Ph.D. Dissertation Defense

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“Method Development and Application of Mass Spectrometry-based Omics Analyses”

Abstract

Endogenous biomolecules, such as metabolites, neuropeptides, and proteins, play important roles in biological and physiological processes. Mass spectrometry (MS) has become a central technology for the study of biomolecules and their biological functions involved in disease mechanisms. However, there are still challenges for biomolecular analyses due to their poor ionization efficiency, low concentration, and various modifications. This dissertation is devoted to the development of novel and improved MS-based omics methodologies and the application to human disease studies. Specifically, this work established a multiplex isobaric dimethylated leucine (DiLeu) strategy combined with advanced bioinformatics tool for metabolomics studies and extended its application to biomarker discovery in mouse models for lower urinary tract symptoms (LUTS). This work also developed a novel MS approach for comparative neuropeptide characterization with a decision-tree driven MS method and applied it to peptidomic analyses of human pituitary tumors and subcommissural organ. Moreover, metabolomics, peptidomics, and proteomics were integrated to investigate how the host immune system is shaped by human microbiome during infection. In summary, this work not only improves current analytical methodologies for characterizing and quantifying biomolecules but also demonstrates its potential applications in the pharmaceutical industry and clinical settings.