Improving Separation and Characterization of Proteoforms and Protein Complexes Using CEMS and ECD Fragmentation

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Join Dr. Liangliang Sun and Xiaojing Shen from the Department of Chemistry at Michigan State University as they share their research on the characterization of proteins in proteoforms for pursuing a better understanding of protein function.

Abstract

Studying the function of proteins in cells is vital for understanding the underlying molecular mechanisms of disease and development. Post-translational modifications (PTMs) can influence protein conformations and function. Understanding protein function requires a deeper characterization of proteoforms and their associated protein complexes.

Top-down proteomics (TDP) aims to delineate proteoforms and protein complexes on a global scale and in discovery mode. It has achieved substantial progress in the last decade. However, many challenges remain, including but not limited to high-capacity separation and extensive fragmentation of proteoforms and protein complexes.

In this talk, we will introduce capillary electrophoresis-mass spectrometry as a useful tool for highly efficient and high-capacity separation of proteoforms and protein complexes as well as the combination of electron capture dissociation and collision-induced dissociation as a powerful technique for nearly 100% backbone cleavage of proteins smaller than 30 kDa. We employed an Agilent G1700 Capillary Electrophoresis with CMP EMASS-II CE-MS ion source interface, 6545XT AdvanceBio LC/Q-TOF mass spectrometer and e-MSion ECD cell in these studies.

Presentation Outline

- Introduction
- CZE-MS with ECD for Denaturing Top-down Proteomics – Find and Characterize the Proteoforms
- CZE-MS for Native Top-down Proteomics of Protein Complexes
- Conclusion