

Workshop Report: MSI: Protein Imaging – Are we there? Are all issues solved?

Moderators:

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Introduction:

MS Imaging allows one to obtain detailed images of the spatial distribution of proteins in tissue and has tremendously progressed over the years. In this workshop experts report to the participants to state-of-the-art protein imaging, covering aspects of specificity, dynamic range, protein identification and data interpretation. Although this field has advanced significantly in the last few years, we still seek to address gaps may remain. The speakers will foster discussions about potentials and limitations of protein imaging. This workshop is addressing everyone in the field, from beginners to experts and also those who are just interested in the method.

Agenda:

17:45 - 17:50 Opening & Announcements

17:50 - 18:00 **Kevin Schey**, Professor of Biochemistry, Vanderbilt University. "Protein Identification in IMS datasets: Key Concepts and Challenges"

18:00 - 18:10 **Meng Xu**, graduate student Lingjun Li Laboratory, University of Wisconsin-Madison. "How to perform on-tissue MS/MS with abundance peptides?"

18:10 - 18:20 **Alice Ly**, MALDI Imaging Division, Bruker Scientific, LLC. "Which are the relevant peaks in MSI datasets? Some surprising examples"

18:20 - 18:30 **Mark Towers**, Waters Corp, "DESI protein imaging, challenges and perspectives"

18:30 - 18:40 **James Hughes**, graduate student Helen Cooper Laboratory, Biosciences at the University of Birmingham. "Univariate and multivariate analysis of DESI protein imaging data from samples of human non-alcoholic fatty liver disease."

18:40 - 18:50 **Emma Sisley**, graduate student Helen Cooper Laboratory, Biosciences at the University of Birmingham. "Development of data processing tools for LESA- TWIMS MSI: Towards conformational MSI."

18:50 Closing

Opening. Martina introduced the session. Peggi and Martina reported upcoming scientific sessions to the group.

This included Asilomar with a focus on Imaging mass spectrometry (October 11-15), Ourcon VII Oct 28-31, and MSACL co-hosted by IMSS March 29- April 2, 2020.

Discussion. Professor Schey gave an overview of state-of-the-art protein imaging followed by presentation from students and vendors. One gap that was discussed was linking image data to the actual pathology, which is critical to defining new molecular signatures related to the pathology. Collaborations with pathologists were emphasized. Additional discussion was on which peaks were useful in developing biomarkers- is acceptable to use the second or third isotope if the first isotope shows interference from another peak? The group was divided on this opinion, as some had experienced challenges in obtaining accurate isotopic signatures from molecules. Statistical considerations for protein and peptide were a significant topic of discussion. This again emphasized that selecting the image data is dependent on determining consistent pathology. Student participants presented on their personal work, seeking advice from the group. This resulted in active discussion on topics covering multivariate analysis of tissue regions. New tools were also presented by student speakers. The conclusion was that the field of protein imaging is challenged by capabilities of laboratories to do advanced data analyses on their images. Identifying proteins and peptides across tissue remains a challenge. Collaboration with pathologists is a requirement to obtain accurate biopatterns in tissue.

Participants: Estimated at 150, the room was at capacity and people stood against the wall.

Next Co-leader: Martina nominated Tiffany Porta, Maastrich University, to be next co-leader.

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