September 18, 2018 – MSDG Meeting

NJ-ACS
MASS SPEC DISCUSSION GROUP

The **NJ Mass Spectrometry Discussion Group** is pleased to announce our **September 2018 Annual Vendor Show and Symposium.**

NJ MSDG is the second largest mass spectrometry professional association in the nation behind ASMS, with over 1,100 members in the tristate area. [***homepage***]

Date: **Tuesday September 18, 2018**

Venue: **Somerville Elks Lodge 1068**
375 Union Avenue
Bridgewater, NJ 08807

908-707-1545

http://somervilleelks.org

Please *register here*. Registration is free, compliments of our sponsors.

A limited number of free drink tickets will be provided to early attendees!

Featuring the following sponsors/vendors/collaborators on site (listed in the order of registration)

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Program

3:00-5:00 PM Registration, vendor show, and poster session
5:00-5:45 PM Prof Hui Zhang (Johns Hopkins University)
5:45-7:00 PM Buffet Dinner (raffle prizes will be announced)
7:00-8:00 PM Prof Jennifer Brodbelt (The University of Texas at Austin)

Speaker 1: Professor Hui Zhang Ph.D., Director, Mass Spectrometry Core Facility, Center for Biomarker Discovery and Translation, Department of Pathology, Johns Hopkins University

Title: Multi-omic analysis of tumor tissues reveals a large number of glycopeptides and their association with glycosylation enzymes

Abstract: Many gene products exhibit extensive structural micro-heterogeneity due to an array of co-occurring post-translational modifications. These protein modifications are not synthesized with genomic template and often affect the functionality of the proteins and therefore need to be characterized in detail in order to determine their structural and functional relationships and their potential linkage with genome and proteome. Protein glycosylation plays fundamental roles in many cellular processes, and previous reports have shown dysregulation to be associated with human diseases. Here, we describe the analysis of proteins from breast cancer xenograft tissues using our recently developed software package GPQuest 2.0, revealing a large number of previously unidentified N-linked glycopeptides. More importantly, we found that using immobilized metal affinity chromatography (IMAC) technology for the enrichment of phosphopeptides had co-enriched a substantial number of sialoglycopeptides, allowing for a large-scale analysis of sialoglycopeptides in conjunction with the analysis of phosphopeptides. Collectively, combined MS/MS analyses of proteomic and phosphoproteomic datasets resulted in the identification of thousands of intact N-linked glycopeptides derived from breast cancer xenograft tissues. This analysis revealed an extensive number of glycopeptides hidden in the proteome and co-enriched in IMAC-based phosphopeptide-enriched proteomic data.

We then performed genomic, proteomic, and glycoproteomic analysis of human high-grade serous ovarian carcinoma (HGSOC) and non-cancerous tissues, we found that abundance at glycosites was regulated by the overall glycoprotein expression, while glycosylation at each individual glycosylation site contained glycosylation-site-specific heterogeneity and it was regulated by the protein abundance of the glycoproteins as well as the levels of glycosylation enzymes that were involved in the glycosylation biosynthesis pathway. This study bridges the gaps among alterations in gene and protein expression, protein glycosylation, and phosphorylation by providing the most complete landscape of glycoproteome in related to proteome and genome, which would be beneficial for stratifying other protein modifications for changes of cancer gene products based on genetic alterations. Furthermore, using the

data from glycoproteomics, proteomics, and genomics, we defined and demonstrated the possibility of classifying the pathological outcome of cancer from normal tissues of HGSOC using glycans on the glycoproteins from tissues.

Speaker 2: Professor Jenny Brodbelt Ph.D., Norman Hackerman Chair, Department of Chemistry, University of Texas at Austin

Title: Ultraviolet Photodissociation Mass Spectrometry for Characterization of Proteins and Protein Complexes

Abstract: Developments in mass spectrometry instrumentation and experimental design have motivated new applications in the field of structural biology. Ultraviolet photodissociation (UVPD) results in broad sequence coverage of intact proteins via more extensive backbone fragmentation than can be obtained using other MS/MS methods, and ion activation/dissociation can be accomplished using a single 5 ns laser pulse. This translates to a compelling MS/MS technology for characterization of intact proteins, including mapping post-translational modifications and ligand binding sites. There has been growing interest in employing top-down approaches to characterize proteins and to examine native-like protein structures by using MS/MS to disassemble the complexes and sequence the constituent proteins. UVPD provides high levels of sequence coverage for native-like protein complexes, and the relative abundances of fragment ions correlate with variations in the intramolecular and intermolecular interactions that stabilize particular regions of the proteins. Products retaining non-covalently bound ligands reflect the fast, high energy activation of UVPD. For multimeric protein complexes, UVPD disassembles the complexes to reflect sub-unit architecture.