**[Research]**

**Comprehensive Characterization of Glycosylation Patterns Using Mass Spectrometry**

【Figure1】

Glycans modify proteins, lipids, and even RNA molecules to form the glycocalyx, a dense regulatory coat on cell surfaces that plays a crucial role in cellular functions. Changes in glycosylation patterns correlate closely with the development and further disease progression. Consequently, the profiling of glycans in biology and medicine is an important approach. This advance regarding glycan analysis, therefore, has been underpinned by mass spectrometry techniques. These allow high-throughput, sensitive, and precise characterization of both composition and structure.

In our lab, we focus on developing state-of-the-art mass spectrometry to enable quantitative structural identification of glycosylation on proteins and RNA molecules. This includes the development of comprehensive workflows, which are tightly integrating advanced sample preparation with data acquisition and computational analysis into unprecedented accuracy and depth in glycosylation profiling. It is in this backdrop that our efforts have gone toward providing an overarching system explaining how different glycan architectures influence molecular interactions, intracellular signaling, and pathogenic mechanisms and thereby link glycomics to functional biology.

**Unraveling Glycan-Mediated Interaction Networks via Chemical Biology Approaches**

【Figure2】

Biological interaction networks play a central role in deciphering complicated molecular machinery and signal transduction pathways active in the cell, affecting development and disease course. Biomolecules are frequently modified, and such modifications determine their functions in various cellular contexts. Of those, glycosylation, which mediates the formation of the glycocalyx, presents several of the biggest challenges to inquiry. So far, the role that various glycan structures play in modulating membrane interaction networks has been only poorly explored, despite their widely recognized key role in cellular signaling and recognition.

In concert with this limitation, we have established expertise in a set of chemical biology toolbox, including proximity labeling, crosslinking mass spectrometry, and affinity purification mass spectrometry, which enable construct of the networks of glycan-mediated interactions at far superior levels of specificity and sensitivity. Using these sophisticated approaches, we aim to achieve a comprehensive molecular understanding of how glycosylation regulates major biological processes. The ultimate goal is to explain how glycosylation acts at the cellular level to change cellular functions and potentially uncover new therapeutic interventions in diseases caused by glycosylation dysregulation.

**Quantitative Mass Spectrometry-Based Epitranscriptomics**

【Figure3】

RNA participates directly in events related to both gene expression and regulation in organisms. More than 150 different chemical modifications have been identified in RNA that participate in significant functions, including mRNA stability, RNA conformation, translation efficiency, and splicing. RNA modifications have been implicated in a variety of diseases, including cancers and neurological disorders, through their dysregulation, underlining their critical relevance to cellular physiology and disease mechanisms. Conventional genomic methods have various limitations in simultaneously characterizing and quantifying multiple RNA modifications, which makes mass spectrometry a unique tool for these tasks. Mass spectrometry enables direct identification of modified entities through their specific mass shifts and provides accurate quantitative information.

Our laboratory is highly motivated to advance mass spectrometry-based methodologies for the high-throughput and quantitative characterization of RNA modifications. Through the creation of novel mass spectrometry techniques, we intend to investigate the dynamics of RNA modifications across different disease conditions, thereby addressing significant gaps in the understanding of RNA biology. This research aspires to uncover the regulatory roles of RNA modifications in gene expression, providing valuable insights into epitranscriptomic processes and identifying prospective biomarkers and therapeutic targets.

**[Available Positions]**

**Postdoctoral Researchers**

We are seeking outstanding postdoctoral researchers interested in a stimulating training environment to expand their expertise in mass spectrometry and glycosylation research. We welcome postdoctoral candidates with diverse training backgrounds, including but not limited to: Mass Spectrometry, Glycobiology, Epitranscriptomics, Epigenetics, Biochemistry, and Molecular Biology. Interested candidates should submit their CV, including the names and contact information for two references, along with a brief description of their doctoral training and research goals, to Dr. Yixuan Xie (xieyixuan@ipm-gba.org.cn). More information: BioArt Link

**Graduate Students and Undergraduate Students**

We are also looking for motivated graduate students with a passion for applying mass spectrometry-based technologies to solve complex biological questions related to glycosylation. At the same time, limited research positions are available for undergraduate students interested in summer or academic-year research projects. Interested students can email Dr. Yixuan Xie (xieyixuan@ipm-gba.org.cn) to inquire about potential projects and the opportunity to join the lab.