Analytical Seminar

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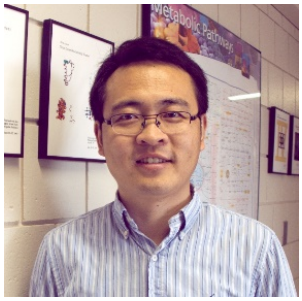

"Top-down proteomics using capillary zone electrophoresis-tandem mass spectrometry"

Top-down proteomics aims to characterize proteoforms in cells. [1] The number of proteoforms in the human proteome has been estimated to be over 1 million. [2] High-resolution liquid-phase separation of proteoforms prior to tandem mass spectrometry (MS/MS) is imperative for large-scale top-down proteomics. The top-down proteomics community has made tremendous efforts in boosting the separation of proteoforms using liquid chromatography (LC). The state-of-the-art LC-MS/MS platforms have approached 3 000-5 000 proteoform identifications (IDs) from mammalian cells. [3,4] However, the number is still far away from the complete human proteome. Better proteoform separation is crucial to improve the proteome coverage.

Capillary zone electrophoresis (CZE)-MS/MS has been recognized as a useful tool for top-down proteomics over 20 years ago. [5] CZE can approach highly efficient separation of intact proteins and CZE-MS has shown obviously higher sensitivity than LC-MS for detection of intact proteins. [6] However, the low sample loading capacity and narrow separation window of CZE has impeded its wide application for top-down proteomics. In my talk, I will first talk about some progress my group has made recently in boosting the sample loading capacity and separation window of CZE. [7] Then I will talk about our work on large-scale top-down proteomics using the CZE-MS/MS.[8, 9] After that, I will introduce our most recent work on top-down proteomics under a native condition using the CZE-MS/MS for identification of protein complexes in cells in discovery mode. In the end, I will talk about deep and highly sensitive bottom-up proteomics using the CZE-MS/MS and introduce our preliminary data on quantitative proteomics of zebrafish embryos during the maternal-to-zygotic transition.

Thursday
September 20

12:15 p.m.
1315 Chemistry

Coffee & cookies
at 12 p.m.

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Chemistry
UNIVERSITY OF WISCONSIN-MADISON