

**Conference:** British Mass Spectrometry Society - British Society for Proteome Research (BSPR) Super Meeting 2024, Warwick Arts Centre (4-6<sup>th</sup> September)

**Sessions:** Applications (Natural and Life Sciences), Chemical Biology, Proteomics (One health and non-human), Instrumentation and fundamental MS, Clinical proteomics, ambient ionisation and imaging, data processing and informatics, native ms and proteomics, small molecules, ion mobility, systems biology and rare diseases, lipidomics and metabolomics, biomacromolecular structure, emerging methods and tech in proteomics

**Keynote Speakers:** Professor Corinne M. Spickett and Professor Bernhard Küster

### **Why did I attend BMSS-BSPR Super Meeting 2024?**

I attended the BMSS-BSPR 2024 super meeting because I am very interested in mass spectrometry research's innovation, diversity and development. It was also a valuable experience to share my own research and learn about the mass spectrometry research and applications of others in academia and industry, as well as to network with others in the mass spectrometry world. As the last conference of my PhD, as I reflect upon this conference, I can see how much my knowledge, experience and contacts have grown.

### **Conference Highlights**

There were many interesting talks throughout the different sessions, with many interesting mass spectrometry applications extending the boundaries of knowledge. Below are a few of the standouts.

#### **1. Lipidomics workshop**

Wanting to know the best methods of processing lipidomics data from experts in the field, this workshop provided an excellent overview of LipidMaps, lipid nomenclature and classification, curation of databases, introduction to MS of lipids, automated data annotation, quality checking and initial analysis using *Lipid Data Analyser (LDA)* software before understanding what they mean using BioPAN and other visualisation tools such as Metaboanalyst. This workshop gave me an insight into the intricacies of lipidomics experiments, the breadth of extraction and detection methods for different lipids and a better understanding of how to analyse and interpret the resultant data in accordance with the biological pathways involved. It was also interesting to note that most lipidomic (targeted and untargeted) experiments are still carried out in DDA, due to the complexity of annotation and analysis. After this, the keynote talk from Corinne Spickett was the perfect continuation, portraying how lipidomics can be applied to a project and the decision points and read-outs involved.

#### **2. Careers workshop**

Coming to the end of my PhD I have been exploring my career options for afterwards and I found the careers workshop hosted by VRS useful. After the opening talk by Angus Hughes, there were three talks covering different career pathways including academic, instrument vendors and start-ups. One of these talks was given by Lucy Woods and it opened my eyes because she mentioned that whilst she had started studying patent law, she had travelled and then decided that she wanted to learn more about mass spectrometry and the technology utilised to produce data, she was passionate about

helping and teaching others, she enjoyed talking to other people (customers) and travelling and as a result she became an application scientist for Bruker. Reflecting on my own experiences, I enjoy those same opportunities, and it led me to starting many subsequent conversations at the conference around peoples' career paths and what being an application scientist or other similar starting roles involve. She highlighted this because along with the other speakers, she suggested that you should play to your strengths, network (because it is often people who can suggest/ offer you a different job) and pick the opportunity which suits you best/ what you enjoy, an echo of the advice which Claire Eyres gave us in my first BSPR conference at Oxford. This session made me reflect upon my time as a PhD student and what I enjoy doing and how this may influence my future career.

### **3. Richard Kay, *University of Cambridge* – LC-MS/MS shows raised maternal plasma levels of GDF15 in pregnancy is produced almost entirely from foetus**

A fascinating talk explaining how a well-designed study, in conjunction with a concerted effort from a team of people together with MS analysis, identified that GDF15 was implicated in the nausea and vomiting of pregnancy and its most severe form, hyperemesis gravidarum (HG), which can unfortunately lead to abortion to preserve the mothers' lives. Identified initially through an additional researcher-suggested question as part of the 23andMe screening questions, GDF15 was found to be 400x higher in cases of HG maternal blood during pregnancy, with most of it originating from the fetoplacental unit. Conversely, women with  $\beta$ -thalassemia (where patients have chronically high GDF15) report very low levels of nausea and vomiting in women. This research has led to a complete shift in the research surrounding HG and the production of GDF15 as a potential supplement to prevent the severe GDF15 spike responsible for HG, highlighting the transformational impact that well-designed and implemented MS studies can have on patients' well-being.

### **4. Brendan Maclean, *University of Washington* – Skyline: Targeted proteomics software free and open source for 15 years**

Brendan Maclean gave a very interesting talk describing skyline's history and how it is funded (50% NIH; 50% vendors). Moreover, one of the comments which has most resounded from the conference was:

*"If the mass spectrometry data has not been checked with Skyline, then it will not be published as it may not show what we think it shows if we have not interrogated the data..."*

The rich data which can be generated with Skyline offer a good data and sanity check, which is now available as a plug-in with FragPipe and DIA-NN to generate the skyline data as part of their processing. As well as a data check, how often do you check your instrument performance? Panorama AutoQC offers an automated method for longitudinally checking the QC of your instruments which works with any vendor, something I am definitely going to have to check into with our instruments...

### **5. Bernhard Kuster – How MS-based phosphoproteomics aids precision oncology by understanding tumours and drugs**

Hearing from Bernhard Kuster was the perfect close to the conference, discussing his group's TOPAS project identifying the right drug for the right patient: the aim of personalised medicine. He emphasised that proteins act in a time- and dose-dependent fashion and that all drugs are proteins,

**make** proteins or **degrade** proteins because the proteins cause the effects seen in the diseases. Moreover, it is a very rare drug which binds to only one target, and for determining a dose-dependent effect of a drug, why not get the hard quantitative data rather than an approximation from a T-test of only two different concentrations? Similarly to the multi-omics analyses, mRNA changes do not necessarily correlate to protein changes, which do not necessarily correlate to the drug target. All points have been highlighted at multiple levels during my own PhD research working in collaboration with Boehringer Ingelheim. Showcasing the project with work from his lab, he presented an innovative 14-day workflow from clinical sample collection to patient recommendation, highlighting the impact on clinical decision-making, which proteomic research can have, and the different mindsets utilised during the clinical decision-making process. However, he also emphasised that this was the collaborative work of many people, which is often what is seen in PI presentations, something to keep in mind the next time we watch a scientific presentation: there is a team behind each one.

## 6. Conclusions

Overall, attending the BMSS-BSPR 2024 super meeting provided me with an invaluable opportunity for both my research and career development. I was very grateful to be able to discuss my work with others, gain insight into their different methods and how they applied them in their own research.

