

The 54th American Society of Mass Spectrometry (ASMS) Conference on Mass Spectrometry and Allied Topics, Seattle, Washington, May 2006

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The conference was held at the WA State Convention and Trade Centre in Seattle that easily accommodated the 54th ASMS Conference on Mass Spectrometry and Allied Topics. The user meetings were held on the Saturday and Sunday prior to the start of the conference. Prof. Roman Zubarev from the Laboratory for Biological and Medical Mass Spectrometry at Uppsala University gave a talk at the Thermo Electron Corporation users meeting entitled “Revealing proteome complexity with tandem mass spectrometry”. He highlighted that there are estimated 100,000 different protein sequences within the human organism, and perhaps 10-100 times as many different protein forms making the proteome far more challenging than the genome. The challenge of mass spectrometry in the subsequent years was to provide sufficient amount of information in experimental datasets to match the underlying complexity. In the post-genome era, the assumed main source of human complexity had been shifted from the genome to pre- and post-translational modifications (pTMs and PTMs) in proteins.

The conference started on the Sunday evening with a tutorial lecture given by Prof. Simon Gaskell from the University of Manchester highlighting the fundamentals of peptide ion fragmentation mechanisms. On Monday the reduction of proteomic oral sessions was welcomed with the new sessions concentrating on problem-solving solutions to areas such as post-translational modifications, protein conformations and hydrophobic peptides. The Membrane Proteins and Hydrophobic Peptides session included interesting talks by Julian Whitelegge from the University of California on how to increase the coverage of transmembrane domains within proteins by electron capture dissociation methods. He was able to locate a fatty acid modification with a mass increase of 266 amu on two possible lysine residues within the protein structure by mass spectrometry. The utility of mapping and quantitation of lipid raft proteins was demonstrated by Josip Blonder of the SAIC-Frederick Inc. and University of Michigan using ¹⁸O-labelling on GAG expressing HeLa cells.

The post-translational modifications sessions discussing phosphorylation and glycosylation were of particular interest and many of the talks highlighted both method development and application-based results. The most prominent new instrument used in many of these reported studies was the Orbitrap mass spectrometer which Alexander Makarov detailed the theory and practice within his Monday afternoon presentation. The rise of interest with glycomics and carbohydrate analysis showed an increased attendance on the Tuesday sessions. Michael Bowman talked about a number of stable isotope labelled-compounds used for reducing terminus derivatization of carbohydrates that were tested on low molecular weight heparins. The initial negative ion mass spectrometry results of the labelled glycans indicated promise but unfortunately the fragmentation data were not presented to show both their sensitivity and sequencing potential. Further investigation of sulphated and phosphorylated glycopeptides was presented by Ying Zhang from Wichita State University using ion-pairing of the sulphate moiety with tri-lysine that increased the information of the glycopeptide by MS/MS as well as differentiated between the sulphate and phosphate by diagnostic ions within the MS/MS mass spectrum.

We presented a poster entitled “Stabilization and linkage determination of sialic acids by selective derivatization for analysis by MALDI and electrospray ionization mass spectrometry”

on Wednesday within the Carbohydrates and Oligosaccharides II selection which was well received. The Wednesday and Thursday oral presentations were of general interest while more time was spent reading posters and catching up with old friends and collaborators. I wish to thank BMSS for the travel grant to attend this conference that, as always, was both informative and invaluable to reinvigorate the weary postdoc back into the lab for those exciting new experiments.