolomics and lipidomics study can be divided into untargeted and targeted approaches The untargeted metabolomics/lipidomics detects as many metabolites/lipids as possible, while the targeted metabolomics/lipidomics focuses on analyzing a number of known metabolites/lipids. In the research seminar, I will present my work on 4 aspects:

1) Integrating multiple MS based platforms for untargeted metabolomics^{1.2}

We extracted polar metabolites from biological samples, then analyzed them by multiple MS based platforms, including GC×GC-MS with MSTFA derivatization, GC×GC-MS with MTBSTFA derivatization, 2DLC-MS/MS in negative ionization mode, and 2DLC-MS/MS in positive ionization mode. Data collected from multiple platforms were merged for further analysis.

2) Targeted metabolomic study of short-chain fatty acids (SCFAs) using GC-MS³

We developed a GC-MS method for simultaneous analysis of eight straight-chain and branched- chain SCFAs. We used DB-225ms column hyphenated with DB-5ms column in tandem to achieve the best separation of SCFAs. This method showed good recovery and sensitivity to quantify the SCFAs in biological samples.

3) Targeted lipidomic study of long-chain fatty acids (LCFAs) and oxylipins using LC-MS/MS⁴ We developed a high-throughput LC-MS method for simultaneous analysis of 51 bioactive LCFAs and oxylipins. LCFAs and oxylipins were extracted via solid-phase extraction, then analyzed using a targeted metabolomics approach by reversed-phase chromatography-mass spectrometry.

4) Developing comprehensive two dimensional LC-MS for untargeted lipidomics

We are developing a comprehensive two dimensional LC-MS for lipid profiling. Lipids extracted from biological samples were separated into several portions by HILIC, each portion were then further separated by RPC.

References:

- 1. Yuan, F.; Harder, J.; Ma, J.; Yin, X.; Zhang, X.; Kosiewicz, M. M., Journal of Proteome Research 2020, 19 (2), 667-676.
- 2. Yuan, F.; Kim, S.; Yin, X.; Zhang, X.; Kato, I., Metabolites 2020, accepted.

3. He, L.; Prodhan, M. A. I.; Yuan, F.; Yin, X.; Lorkiewicz, P. K.; Wei, X.; Feng, W.; McClain, C.; Zhang, X., Journal of Chromatography B 2018, 1092, 359-367.

4. Warner, D. R.; Warner, J. B.; Hardesty, J. E.; Song, Y. L.; King, T. N.; Kang, J. X.; Chen, C.-Y.; Xie, S.; Yuan, F.; Prodhan, M. A. I.; Ma, X.; Zhang, X.; Rouchka, E. C.; Maddipati, K. R.; Whitlock, J.; Li, E. C.; Wang, G. P.; McClain, C. J.; Kirpich, I. A., *Journal of Lipid Research* 2019, 60 (12), 2034-2049.