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Editorial

Emerging Technologies in Proteomics: Insights from the HUPO ETC Webinar Series

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INTRODUCTION

Proteomics is undergoing a technological revolution, propelled by advances in mass spectrometry (MS), chromatography, protein arrays, and automation systems. These innovations enable deeper proteome coverage, higher throughput, and involvement in direct clinical applications. As precision medicine becomes a reality, technologies that refine protein identification, quantification, and characterization are essential for bridging basic discovery with translational practice.[1−3] To highlight these frontiers, the International HUPO Education and Training Committee (ETC) organized its second webinar series, featuring academic and industry experts who showcased cutting-edge platforms ranging from advanced ion mobility MS to antibody-based arrays and automated sample preparation workflows.

- Daniel DeBord, MOBILion SYSTEMS, Inc., "Why Size Matters: Revolutionizing Protein and Peptide Detection with Ion Mobility"
- Rosa Isela Gallagher, Center of Applied Proteomics and Molecular Medicine, "Reverse Phase Protein Array (RPPA) Applications: Molecular Profiling and Predicting Response to Targeted Therapies"
- Oliver Raether, Bruker Daltonics, "Past, Actual & Future Directions of Trapped Ion Mobility Time of Flight Mass Spectrometry"
- Philip M. Remes, Thermo Fisher Scientific, "The Past, Present and Future of Quadruple Ion Trap Mass Spectrometers in Proteomics"
- Ruijun Tian, Research Center for Chemical Biology and Omics Analysis, "Fully automated proteomics sample prep applied to chemical proteomics and plasma proteomics"

All webinars can be freely watched on the YouTube channel of HUPO in the ETC Webinar playlist.

ADVANCES IN MASS SPECTROMETRY

Three webinars emphasized the rapid evolution of MS instrumentation. Dr. Philip Remes (Thermo Fisher Scientific) traced the trajectory of quadrupole ion traps, from qualitative analyzers to highly sensitive quantitative proteomics engines. Ion traps are prized for sensitivity but have traditionally been limited by throughput and target capacity. In 2024, Remes et al. introduced a hybrid quadrupole−radial ejection linear ion trap (Stellar MS), which integrates a quadrupole mass filter, a collision cell, and a linear ion trap with intelligent data acquisition.[4] This platform supports multiplexed targeting of 5,000−8,000 peptides per hour, with acquisition rates of 70−100 Hz and real-time chromatogram alignment, markedly improving efficiency and reducing missing data compared with conventional targeted assays, including selected reaction monitoring (SRM) and parallel reaction monitoring (PRM) assays.

Ion mobility spectrometry (IMS) has also emerged as transformative for proteomics. Daniel DeBord (MOBILion Systems) presented the MOBIE platform, which uses structures for lossless ion manipulation (SLIM) to achieve high-resolution gas−phase separations. Compared with conventional LC−MS, SLIM offers greater reproducibility, faster acquisition, and enhanced structural resolution, directly addressing the bottlenecks of chromatographic separations. These developments echo the vision outlined by Jiang et al.,[5] who argue that IMS may ultimately replace LC approaches for high-throughput proteomics, offering unmatched speed and reproducibility for large-scale and clinical studies.

Oliver Raether (Bruker Daltonics) provided an overview of trapped ion mobility spectrometry (TIMS), which trap ions in a flowing gas using an electric field gradient and releases them selectively. A compact 5 cm TIMS device achieves the resolution of a 2 m drift tube without the high voltages or ion losses of traditional systems. When coupled with TOF analyzers, TIMS significantly enhances peak capacity and throughput, reduces chemical noise, and enables multiplexed analysis.[6] The TIMS−Parallel Accumulation Serial Fragmentation (PASEF) method, commercialized through Bruker's timsTOF instruments, has proven to be a powerful tool for high-throughput proteomics, enabling deep coverage in plasma and urine studies, single-cell analyses,[7] immunopeptidomics,[8] biopsy-scale proteomics,[9] and diverse workflows, including label-free quantification, SILAC,[10] DIA,[11] and PRM.[12]

ANTIBODY-BASED PROTEIN ARRAYS

In addition to mass spectrometry, Dr. Rosa Isela Gallagher (George Mason University) presented reverse-phase protein arrays (RPPAs), which enable precise quantification of proteins and PTMs across thousands of samples with minimal

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input. RPPA is particularly well suited to rare clinical materials, such as laser-captured microdissected biopsies.[13] Gallagher and colleagues recently profiled over 700 tumors using RPPA, revealing phosphoproteomic signatures that are predictive of therapeutic response.[14] These advances highlight the translational value of antibody-based proteomics in personalized medicine.

AUTOMATION AND CHEMICAL PROTEOMICS

Dr. Ruijun Tian (Shanghai Institute of Organic Chemistry) presented automated workflows for sample preparation, accelerating chemical proteomics and plasma biomarker studies. Automation improves reproducibility and scalability, paving the way for population-level proteomics, which is increasingly vital for biomarker validation and epidemiological applications.[15]

CONCLUSIONS AND OUTLOOK

The webinar series underscored how converging technologies, including high-resolution MS, ion mobility separations, protein arrays, and automation of sample preparation, are expanding the reach of proteomics toward clinical translation. Several key themes have emerged for the field's upward trajectory.

Clinical translation and validation will require rigorous standardization, reproducibility, and regulatory frameworks before advanced technologies can be deployed in diagnostics. Population-scale applications, as highlighted in many studies,[16−18] emphasize the need for harmonized workflows to translate discovery into clinical assays. Single-cell, spatial, and multimodal proteomics are rapidly advancing to resolve tissue heterogeneity and PTM landscapes, aligning with calls for "4D proteomics".[19] Automation and high-throughput pipelines will be essential for handling large cohorts. Furthermore, the integration with informatics and software platforms that are designed to manage, track samples, data, and laboratory workflows will higher data quality. Moreover, computational advances, particularly AI-powered approaches like deep learning and neural network for DIA data, PTM prediction, and multiomics integration, are expected to shift hypothesis-driven process fueling advancements in precision medicine and therapeutic development.[20,21]

Ultimately, proteome characterization is moving from a discovery-driven discipline into a core pillar of translational research and of precision medicine. This shift will depend not only on instrumental and methodological innovation but also on community-wide efforts to establish robust standards, ethical frameworks, and training opportunities. The HUPO ETC webinar series plays a vital role in this transformation by fostering knowledge exchange, showcasing best practices, and equipping the next generation of researchers. By continuing to democratize access to advanced tools and expertise, the proteomics community is positioning itself to have a tangible impact on diagnostics, therapeutics, and mechanistic insights into human disease.

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Notes

Views expressed in this editorial are those of the authors and not necessarily the views of the ACS.

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